

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:06:22 ; Search time 7.91209 Seconds
(without alignments)
141.522 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VFPSVAKSVKSLVIG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	678	1	US-08-282-141-2
2	72	100.0	678	1	US-08-435-434-2
3	72	100.0	678	1	US-08-435-436-2
4	72	100.0	678	2	US-08-438-863-2
5	72	100.0	678	2	US-08-438-864-2
6	72	100.0	678	3	US-08-438-862-2
7	72	100.0	678	3	US-08-438-862-2
8	72	100.0	678	3	US-08-402-253-2
9	72	100.0	678	3	US-08-443-866B-2
10	69	95.8	673	1	US-08-282-141-3
11	69	95.8	673	1	US-08-435-434-1
12	69	95.8	673	1	US-08-435-436-1
13	69	95.8	673	2	US-08-438-863-1
14	69	95.8	673	2	US-08-438-864-1
15	69	95.8	673	3	US-08-438-862-1
16	69	95.8	673	3	US-08-402-253-1
17	69	95.8	673	3	US-08-443-866B-1
18	69	95.8	673	3	US-09-107-532A-4410
19	44	61.1	77	4	US-09-721-870-24
20	44	61.1	374	4	US-09-270-767-60047
21	42	58.3	186	4	US-08-843-530B-36
22	42	58.3	1220	2	US-09-636-728-32
23	42	58.3	1220	4	US-09-248-796A-15046
24	41	56.9	292	4	US-08-416-603-4
25	41	56.9	3457	2	US-08-416-603-4
26	39	54.2	99	4	US-09-248-796A-18222
27	39	54.2	369	4	US-09-519-232-74

28	37	51.4	169	4	US-09-270-767-60047	Sequence 60047, A
29	37	51.4	224	4	US-09-270-767-44600	Sequence 44600, A
30	37	51.4	266	4	US-09-489-039A-8199	Sequence 8199, A
31	37	51.4	316	4	US-09-107-532A-5019	Sequence 5019, A
32	37	51.4	334	1	US-08-118-270-22	Sequence 22, Appl
33	37	51.4	334	5	PCT-US93-08528-22	Sequence 22, Appl
34	37	51.4	729	4	US-09-248-796A-17702	Sequence 17702, A
35	36.5	50.7	974	4	US-09-949-016-11563	Sequence 11563, A
36	36	50.0	12	3	US-09-185-501B-6	Sequence 6, Appl
37	36	50.0	74	4	US-09-489-039A-8829	Sequence 8829, A
38	36	50.0	207	3	US-09-185-501B-14	Sequence 14, Appl
39	36	50.0	297	3	US-09-632-947B-4	Sequence 4, Appl
40	36	50.0	551	3	US-09-503-391-2	Sequence 2, Appl
41	36	50.0	551	3	US-09-503-391-2	Sequence 2, Appl
42	36	50.0	15281	2	US-08-471-119A-2	Sequence 4, Appl
43	35	48.6	148	4	US-09-902-540-13147	Sequence 13147, A
44	35	48.6	279	4	US-09-252-991A-32921	Sequence 32921, A
45	35	48.6	303	4	US-09-328-352-4879	Sequence 4879, A
46	35	48.6	332	4	US-09-489-039A-7261	Sequence 7261, A
47	35	48.6	379	1	US-08-121-714-4	Sequence 4, Appl
48	35	48.6	379	1	US-08-477-108A-4	Sequence 4, Appl
49	35	48.6	379	2	US-08-477-112-4	Sequence 4, Appl
50	35	48.6	379	5	PCT-US93-08322-4	Sequence 4, Appl
51	35	48.6	386	4	US-09-328-352-7556	Sequence 7556, A
52	35	48.6	391	5	PCT-US91-08177-3	Sequence 3, Appl
53	35	48.6	396	4	US-09-567-458A-5	Sequence 5, Appl
54	35	48.6	413	4	US-09-543-681A-6252	Sequence 6252, A
55	35	48.6	445	4	US-09-252-991A-24335	Sequence 24335, A
56	35	48.6	452	4	US-09-530-836-6	Sequence 6, Appl
57	35	48.6	452	4	US-09-530-838-2	Sequence 2, Appl
58	35	48.6	460	4	US-09-252-991A-19007	Sequence 19007, A
59	35	48.6	465	4	US-09-328-352-6141	Sequence 6141, A
60	35	48.6	469	4	US-09-538-092-416	Sequence 416, App
61	35	48.6	606	4	US-09-134-000C-4093	Sequence 4093, A
62	35	48.6	922	4	US-09-248-796A-18806	Sequence 18806, A
63	34.5	47.9	335	3	US-09-247-155-176	Sequence 176, App
64	34.5	47.9	346	4	US-09-540-236-2411	Sequence 2411, A
65	34.5	47.9	348	3	US-09-286-803-2	Sequence 2, Appl
66	34.5	47.9	350	4	US-09-800-729-91	Sequence 91, Appl
67	34.5	47.9	350	4	US-09-800-729-127	Sequence 127, App
68	34	47.2	72	4	US-09-134-000C-6242	Sequence 6242, A
69	34	47.2	72	4	US-09-248-796A-27413	Sequence 27413, A
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76	34	47.2	267	3	US-09-290-602-4	Sequence 4, Appl
77	34	47.2	291	4	US-09-248-796A-20693	Sequence 20693, A
78	34	47.2	300	4	US-09-248-796A-14150	Sequence 14150, A
79	34	47.2	324	4	US-09-543-681A-8220	Sequence 8220, A
80	34	47.2	325	4	US-09-270-767-44984	Sequence 44984, A
81	34	47.2	330	1	US-08-118-270-19	Sequence 19, Appl
82	34	47.2	330	5	PCT-US93-08528-19	Sequence 19, Appl
83	34	47.2	335	4	US-08-961-083-110	Sequence 110, App
84	34	47.2	335	4	US-09-536-784-110	Sequence 110, App
85	34	47.2	358	4	US-09-270-767-44738	Sequence 44738, A
86	34	47.2	371	4	US-09-583-110-3815	Sequence 3815, A
87	34	47.2	378	4	US-09-107-433-4822	Sequence 4822, A
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89	34	47.2	415	4	US-09-540-236-2600	Sequence 2600, A
90	34	47.2	415	4	US-09-902-540-12194	Sequence 12194, A
91	34	47.2	416	4	US-09-543-681A-5020	Sequence 5020, A
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93	34	47.2	427	4	US-09-489-039A-12022	Sequence 12022, A
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98	34	47.2	450	4	US-09-583-110-2858	Sequence 2858, A
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101	34	47.2	453	4	US-09-270-767-42936	Sequence 42936, A	174	33	45.8	258	4	US-09-315-574-5	Sequence 5, Appli
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103	34	47.2	487	4	US-09-107-433-3203	Sequence 3203, Ap	176	33	45.8	262	4	US-09-956-086-4	Sequence 4, Appli
104	34	47.2	496	4	US-10-146-704-3	Sequence 3, Appli	177	33	45.8	262	4	US-09-956-087-4	Sequence 4, Appli
105	34	47.2	536	4	US-09-902-540-14532	Sequence 14532, A	178	33	45.8	282	3	US-09-420-592A-7	Sequence 7, Appli
106	34	47.2	547	4	US-09-583-110-3718	Sequence 3718, Ap	179	33	45.8	282	4	US-09-985-442-7	Sequence 7, Appli
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108	34	47.2	578	1	US-08-458-120-2	Sequence 2, Appli	181	33	45.8	293	4	US-09-248-796A-17601	Sequence 17601, A
109	34	47.2	578	2	US-08-867-970-2	Sequence 2, Appli	182	33	45.8	297	2	US-09-027-013-3	Sequence 3, Appli
110	34	47.2	578	3	US-09-326-217-2	Sequence 2, Appli	183	33	45.8	297	3	US-09-244-213-3	Sequence 3, Appli
111	34	47.2	578	3	US-09-732-020-2	Sequence 2, Appli	184	33	45.8	300	3	US-09-134-001C-4762	Sequence 4762, Ap
112	34	47.2	753	4	US-09-248-796A-19291	Sequence 19291, A	185	33	45.8	310	4	US-09-107-532A-4185	Sequence 4185, Ap
113	34	47.2	764	1	US-08-424-567-2	Sequence 2, Appli	186	33	45.8	321	3	US-09-171-461-22	Sequence 22, Appli
114	34	47.2	764	2	US-08-711-928-2	Sequence 2, Appli	187	33	45.8	321	4	US-09-970-711-22	Sequence 22, Appli
115	34	47.2	764	3	US-09-184-937-2	Sequence 2, Appli	188	33	45.8	332	4	US-09-252-991A-29420	Sequence 29420, A
116	34	47.2	790	4	US-09-949-016-11220	Sequence 11220, A	189	33	45.8	338	4	US-09-248-796A-18170	Sequence 18170, A
117	34	47.2	792	4	US-09-995-587A-11	Sequence 11, Appli	190	33	45.8	341	4	US-09-580-929-3	Sequence 3, Appli
118	34	47.2	989	4	US-09-302-540-15948	Sequence 15948, A	191	33	45.8	346	4	US-09-328-352-5625	Sequence 5625, Ap
119	34	47.2	2802	3	US-09-542-331-1	Sequence 1, Appli	192	33	45.8	351	2	US-08-933-750C-19	Sequence 19, Appli
120	34	47.2	2802	3	US-09-510-791-1	Sequence 1, Appli	193	33	45.8	351	3	US-09-234-613-19	Sequence 19, Appli
121	33.5	46.5	322	4	US-09-489-039A-14170	Sequence 14170, A	194	33	45.8	352	4	US-09-580-929-2	Sequence 2, Appli
122	33.5	46.5	343	2	US-08-788-539A-2	Sequence 2, Appli	195	33	45.8	354	4	US-09-949-016-7936	Sequence 7936, Ap
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124	124	33	45.8	27	US-08-218-369-4	Sequence 4, Appli	197	33	45.8	357	4	US-09-710-279-410	Sequence 410, App
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126	33	45.8	27	5	PCT-US95-03742-4	Sequence 4, Appli	199	33	45.8	362	3	US-09-875-223-1	Sequence 1, Appli
127	33	45.8	57	4	US-09-621-976-5488	Sequence 5488, Ap	200	33	45.8	362	4	US-09-875-114-1	Sequence 1, Appli
128	33	45.8	66	4	US-09-302-540-14950	Sequence 14950, A	201	33	45.8	366	3	US-09-134-001C-3198	Sequence 3198, Ap
129	33	45.8	97	4	US-09-270-767-44415	Sequence 44415, A	202	33	45.8	366	3	US-07-864-004B-2	Sequence 2, Appli
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131	33	45.8	101	3	US-09-134-001C-4755	Sequence 4755, Ap	204	33	45.8	367	5	PCT-US93-03275-2	Sequence 2, Appli
132	33	45.8	101	3	US-09-134-001C-5624	Sequence 5624, Ap	205	33	45.8	367	5	PCT-US93-03275-2	Sequence 2, Appli
133	33	45.8	101	4	US-09-134-000C-5291	Sequence 5291, Ap	206	33	45.8	368	1	US-08-212-133A-6	Sequence 6, Appli
134	33	45.8	111	4	US-09-513-999C-7798	Sequence 7798, Ap	207	33	45.8	368	1	US-08-474-503-4	Sequence 4, Appli
135	33	45.8	125	2	US-08-665-202-44	Sequence 44, Appli	208	33	45.8	368	2	US-08-670-707A-4	Sequence 4, Appli
136	33	45.8	125	2	US-08-665-202-45	Sequence 45, Appli	209	33	45.8	368	3	US-09-037-601-4	Sequence 4, Appli
137	33	45.8	125	2	US-08-665-202-47	Sequence 47, Appli	210	33	45.8	368	3	US-09-315-179-4	Sequence 4, Appli
138	33	45.8	125	2	US-08-665-202-48	Sequence 48, Appli	211	33	45.8	368	4	US-09-523-656-4	Sequence 4, Appli
139	33	45.8	125	2	US-08-665-202-49	Sequence 49, Appli	212	33	45.8	368	5	PCT-US94-13200-4	Sequence 4, Appli
140	33	45.8	125	2	US-08-665-202-50	Sequence 50, Appli	213	33	45.8	379	1	US-07-723-002C-4	Sequence 4, Appli
141	33	45.8	125	2	US-08-665-202-51	Sequence 51, Appli	214	33	45.8	379	2	US-08-257-963B-3	Sequence 3, Appli
142	33	45.8	125	2	US-08-665-202-52	Sequence 52, Appli	215	33	45.8	379	3	US-08-367-841A-3	Sequence 3, Appli
143	33	45.8	125	2	US-08-665-202-55	Sequence 55, Appli	216	33	45.8	379	5	PCT-US95-07201-3	Sequence 3, Appli
144	33	45.8	125	2	US-08-665-202-57	Sequence 57, Appli	217	33	45.8	389	4	US-09-248-796A-17443	Sequence 17443, A
145	33	45.8	125	2	US-08-665-202-58	Sequence 58, Appli	218	33	45.8	409	4	US-09-540-236-2952	Sequence 2952, Ap
146	33	45.8	125	2	US-08-665-202-59	Sequence 59, Appli	219	33	45.8	415	4	US-09-134-000C-6391	Sequence 6391, Ap
147	33	45.8	125	4	US-09-315-574-44	Sequence 44, Appli	220	33	45.8	418	2	US-08-257-963B-2	Sequence 2, Appli
148	33	45.8	125	4	US-09-315-574-45	Sequence 45, Appli	221	33	45.8	418	4	US-08-520-373D-2	Sequence 2, Appli
149	33	45.8	125	4	US-09-315-574-47	Sequence 47, Appli	222	33	45.8	418	4	US-09-603-478-1	Sequence 1, Appli
150	33	45.8	125	4	US-09-315-574-48	Sequence 48, Appli	223	33	45.8	418	5	PCT-US95-07201-2	Sequence 2, Appli
151	33	45.8	125	4	US-09-315-574-49	Sequence 49, Appli	224	33	45.8	435	4	US-09-489-039A-10088	Sequence 10088, A
152	33	45.8	125	4	US-09-315-574-50	Sequence 50, Appli	225	33	45.8	435	4	US-09-543-681A-6358	Sequence 6358, Ap
153	33	45.8	125	4	US-09-315-574-51	Sequence 51, Appli	226	33	45.8	437	4	US-09-328-352-7853	Sequence 7853, Ap
154	33	45.8	125	4	US-09-315-574-52	Sequence 52, Appli	227	33	45.8	519	4	US-08-121-202-4	Sequence 4, Appli
155	33	45.8	125	4	US-09-315-574-55	Sequence 55, Appli	228	33	45.8	541	1	US-08-121-202-4	Sequence 4, Appli
156	33	45.8	125	4	US-09-315-574-57	Sequence 57, Appli	229	33	45.8	645	4	US-09-270-767-45647	Sequence 45647, A
157	33	45.8	125	4	US-09-315-574-58	Sequence 58, Appli	230	33	45.8	661	1	US-08-514-014-4	Sequence 4, Appli
158	33	45.8	125	4	US-09-315-574-59	Sequence 59, Appli	231	33	45.8	661	2	US-08-833-823-4	Sequence 4, Appli
159	33	45.8	129	2	US-08-665-202-32	Sequence 32, Appli	232	33	45.8	719	4	US-09-708-426-4	Sequence 32, Appli
160	33	45.8	129	4	US-09-315-574-32	Sequence 32, Appli	233	33	45.8	751	2	US-08-843-530B-32	Sequence 29, Appli
161	33	45.8	132	4	US-09-661-322A-16	Sequence 16, Appli	234	33	45.8	751	4	US-09-636-728-29	Sequence 110, App
162	33	45.8	133	4	US-09-900-920-58	Sequence 58, Appli	235	33	45.8	787	1	US-08-453-695A-110	Sequence 110, App
163	33	45.8	148	4	US-09-270-767-37439	Sequence 37439, A	236	33	45.8	787	2	US-08-268-161A-110	Sequence 110, App
164	33	45.8	148	4	US-09-270-767-52656	Sequence 52656, A	237	33	45.8	787	2	US-08-453-702A-110	Sequence 110, App
165	33	45.8	153	2	US-08-476-254-7	Sequence 7, Appli	238	33	45.8	787	3	US-09-099-639-110	Sequence 110, App
166	33	45.8	153	6	5474933-4	Patent No. 5474933	239	33	45.8	787	5	PCT-US95-08071-110	Sequence 110, App
167	33	45.8	153	6	5474933-4	Patent No. 5474933	240	33	45.8	907	4	US-09-198-452A-306	Sequence 306, App
168	33	45.8	194	4	US-09-902-540-15449	Sequence 15449, A	241	33	45.8	928	4	US-09-438-185A-295	Sequence 295, App
169	33	45.8	196	4	US-09-710-279-3070	Sequence 3070, Ap	242	33	45.8	931	4	US-09-949-016-8988	Sequence 8988, Ap
170	33	45.8	227	4	US-09-270-767-44321	Sequence 44321, A	243	33	45.8	954	4	US-09-351-150A-17	Sequence 17, Appli
171	33	45.8	230	4	US-09-543-681A-4173	Sequence 4173, Ap	244	33	45.8	974	4	US-10-101-464A-321	Sequence 921, App
172	33	45.8	243	4	US-09-508-710-18	Sequence 18, Appli	245	33	45.8	978	4	US-09-549-016-9882	Sequence 9882, Ap
173	33	45.8	258	2	US-08-665-202-5	Sequence 5, Appli	246	33	45.8	1125	4	US-09-900-920-60	Sequence 60, Appli

247	33	45.8	1137	4	US-09-252-991A-24829	Sequence 24829, A	320	44.4	372	2	US-08-984-246-3	Sequence 3, Appli
248	33	45.8	1443	2	US-08-670-707A-39	Sequence 39, Appl	321	44.4	372	2	US-09-149-674-3	Sequence 3, Appli
249	33	45.8	1443	3	US-09-037-601-39	Sequence 39, Appl	322	44.4	372	2	US-09-134-000C-6593	Sequence 6593, Ap
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251	33	45.8	1467	4	US-09-523-656-38	Sequence 38, Appl	324	44.4	382	1	US-08-487-823B-3	Sequence 3, Appli
252	33	45.8	2115	3	US-09-324-867-5	Sequence 5, Appli	325	44.4	382	2	US-08-997-040-3	Sequence 3, Appli
253	33	45.8	2133	2	US-08-670-707A-37	Sequence 37, Appl	326	44.4	382	2	US-09-203-237-3	Sequence 3, Appli
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255	33	45.8	2133	3	US-09-315-179-37	Sequence 37, Appl	328	44.4	392	4	US-09-583-110-3827	Sequence 3827, Ap
256	33	45.8	2133	3	US-09-523-656-30	Sequence 30, Appl	329	44.4	394	4	US-07-603-133B-11	Sequence 11, Appl
257	32.5	45.1	314	3	US-08-927-219-6	Sequence 6, Appli	330	44.4	395	3	US-09-088-216-4	Sequence 4, Appli
258	32.5	45.1	314	4	US-09-710-099-6	Sequence 4, Appli	331	44.4	395	3	US-09-088-216-2	Sequence 4, Appli
259	32.5	45.1	314	4	US-09-710-099-12	Sequence 12, Appl	332	44.4	400	4	US-09-889-746-2	Sequence 2, Appli
260	32.5	45.1	314	4	US-10-200-910-4	Sequence 4, Appli	333	44.4	405	1	US-08-121-714-7	Sequence 7, Appli
261	32.5	45.1	314	4	US-10-200-910-12	Sequence 12, Appl	334	44.4	405	1	US-08-477-108A-7	Sequence 7, Appli
262	32.5	45.1	351	4	US-09-710-099-2	Sequence 2, Appli	335	44.4	405	1	US-08-477-112-7	Sequence 7, Appli
263	32.5	45.1	351	4	US-09-710-099-10	Sequence 10, Appl	336	44.4	405	5	PCT-US93-08322-7	Sequence 7, Appli
264	32.5	45.1	351	4	US-10-200-910-2	Sequence 2, Appli	337	44.4	415	1	US-07-911-531-19	Sequence 19, Appl
265	32.5	45.1	351	4	US-10-200-910-10	Sequence 10, Appl	338	44.4	415	1	US-07-693-636A-19	Sequence 19, Appl
266	32.5	45.1	399	4	US-09-710-099-8	Sequence 8, Appli	339	44.4	415	1	US-07-768-286B-2	Sequence 2, Appli
267	32.5	45.1	399	4	US-10-200-910-8	Sequence 8, Appli	340	44.4	415	3	US-09-026-408-4	Sequence 4, Appli
268	32.5	45.1	415	3	US-08-927-219-8	Sequence 8, Appli	341	44.4	415	3	US-09-902-684-4	Sequence 4, Appli
269	32.5	45.1	436	4	US-09-710-099-6	Sequence 6, Appli	342	44.4	417	4	US-09-252-991A-25870	Sequence 25870, A
270	32.5	45.1	436	4	US-10-200-910-6	Sequence 6, Appli	343	44.4	434	1	US-07-679-052A-15	Sequence 15, Appl
271	32.5	45.1	630	3	US-08-927-219-2	Sequence 2, Appli	344	44.4	436	3	US-09-150-213-4	Sequence 4, Appli
272	32.5	45.1	630	3	US-08-927-219-4	Sequence 4, Appli	345	44.4	436	4	US-09-328-352-6067	Sequence 6067, Ap
273	32.5	45.1	631	3	US-08-927-219-127	Sequence 127, App	346	44.4	438	1	US-07-679-052A-17	Sequence 17, Appl
274	32.5	45.1	670	2	US-08-473-750-11	Sequence 11, Appl	347	44.4	444	4	US-09-107-532A-4848	Sequence 4848, Ap
275	32.5	45.1	670	2	US-08-477-326-11	Sequence 11, Appl	348	44.4	447	4	US-09-270-767-45673	Sequence 45673, A
276	32.5	45.1	949	4	US-10-164-595-65	Sequence 65, Appl	349	44.4	457	4	US-09-270-767-44881	Sequence 44881, A
277	32.5	45.1	1214	4	US-10-164-595-24	Sequence 24, Appl	350	44.4	462	4	US-09-252-991A-31372	Sequence 31372, A
278	32	44.4	20	4	US-09-157-689-31	Sequence 31, Appl	351	44.4	471	4	US-09-325-256-26	Sequence 26, Appl
279	32	44.4	20	4	US-08-447-398-31	Sequence 31, Appl	352	44.4	471	4	US-09-704-917-20	Sequence 20, Appl
280	32	44.4	20	4	US-09-953-510-31	Sequence 31, Appl	353	44.4	471	4	US-09-151-999-20	Sequence 20, Appl
281	32	44.4	28	4	US-09-270-767-58413	Sequence 58413, A	354	44.4	471	4	US-09-418-212-18	Sequence 18, Appl
282	32	44.4	85	4	US-09-732-210-1119	Sequence 1119, Ap	355	44.4	485	3	US-09-384-212-2	Sequence 2, Appli
283	32	44.4	85	4	US-09-621-376-6425	Sequence 6425, Ap	356	44.4	500	1	US-07-755-573C-8	Sequence 8, Appli
284	32	44.4	86	4	US-09-543-681A-8300	Sequence 8300, Ap	357	44.4	500	4	US-09-519-878-2	Sequence 2, Appli
285	32	44.4	91	4	US-09-513-990C-4169	Sequence 4169, Ap	358	44.4	504	4	US-09-519-878-4	Sequence 4, Appli
286	32	44.4	115	4	US-09-543-681A-7586	Sequence 7586, Ap	359	44.4	520	4	US-09-949-016-10586	Sequence 10586, A
287	32	44.4	133	4	US-09-270-767-34410	Sequence 34410, A	360	44.4	524	4	US-09-248-796A-20256	Sequence 20256, A
288	32	44.4	133	4	US-09-270-767-49627	Sequence 49627, A	361	44.4	540	4	US-09-513-057C-33	Sequence 33, Appl
289	32	44.4	134	4	US-09-270-767-60352	Sequence 60352, A	362	44.4	540	4	US-09-746-801A-33	Sequence 33, Appl
290	32	44.4	140	4	US-09-270-767-38533	Sequence 38533, A	363	44.4	540	4	US-08-311-731A-142	Sequence 142, App
291	32	44.4	140	4	US-09-270-767-53750	Sequence 53750, A	364	44.4	567	3	US-09-347-878-42	Sequence 42, Appl
292	32	44.4	142	4	US-09-248-796A-15418	Sequence 15418, A	365	44.4	591	4	US-09-519-232-66	Sequence 66, Appl
293	32	44.4	146	3	US-09-373-750-3	Sequence 3, Appli	366	44.4	597	4	US-09-252-991A-32073	Sequence 32073, A
294	32	44.4	146	3	US-09-373-750-4	Sequence 4, Appli	367	44.4	615	4	US-09-898-165B-7	Sequence 7, Appli
295	32	44.4	158	4	US-09-270-767-31923	Sequence 31923, A	368	44.4	619	4	US-09-786-240-6	Sequence 6, Appli
296	32	44.4	158	4	US-09-270-767-47140	Sequence 47140, A	369	44.4	628	4	US-09-602-787A-550	Sequence 550, App
297	32	44.4	172	4	US-09-270-767-43079	Sequence 43079, A	370	44.4	628	4	US-09-602-787A-666	Sequence 666, App
298	32	44.4	189	4	US-09-270-767-61188	Sequence 61188, A	371	44.4	641	4	US-09-949-016-7796	Sequence 7796, Ap
299	32	44.4	201	4	US-09-902-540-12974	Sequence 12974, A	372	44.4	649	4	US-09-270-767-61886	Sequence 61886, A
300	32	44.4	202	4	US-09-248-796A-25290	Sequence 25290, A	373	44.4	664	4	US-09-328-352-6193	Sequence 6193, Ap
301	32	44.4	218	4	US-09-107-433-3813	Sequence 3813, Ap	374	44.4	682	1	US-07-998-003A-107	Sequence 107, App
302	32	44.4	233	4	US-09-270-767-45122	Sequence 45122, A	375	44.4	682	1	US-08-453-274B-107	Sequence 107, App
303	32	44.4	245	4	US-09-248-796A-17097	Sequence 17097, A	376	44.4	682	1	US-08-453-695A-107	Sequence 107, App
304	32	44.4	256	4	US-09-270-767-42933	Sequence 42933, A	377	44.4	682	1	US-08-268-161A-107	Sequence 107, App
305	32	44.4	257	4	US-09-543-681A-4193	Sequence 4193, Ap	378	44.4	682	2	US-08-453-702A-107	Sequence 107, App
306	32	44.4	259	2	US-08-808-550-39	Sequence 39, Appl	379	44.4	682	3	US-09-099-639-107	Sequence 107, App
307	32	44.4	265	4	US-09-134-000C-5847	Sequence 5847, Ap	380	44.4	682	5	PCT-US93-12588-107	Sequence 107, App
308	32	44.4	294	4	US-09-248-796A-20697	Sequence 20697, A	381	44.4	682	5	PCT-US95-08071-107	Sequence 107, App
309	32	44.4	296	4	US-09-540-236-2650	Sequence 2650, Ap	382	44.4	725	4	US-09-540-236-2026	Sequence 2026, Ap
310	32	44.4	298	4	US-09-252-991A-20712	Sequence 20712, A	383	44.4	789	1	US-08-431-080-20	Sequence 20, Appl
311	32	44.4	308	4	US-09-328-352-8155	Sequence 8155, Ap	384	44.4	789	2	US-08-938-534-20	Sequence 20, Appl
312	32	44.4	309	1	US-08-729-202-1	Sequence 1, Appli	385	44.4	789	3	US-09-345-294-20	Sequence 20, Appl
313	32	44.4	309	1	US-08-896-371-1	Sequence 1, Appli	386	44.4	828	4	US-09-540-236-3107	Sequence 3107, Ap
314	32	44.4	327	4	US-09-134-000C-4685	Sequence 4685, Ap	387	44.4	836	1	US-07-998-003A-105	Sequence 105, App
315	32	44.4	354	1	US-08-753-233-2	Sequence 2, Appli	388	44.4	836	1	US-08-453-274B-105	Sequence 105, App
316	32	44.4	354	1	US-08-984-246-2	Sequence 2, Appli	389	44.4	836	1	US-08-453-695A-105	Sequence 105, App
317	32	44.4	354	2	US-09-149-674-2	Sequence 2, Appli	390	44.4	836	1	US-08-268-161A-105	Sequence 105, App
318	32	44.4	364	4	US-09-270-767-46731	Sequence 46731, A	391	44.4	836	2	US-08-453-702A-105	Sequence 105, App
319	32	44.4	372	1	US-08-753-233-3	Sequence 3, Appli	392	44.4	836	3	US-09-099-639-105	Sequence 105, App

393	32	44.4	836	5	PCT-US93-12588-105	Sequence 105, App	466	31	43.1	265	4	US-09-543-681A-5083	Sequence 5083, Ap
394	32	44.4	836	5	PCT-US95-08071-105	Sequence 105, App	467	31	43.1	266	4	US-09-489-039A-7484	Sequence 7484, Ap
395	32	44.4	904	1	US-07-988-003A-97	Sequence 97, Appl	468	31	43.1	268	4	US-09-248-796A-19955	Sequence 19955, A
396	32	44.4	904	1	US-08-453-274B-97	Sequence 97, Appl	469	31	43.1	272	4	US-09-943-016-6331	Sequence 6331, Ap
397	32	44.4	904	1	US-08-453-695A-97	Sequence 97, Appl	470	31	43.1	281	4	US-09-543-681A-6233	Sequence 6233, Ap
398	32	44.4	904	1	US-08-268-163A-97	Sequence 97, Appl	471	31	43.1	281	4	US-09-854-864-10	Sequence 10, Appl
399	32	44.4	904	2	US-08-453-702A-97	Sequence 97, Appl	472	31	43.1	309	4	US-09-252-991A-25953	Sequence 25953, A
400	32	44.4	904	2	US-09-099-639-97	Sequence 97, Appl	473	31	43.1	317	4	US-09-540-236-3830	Sequence 3830, Ap
401	32	44.4	904	5	PCT-US93-12588-97	Sequence 97, Appl	474	31	43.1	320	4	US-09-489-039A-13989	Sequence 13989, A
402	32	44.4	904	5	PCT-US95-08071-97	Sequence 97, Appl	475	31	43.1	330	4	US-09-489-039A-12859	Sequence 12859, A
403	32	44.4	910	3	US-09-228-986-72	Sequence 72, Appl	476	31	43.1	332	4	US-09-943-016-10159	Sequence 10159, A
404	32	44.4	910	4	US-10-101-464A-72	Sequence 72, Appl	477	31	43.1	338	4	US-09-252-991A-28498	Sequence 28498, A
405	32	44.4	932	4	US-09-949-016-8989	Sequence 8989, Ap	478	31	43.1	342	4	US-09-107-532A-4845	Sequence 4845, Ap
406	32	44.4	934	4	US-09-949-016-6242	Sequence 6242, Ap	479	31	43.1	361	4	US-09-902-540-12257	Sequence 12257, A
407	32	44.4	941	4	US-09-949-016-10983	Sequence 10983, A	480	31	43.1	362	2	US-08-290-731C-15	Sequence 15, Appl
408	32	44.4	941	4	US-09-949-016-10984	Sequence 10984, A	481	31	43.1	365	4	US-09-248-796A-20907	Sequence 20907, A
409	32	44.4	941	4	US-09-949-016-10985	Sequence 10985, A	482	31	43.1	371	3	US-09-382-155-22	Sequence 22, Appl
410	32	44.4	982	4	US-09-023-905A-7	Sequence 7, Appl1	483	31	43.1	371	3	US-09-074-044A-22	Sequence 22, Appl
411	32	44.4	1005	4	US-09-134-000C-6322	Sequence 6322, Ap	484	31	43.1	376	4	US-09-564-954-2	Sequence 2, Appl1
412	32	44.4	1022	4	US-09-949-016-8864	Sequence 8864, Ap	485	31	43.1	379	4	US-09-492-709A-355	Sequence 355, App
413	32	44.4	1222	4	US-09-949-016-9041	Sequence 9041, Ap	486	31	43.1	385	4	US-09-380-287A-2	Sequence 2, Appl1
414	32	44.4	1505	4	US-09-538-092-1102	Sequence 1102, Ap	487	31	43.1	397	4	US-09-459-133-2	Sequence 2, Appl1
415	32	44.4	1693	4	US-09-560-385A-4	Sequence 4, Appl1	488	31	43.1	405	4	US-09-603-208A-262	Sequence 262, App
416	32	44.4	1693	4	US-09-560-385A-8	Sequence 8, Appl1	489	31	43.1	412	3	US-09-134-001C-4885	Sequence 4885, Ap
417	32	44.4	1713	3	US-08-600-982-24	Sequence 24, Appl	490	31	43.1	424	2	US-08-951-148-9	Sequence 9, Appl1
418	32	44.4	1713	4	US-09-560-385A-6	Sequence 6, Appl1	491	31	43.1	424	2	US-09-165-234-9	Sequence 9, Appl1
419	32	44.4	1713	4	US-09-538-092-1359	Sequence 1359, Ap	492	31	43.1	424	2	US-09-274-570-9	Sequence 9, Appl1
420	32	44.4	1713	5	PCT-US94-10261A-24	Sequence 24, Appl	493	31	43.1	424	4	US-09-538-092-1317	Sequence 1317, Ap
421	32	44.4	1724	4	US-09-560-385A-2	Sequence 2, Appl1	494	31	43.1	433	4	US-09-380-287A-6	Sequence 6, Appl1
422	32	44.4	1824	2	US-08-680-327-3	Sequence 3, Appl1	495	31	43.1	434	4	US-09-248-796A-14315	Sequence 14315, A
423	32	44.4	2763	3	US-08-496-944-2	Sequence 2, Appl1	496	31	43.1	440	4	US-09-380-287A-4	Sequence 4, Appl1
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425	31.5	43.8	432	4	US-09-248-796A-16603	Sequence 16603, A	498	31	43.1	457	4	US-09-328-352-7471	Sequence 7471, Ap
426	31.5	43.8	439	4	US-09-502-540-13695	Sequence 13695, A	499	31	43.1	458	4	US-09-489-039A-10215	Sequence 10215, A
427	31.5	43.8	510	4	US-09-121-211-16	Sequence 16, Appl	500	31	43.1	465	4	US-09-270-767-37268	Sequence 37268, A
428	31	43.1	26	3	US-09-066-046-19	Sequence 6, Appl1	501	31	43.1	465	4	US-09-270-767-52485	Sequence 52485, A
429	31	43.1	36	1	US-08-139-862-6	Sequence 6, Appl1	502	31	43.1	484	4	US-09-902-540-11231	Sequence 11231, A
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431	31	43.1	47	4	US-09-270-767-50482	Sequence 50482, A	504	31	43.1	510	4	US-09-252-991A-25076	Sequence 25076, A
432	31	43.1	72	4	US-09-270-767-41152	Sequence 41152, A	505	31	43.1	518	4	US-09-198-452A-172	Sequence 172, App
433	31	43.1	72	4	US-09-270-767-56368	Sequence 56368, A	506	31	43.1	518	4	US-09-438-185A-153	Sequence 153, App
434	31	43.1	88	4	US-09-726-219A-172	Sequence 172, App	507	31	43.1	529	4	US-09-902-540-15802	Sequence 15802, A
435	31	43.1	95	4	US-09-153-447-31	Sequence 31, Appl	508	31	43.1	555	4	US-09-134-000C-3906	Sequence 3906, Ap
436	31	43.1	106	4	US-09-270-767-58711	Sequence 58711, A	509	31	43.1	556	4	US-09-134-000C-5850	Sequence 5850, Ap
437	31	43.1	109	4	US-09-248-796A-26362	Sequence 26362, A	510	31	43.1	562	4	US-09-252-991A-20178	Sequence 20178, A
438	31	43.1	110	4	US-09-248-796A-22555	Sequence 22555, A	511	31	43.1	568	4	US-09-248-796A-20839	Sequence 20839, A
439	31	43.1	124	3	US-08-905-223-343	Sequence 223343, App	512	31	43.1	590	4	US-09-248-796A-20379	Sequence 20379, A
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441	31	43.1	125	4	US-09-543-681A-7941	Sequence 7941, Ap	514	31	43.1	616	1	US-08-453-695A-115	Sequence 115, App
442	31	43.1	127	4	US-09-252-991A-28758	Sequence 28758, A	515	31	43.1	616	2	US-08-268-161A-115	Sequence 115, App
443	31	43.1	141	4	US-09-732-210-789	Sequence 789, App	516	31	43.1	616	2	US-08-453-702A-115	Sequence 115, App
444	31	43.1	142	4	US-09-732-210-786	Sequence 786, App	517	31	43.1	616	3	US-09-099-639-115	Sequence 115, App
445	31	43.1	144	4	US-09-328-352-7108	Sequence 7108, Ap	518	31	43.1	616	5	PCT-US95-08071-115	Sequence 115, App
446	31	43.1	155	4	US-09-134-000C-3920	Sequence 3920, Ap	519	31	43.1	653	4	US-09-438-185A-730	Sequence 730, App
447	31	43.1	157	4	US-09-270-767-37758	Sequence 37758, A	520	31	43.1	660	4	US-09-902-540-10693	Sequence 10693, A
448	31	43.1	157	4	US-09-270-767-52975	Sequence 52975, A	521	31	43.1	668	4	US-09-328-352-6586	Sequence 6586, Ap
449	31	43.1	157	4	US-10-101-464A-788	Sequence 788, App	522	31	43.1	676	4	US-09-252-991A-24713	Sequence 24713, A
450	31	43.1	177	4	US-09-943-681A-8325	Sequence 8325, Ap	523	31	43.1	676	4	US-09-107-532A-6028	Sequence 6028, Ap
451	31	43.1	188	4	US-09-270-767-61853	Sequence 61853, A	524	31	43.1	689	4	US-09-489-039A-7677	Sequence 7677, Ap
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453	31	43.1	195	4	US-09-248-796A-14170	Sequence 14170, A	526	31	43.1	724	1	US-08-121-713D-62	Sequence 62, Appl
454	31	43.1	207	2	US-08-793-229-30	Sequence 30, Appl	527	31	43.1	724	2	US-08-835-268-62	Sequence 62, Appl
455	31	43.1	207	3	US-09-285-957-30	Sequence 30, Appl	528	31	43.1	724	2	US-09-060-692-62	Sequence 62, Appl
456	31	43.1	208	3	US-09-134-001C-4007	Sequence 4007, Ap	529	31	43.1	724	3	US-08-833-391-62	Sequence 62, Appl
457	31	43.1	215	4	US-09-270-767-43363	Sequence 43363, A	530	31	43.1	724	3	US-09-060-610-62	Sequence 62, Appl
458	31	43.1	216	4	US-09-540-236-2124	Sequence 2124, Ap	531	31	43.1	724	5	PCT-US94-10151A-62	Sequence 62, Appl
459	31	43.1	219	4	US-09-270-767-46282	Sequence 46282, A	532	31	43.1	727	3	US-09-134-001C-4067	Sequence 4067, Ap
460	31	43.1	223	4	US-10-112-802-4	Sequence 4, Appl1	533	31	43.1	792	2	US-09-645-835A-4	Sequence 4, Appl1
461	31	43.1	228	4	US-09-710-279-2936	Sequence 2936, Ap	534	31	43.1	798	2	US-08-222-617A-8	Sequence 8, Appl1
462	31	43.1	228	4	US-09-710-279-3196	Sequence 3196, Ap	535	31	43.1	823	4	US-09-252-991A-21027	Sequence 21027, A
463	31	43.1	228	4	US-09-538-092-360	Sequence 360, App	536	31	43.1	857	4	US-09-107-532A-4201	Sequence 4201, Ap
464	31	43.1	233	3	US-09-134-001C-3643	Sequence 3643, Ap	537	31	43.1	884	4	US-09-741-150-4	Sequence 4, Appl1
465	31	43.1	246	4	US-09-248-796A-15053	Sequence 15053, A	538	31	43.1	884	4	US-10-160-187-4	Sequence 4, Appl1

539	31	43.1	932	4	US-09-949-016-8990	Sequence 8990, Ap	612	30	41.7	179	6	5463025-4	Patent No. 5463025
540	31	43.1	1039	4	US-09-252-991A-24417	Sequence 24417, A	613	30	41.7	179	6	5463025-4	Patent No. 5463025
541	31	43.1	1047	4	US-09-543-681A-78616	Sequence 6186, Ap	614	30	41.7	192	4	US-09-543-681A-78616	Sequence 7861, Ap
542	31	43.1	1085	1	US-08-431-080-28	Sequence 28, Appl	615	30	41.7	199	4	US-09-248-796A-16876	Sequence 16876, A
543	31	43.1	1085	2	US-08-938-534-28	Sequence 28, Appl	616	30	41.7	202	4	US-09-583-110-3500	Sequence 3500, Ap
544	31	43.1	1085	3	US-09-345-294-28	Sequence 28, Appl	617	30	41.7	209	4	US-09-270-767-41759	Sequence 41759, A
545	31	43.1	1129	4	US-09-023-905A-2	Sequence 2, Appli	618	30	41.7	217	4	US-09-270-767-48082	Sequence 48082, A
546	31	43.1	1151	4	US-09-023-905A-4	Sequence 4, Appli	619	30	41.7	218	3	US-09-651-656-105	Sequence 105, App
547	31	43.1	1180	4	US-09-543-681A-6436	Sequence 6436, Ap	620	30	41.7	218	3	US-09-650-855-105	Sequence 105, App
548	31	43.1	1259	4	US-09-902-540-16442	Sequence 16442, A	621	30	41.7	220	1	US-07-991-867B-11	Sequence 11, Appl
549	31	43.1	1734	4	US-09-724-126A-19	Sequence 19, Appl	622	30	41.7	220	1	US-08-107-755A-11	Sequence 11, Appl
550	31	43.1	1749	4	US-09-724-126A-2	Sequence 2, Appli	623	30	41.7	220	2	US-08-544-332-11	Sequence 11, Appl
551	31	43.1	1824	3	US-09-228-246-2	Sequence 2, Appli	624	30	41.7	220	4	US-09-370-861A-11	Sequence 11, Appl
552	31	43.1	2175	4	US-09-693-205A-8	Sequence 8, Appli	625	30	41.7	221	4	US-09-252-991A-22003	Sequence 22003, A
553	31	43.1	2595	3	US-09-316-987A-2	Sequence 2, Appli	626	30	41.7	225	4	US-09-248-796A-19486	Sequence 19486, A
554	31	43.1	2595	3	US-09-370-700-2	Sequence 2, Appli	627	30	41.7	225	4	US-09-194-905-8	Sequence 8, Appli
555	31	43.1	2595	3	US-09-603-207-2	Sequence 2, Appli	628	30	41.7	240	4	US-09-270-767-42421	Sequence 42421, A
556	31	43.1	3165	2	US-08-459-146-3	Sequence 3, Appli	629	30	41.7	240	4	US-09-922-683-8	Sequence 8, Appli
557	31	43.1	3165	2	US-08-459-065-3	Sequence 3, Appli	630	30	41.7	240	4	US-09-438-185A-414	Sequence 414, App
558	31	43.1	3594	4	US-09-911-842A-4	Sequence 4, Appli	631	30	41.7	246	4	US-09-248-796A-16241	Sequence 16241, A
559	31	43.1	3829	4	US-09-693-205A-2	Sequence 2, Appli	632	30	41.7	248	4	US-09-107-532A-4367	Sequence 4367, Ap
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562	30.5	42.4	69	4	US-09-732-210-484	Sequence 484, App	635	30	41.7	255	4	US-09-270-767-59674	Sequence 59674, A
563	30.5	42.4	111	4	US-09-732-210-1309	Sequence 1309, Ap	636	30	41.7	259	4	US-09-248-796A-19367	Sequence 18367, A
564	30.5	42.4	139	4	US-09-252-991A-20476	Sequence 20476, A	637	30	41.7	260	4	US-09-328-352-6613	Sequence 6613, Ap
565	30.5	42.4	135	4	US-09-248-796A-17198	Sequence 17198, A	638	30	41.7	262	4	US-09-252-991A-27182	Sequence 27182, A
566	30.5	42.4	327	4	US-09-248-796A-18802	Sequence 18802, A	639	30	41.7	276	4	US-09-134-000C-4646	Sequence 4646, Ap
567	30.5	42.4	330	1	US-08-118-270-21	Sequence 21, Appl	640	30	41.7	284	4	US-09-543-681A-6652	Sequence 6652, Ap
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570	30.5	42.4	544	4	US-09-583-110-3538	Sequence 3538, Ap	643	30	41.7	295	4	US-09-248-796A-19392	Sequence 19392, A
571	30.5	42.4	568	4	US-09-107-433-2849	Sequence 2849, Ap	644	30	41.7	299	4	US-09-393-634-41	Sequence 41, Appl
572	30.5	42.4	606	3	US-08-620-077B-3	Sequence 3, Appli	645	30	41.7	302	4	US-09-248-796A-25270	Sequence 25270, A
573	30.5	42.4	617	4	US-09-198-452A-155	Sequence 155, App	646	30	41.7	304	4	US-09-248-796A-19355	Sequence 19355, A
574	30.5	42.4	617	4	US-09-438-185A-138	Sequence 138, App	647	30	41.7	306	4	US-09-543-681A-6571	Sequence 6571, Ap
575	30.5	42.4	1788	2	US-08-962-284-2	Sequence 2, Appli	648	30	41.7	312	3	US-08-821-872-2	Sequence 2, Appli
576	30.5	42.4	1897	4	US-09-732-024-98	Sequence 98, Appl	649	30	41.7	312	3	US-09-171-517B-11	Sequence 11, Appl
577	30.5	42.4	3665	2	US-08-222-617A-13	Sequence 13, Appl	650	30	41.7	312	4	US-09-769-086-5	Sequence 5, Appli
578	30.5	42.4	3712	2	US-08-222-617A-4	Sequence 4, Appli	651	30	41.7	313	2	US-08-671-320-15	Sequence 15, Appl
579	30.5	42.4	3712	2	US-08-222-617A-25	Sequence 25, Appl	652	30	41.7	313	2	US-08-868-577-15	Sequence 15, Appl
580	30	41.7	36	3	US-08-974-549A-143	Sequence 143, App	653	30	41.7	313	4	US-09-207-914-15	Sequence 15, Appl
581	30	41.7	36	4	US-09-402-181B-143	Sequence 143, App	654	30	41.7	314	3	US-09-171-517B-6	Sequence 6, Appli
582	30	41.7	36	4	US-09-721-456-143	Sequence 143, App	655	30	41.7	314	3	US-09-171-517B-9	Sequence 9, Appli
583	30	41.7	44	4	US-09-270-767-36209	Sequence 36209, A	656	30	41.7	314	3	US-09-171-517B-10	Sequence 10, Appl
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585	30	41.7	61	4	US-09-248-796A-27150	Sequence 27150, A	658	30	41.7	320	4	US-09-543-681A-6146	Sequence 6146, Ap
586	30	41.7	63	4	US-09-248-796A-27500	Sequence 27500, A	659	30	41.7	323	4	US-09-489-039A-8462	Sequence 8462, Ap
587	30	41.7	63	4	US-09-248-796A-28053	Sequence 28053, A	660	30	41.7	333	1	US-07-991-587A-2	Sequence 2, Appli
588	30	41.7	66	3	US-09-134-001C-5121	Sequence 5121, Ap	661	30	41.7	333	1	US-08-309-985-2	Sequence 2, Appli
589	30	41.7	72	4	US-09-328-352-7355	Sequence 7355, Ap	662	30	41.7	338	4	US-09-252-991A-31928	Sequence 31928, A
590	30	41.7	74	4	US-09-270-767-40827	Sequence 40827, A	663	30	41.7	343	4	US-09-887-054-2	Sequence 2, Appli
591	30	41.7	74	4	US-09-270-767-56043	Sequence 56043, A	664	30	41.7	344	3	US-09-389-341-72	Sequence 72, Appl
592	30	41.7	78	4	US-09-134-000C-6444	Sequence 6444, Ap	665	30	41.7	348	4	US-09-602-787A-190	Sequence 190, App
593	30	41.7	101	4	US-09-621-976-4489	Sequence 4489, Ap	666	30	41.7	353	4	US-09-902-540-14304	Sequence 14304, A
594	30	41.7	103	4	US-09-248-796A-19261	Sequence 19261, A	667	30	41.7	354	1	US-07-868-353A-13	Sequence 13, Appl
595	30	41.7	111	3	US-08-899-330-11	Sequence 11, Appl	668	30	41.7	354	3	US-08-407-804-22	Sequence 22, Appl
596	30	41.7	111	4	US-09-756-541-11	Sequence 11, Appl	669	30	41.7	354	3	US-09-124-807-22	Sequence 22, Appl
597	30	41.7	116	4	US-09-902-540-13423	Sequence 13423, A	670	30	41.7	354	4	US-09-583-110-4997	Sequence 4997, Ap
598	30	41.7	118	4	US-09-270-767-48353	Sequence 48353, A	671	30	41.7	357	4	US-09-535-909-8	Sequence 8, Appli
599	30	41.7	120	4	US-09-489-039A-14308	Sequence 14308, A	672	30	41.7	358	4	US-09-270-767-37254	Sequence 37254, A
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601	30	41.7	122	3	US-09-134-001C-3014	Sequence 3014, Ap	674	30	41.7	359	4	US-09-107-433-2619	Sequence 2619, Ap
602	30	41.7	128	4	US-09-949-016-6563	Sequence 6563, Ap	675	30	41.7	360	4	US-09-107-532A-4523	Sequence 4523, A
603	30	41.7	135	4	US-09-513-999C-5817	Sequence 5817, Ap	676	30	41.7	362	4	US-09-252-991A-26917	Sequence 26917, A
604	30	41.7	144	4	US-09-328-352-7792	Sequence 7792, Ap	677	30	41.7	364	4	US-09-755-630B-281	Sequence 281, App
605	30	41.7	149	4	US-09-328-352-6256	Sequence 6256, Ap	678	30	41.7	364	4	US-09-755-274-3	Sequence 3, Appli
606	30	41.7	152	4	US-09-270-767-37006	Sequence 37006, A	679	30	41.7	364	4	US-09-949-016-9994	Sequence 9994, Ap
607	30	41.7	152	4	US-09-270-767-52223	Sequence 52223, A	680	30	41.7	366	4	US-09-755-630B-247	Sequence 247, App
608	30	41.7	164	4	US-09-902-540-15953	Sequence 15953, A	681	30	41.7	366	4	US-09-755-630B-251	Sequence 251, App
609	30	41.7	168	4	US-09-198-452A-431	Sequence 431, App	682	30	41.7	366	4	US-09-755-630B-255	Sequence 255, App
610	30	41.7	176	4	US-09-248-796A-20480	Sequence 20480, A	683	30	41.7	366	4	US-09-755-630B-259	Sequence 259, App
611	30	41.7	179	4	US-09-248-796A-22488	Sequence 22488, A	684	30	41.7	366	4	US-09-755-630B-263	Sequence 263, App

685	30	41.7	366	4	US-09-755-274-21	Sequence 21, Appl	758	30	41.7	461	4	US-09-043-944-6	Sequence 6, Appl
686	30	41.7	366	4	US-09-755-274-23	Sequence 23, Appl	759	30	41.7	461	4	US-09-866-570B-70	Sequence 70, Appl
687	30	41.7	366	4	US-09-755-274-25	Sequence 25, Appl	760	30	41.7	464	6	5463025-1	Patent No. 5463025
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695	30	41.7	368	3	US-09-353-688-3	Sequence 3, Appl	767	30	41.7	487	4	US-09-321-969-8	Sequence 8, Appl
696	30	41.7	371	4	US-09-265-585C-122	Sequence 122, App	768	30	41.7	488	4	US-09-328-352-4363	Sequence 4363, Ap
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699	30	41.7	373	4	US-09-489-039A-7685	Sequence 7685, Ap	771	30	41.7	490	1	US-09-071-296-10	Sequence 10, Appl
700	30	41.7	375	1	US-08-121-714-8	Sequence 8, Appl	772	30	41.7	490	3	US-09-196-268-10	Sequence 10, Appl
701	30	41.7	375	1	US-08-477-108A-8	Sequence 8, Appl	773	30	41.7	490	3	US-09-015-683-10	Sequence 10, Appl
702	30	41.7	375	2	US-08-477-112-8	Sequence 8, Appl	774	30	41.7	490	3	US-09-191-998-10	Sequence 10, Appl
703	30	41.7	375	4	US-09-252-991A-25072	Sequence 25072, A	775	30	41.7	490	3	US-09-438-185A-1032	Sequence 1032, Ap
704	30	41.7	375	4	US-09-540-236-3290	Sequence 3290, Ap	776	30	41.7	490	4	US-09-321-969-10	Sequence 10, Appl
705	30	41.7	375	5	PCT-US93-08322-8	Sequence 8, Appl	777	30	41.7	491	4	US-09-321-969-10	Sequence 10, Appl
706	30	41.7	376	4	US-09-802-540-13915	Sequence 13915, A	778	30	41.7	491	4	US-09-949-016-6005	Sequence 6005, Ap
707	30	41.7	379	2	US-08-887-365-36	Sequence 36, Appl	779	30	41.7	492	4	US-09-321-969-9	Sequence 9, Appl
708	30	41.7	381	1	US-07-936-163-3	Sequence 3, Appl	780	30	41.7	492	4	US-09-949-016-9657	Sequence 9657, Ap
709	30	41.7	383	1	US-07-936-163-4	Sequence 4, Appl	781	30	41.7	493	3	US-08-868-373-4	Sequence 4, Appl
710	30	41.7	384	4	US-09-489-039A-13229	Sequence 13229, A	782	30	41.7	497	4	US-09-107-433-4571	Sequence 4571, Ap
711	30	41.7	384	4	US-09-248-796A-18614	Sequence 18614, A	783	30	41.7	497	4	US-08-357-598-9	Sequence 9, Appl
712	30	41.7	385	4	US-09-583-110-3969	Sequence 3969, Ap	784	30	41.7	498	2	US-09-003-289-9	Sequence 9, Appl
713	30	41.7	386	4	US-09-755-6308-2	Sequence 2, Appl	785	30	41.7	498	5	PCT-US95-16435-9	Sequence 9, Appl
714	30	41.7	386	4	US-09-755-6308-265	Sequence 265, Appl	786	30	41.7	509	4	US-09-252-991A-28680	Sequence 28680, A
715	30	41.7	386	4	US-09-755-6308-278	Sequence 278, App	787	30	41.7	517	3	US-09-457-040B-14	Sequence 14, Appl
716	30	41.7	386	4	US-09-755-6308-279	Sequence 279, App	788	30	41.7	517	4	US-09-540-236-2403	Sequence 2403, Ap
717	30	41.7	386	4	US-09-755-6308-282	Sequence 282, App	789	30	41.7	523	4	US-09-328-352-4880	Sequence 4880, Ap
718	30	41.7	386	4	US-09-755-6308-286	Sequence 286, App	790	30	41.7	524	4	US-09-265-585C-35	Sequence 35, Appl
719	30	41.7	386	4	US-09-755-274-1	Sequence 1, Appl	791	30	41.7	527	4	US-09-107-532A-6562	Sequence 6562, Ap
720	30	41.7	386	4	US-09-755-274-4	Sequence 4, Appl	792	30	41.7	542	4	US-09-693-746-18	Sequence 18, Appl
721	30	41.7	386	4	US-09-755-274-5	Sequence 5, Appl	793	30	41.7	552	4	US-09-356-643B-11	Sequence 11, Appl
722	30	41.7	386	4	US-09-755-274-6	Sequence 6, Appl	794	30	41.7	552	4	US-10-053-510-11	Sequence 11, Appl
723	30	41.7	386	4	US-09-755-274-31	Sequence 31, Appl	795	30	41.7	559	4	US-09-081-149-2	Sequence 2, Appl
724	30	41.7	389	4	US-09-755-6308-271	Sequence 39, Appl	796	30	41.7	562	3	US-08-851-843A-5	Sequence 5, Appl
725	30	41.7	389	4	US-09-755-6308-275	Sequence 271, App	797	30	41.7	562	3	US-08-854-050-5	Sequence 5, Appl
726	30	41.7	389	4	US-09-755-6308-275	Sequence 275, App	798	30	41.7	562	3	US-09-430-323-5	Sequence 5, Appl
727	30	41.7	389	4	US-09-755-274-33	Sequence 33, Appl	799	30	41.7	562	4	US-09-766-253-5	Sequence 5, Appl
728	30	41.7	389	4	US-09-755-274-33	Sequence 35, Appl	800	30	41.7	574	4	US-09-902-540-10370	Sequence 10370, A
729	30	41.7	392	4	US-09-755-274-33	Sequence 35, Appl	801	30	41.7	574	4	US-09-248-796A-16619	Sequence 16619, A
730	30	41.7	393	4	US-09-107-433-4281	Sequence 4281, Ap	802	30	41.7	586	4	US-09-519-232-8	Sequence 8, Appl
731	30	41.7	393	4	US-09-489-039A-13122	Sequence 13122, A	803	30	41.7	588	4	US-09-538-092-1040	Sequence 1040, Ap
732	30	41.7	406	4	US-09-248-796A-16393	Sequence 16393, A	804	30	41.7	589	4	US-09-410-416-5	Sequence 5, Appl
733	30	41.7	406	4	US-09-248-796A-16393	Sequence 16393, A	805	30	41.7	599	1	US-08-391-615-4	Sequence 4, Appl
734	30	41.7	408	4	US-09-265-585C-150	Sequence 150, App	806	30	41.7	601	4	US-09-410-416-1	Sequence 1, Appl
735	30	41.7	409	4	US-09-107-433-3810	Sequence 3810, Ap	807	30	41.7	602	4	US-09-410-416-3	Sequence 3, Appl
736	30	41.7	413	4	US-09-491-577-72	Sequence 72, Appl	808	30	41.7	602	4	US-09-949-016-7417	Sequence 7417, Ap
737	30	41.7	420	4	US-09-252-991A-30038	Sequence 30038, A	809	30	41.7	606	4	US-09-949-016-7418	Sequence 7418, Ap
738	30	41.7	431	4	US-09-103-331-39	Sequence 39, Appl	810	30	41.7	606	4	US-09-949-016-11431	Sequence 11431, A
739	30	41.7	431	4	US-09-631-594-48	Sequence 48, Appl	811	30	41.7	611	4	US-09-949-016-10530	Sequence 10530, A
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741	30	41.7	443	4	US-09-302-540-11164	Sequence 11164, A	813	30	41.7	624	2	US-08-879-561-3	Sequence 3, Appl
742	30	41.7	444	3	US-08-482-746-15	Sequence 15, Appl	814	30	41.7	624	2	US-08-879-561-9	Sequence 9, Appl
743	30	41.7	444	4	US-08-580-734-15	Sequence 15, Appl	815	30	41.7	624	4	US-09-949-016-7339	Sequence 7339, Ap
744	30	41.7	444	4	US-08-374-009-15	Sequence 15, Appl	816	30	41.7	625	4	US-09-538-092-1064	Sequence 1064, Ap
745	30	41.7	444	4	US-09-191-724-15	Sequence 15, Appl	817	30	41.7	625	4	US-09-949-016-6671	Sequence 6671, Ap
746	30	41.7	446	4	US-09-631-603-11	Sequence 11, Appl	818	30	41.7	631	4	US-09-949-016-6325	Sequence 6325, Ap
747	30	41.7	446	4	US-09-134-000C-4163	Sequence 4163, Ap	819	30	41.7	638	4	US-09-902-540-11575	Sequence 11575, A
748	30	41.7	447	4	US-09-107-532A-6751	Sequence 6751, Ap	820	30	41.7	641	4	US-09-949-016-6746	Sequence 6746, Ap
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832	30	41.7	660	4	US-09-949-016-6843	Sequence 6843, Ap	905	30	41.7	4302	3	US-08-658-136-5	Sequence 5, Appli
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ALIGNMENTS

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RESULT 1
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; Sequence 2, Application US/08282141
; Patent No. 5538861
; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manfioletti, Guidoalberto
; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-282-141-2

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Query Match 100.0%; Score 72; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
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Db 284 VPFSVAKSVKSLYL 298

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; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-2

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Best Local Similarity 100.0%; Pred. No. 0.0001;
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Qy 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298

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; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

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; SOFTWARE: patin (Genentech)
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; APPLICATION NUMBER: US/08/435,436
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
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; TYPE: amino acid
; TOPOLOGY: linear
; US-08-435-436-2

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Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 4
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; Sequence 2, Application US/08438863
; Patent No. 5849585
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Ronghao Li
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,863
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-863-2

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 5
US-08-438-864-2
; Sequence 2, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
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; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929p1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-864-2

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 6
US-08-438-862-2


```
; Sequence 2, Application US/08438862
; Patent No. 6033660
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,862
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-862-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15
Db 284 VPFSVAKSVKSLYLG 298

RESULT 7
US-08-628-747-2
; Sequence 2, Application US/08628747
; Patent No. 6169070
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: One DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,747
; FILING DATE: 17-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/402,253
; FILING DATE: 10-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,861
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P929P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-225-1994
; TELEFAX: 650-952-9881
; TELEX: 910-371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-628-747-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15
Db 284 VPFSVAKSVKSLYLG 298

RESULT 8
US-08-402-253-2
; Sequence 2, Application US/08402253
; Patent No. 6211142
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-402-253-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 284 VPFSVAKSVKSLYLIG 298

;
; US-08-443-866B-2
; Sequence 2, Application US/08443866B
; Patent No. 6255068
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
; FILING DATE: 31-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0929D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-443-866B-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 284 VPFSVAKSVKSLYLIG 298

;
; US-08-443-866B-3
; Sequence 3, Application US/08282141
; Patent No. 5538861
; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manioletti, Guido
; TITLE OF INVENTION: Stimulating factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-282-141-3

Query Match 95.8%; Score 69; DB 1; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 281 VPFSVAKSVKSLYLIG 295

;
; US-08-435-434-1
; Sequence 1, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;
; US-08-435-434-1
```

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-434-1

Query Match 95.8%; Score 69; DB 1; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295

RESULT 12
US-08-435-436-1
Sequence 1, Application US/08435436
Patent No. 5721139
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
APPLICATION NUMBER:
PRIORITY APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-436-1

Query Match 95.8%; Score 69; DB 1; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295

RESULT 13
US-08-438-863-1
Sequence 1, Application US/08438863
Patent No. 5849585
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Ronghao Li
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
APPLICATION NUMBER:
PRIORITY APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-863-1

Query Match 95.8%; Score 69; DB 2; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295

RESULT 14
US-08-438-864-1
Sequence 1, Application US/08438864
Patent No. 5955420
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Hammonds, R. Glenn
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,864
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402253
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 929P1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-864-1

Query Match 95.8%; Score 69; DB 2; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 15
US-08-438-862-1
Sequence 1, Application US/08438862
Patent No. 6033660
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-1

Query Match 95.8%; Score 69; DB 3; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 16
US-08-628-747-1
Sequence 1, Application US/08628747
Patent No. 6169070
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Godowski, Paul J.
APPLICANT: Hammonds, R. Glenn
APPLICANT: Mark, Melanie
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: One DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,747
FILING DATE: 17-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,253
FILING DATE: 10-MAR-1995
APPLICATION NUMBER: US 08/438,861
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P929P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-225-1994
TELEFAX: 650-952-9881
TELEX: 910-371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-628-747-1

Query Match 95.8%; Score 69; DB 3; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSMAKSVKSLYL 295

RESULT 17
US-08-402-253-1
Sequence 1, Application US/08402253
Patent No. 6211142
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Hammonds, R. Glenn
APPLICANT: Godowski, Paul J.
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,253
FILING DATE: 10-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 929
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear

Query Match 95.8%; Score 69; DB 3; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSMAKSVKSLYL 295

RESULT 18
US-08-443-866B-1
Sequence 1, Application US/08443866B
Patent No. 6255068
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Hammonds, R. Glenn
APPLICANT: Mark, Melanie R.
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,866B
FILING DATE: 31-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402253
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0929D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-443-866B-1
Query Match 95.8%; Score 69; DB 3; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSMAKSVKSLYL 295

RESULT 19
US-09-107-532A-4410
Sequence 4410, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...77
; SEQUENCE DESCRIPTION: SEQ ID NO: 4410:
US-09-107-532A-4410

Query Match 61.1%; Score 44; DB 4; Length 77;
Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 44 IPISIAKVKVEILYL 57

RESULT 20
US-09-721-870-24
; Sequence 24, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Rubiak, Teresa M.
; APPLICANT: Larsen, Marsha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-24

Query Match 61.1%; Score 44; DB 4; Length 374;
Best Local Similarity 61.5%; Pred. No. 6.7;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13
Db 142 LPFAIAASVNSLY 154

RESULT 21
US-09-270-767-60337
; Sequence 60337, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 60337
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60337

Query Match 58.3%; Score 42; DB 4; Length 186;
Best Local Similarity 53.3%; Pred. No. 7;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
Db 65 IAFSTTKGVRQYLG 79

RESULT 22
US-08-843-530B-36
; Sequence 36, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,530B
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1220 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-843-530B-36

Query Match 58.3%; Score 42; DB 2; Length 1220;
Best Local Similarity 81.8%; Pred. No. 59;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKS 11
Db 955 VKFSVAKSVKS 965

RESULT 23
US-09-636-728-32
; Sequence 32, Application US/09636728
; Patent No. 6716625
```

RESULT 27
US-09-519-232-74
; Sequence 74, Application US/09519232
; Patent No. 6528702


```

; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-10857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; ORGANISM: Nicotiana tabacum
US-09-519-232-74

Query Match 54.2%; Score 39; DB 4; Length 369;
Best Local Similarity 53.8%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 4; Indels 2; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13
   ||| ||| |||
Db 237 VPPEVAENIKLLW 249

RESULT 28
US-09-270-767-60047
; Sequence 60047, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60047
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60047

Query Match 51.4%; Score 37; DB 4; Length 169;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

Qy 3 FSVAKSVKSLYL 14
   ||| ||| |||
Db 154 FSVKSKXKGAYL 165

RESULT 29
US-09-270-767-44600
; Sequence 44600, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44600
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44600

Query Match 51.4%; Score 37; DB 4; Length 224;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FSVAKSVKSLYL 14
   ||| ||| |||
Db 154 FSVKSKXKGAYL 165

US-09-270-767-44600

Query Match 51.4%; Score 37; DB 4; Length 224;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FSVAKSVKSLYL 14
   ||| ||| |||
Db 154 FSVKSKXKGAYL 165

RESULT 30
US-09-489-039A-8199
; Sequence 8199, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8199
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8199

Query Match 51.4%; Score 37; DB 4; Length 266;
Best Local Similarity 58.3%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSL 12
   :||| ||| :|||
Db 83 IPFCVAGGIRKSL 94

RESULT 31
US-09-107-532A-5019
; Sequence 5019, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Atinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
```

```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781)893-5007
/ TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 5019:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 316 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Enterococcus faecium
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...316
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5019:
US-09-107-532A-5019

Query Match 51.4%; Score 37; DB 4; Length 316;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 FSVSVKSKSLYL 14
Db 119 FAVSKNVEPLYL 130

RESULT 32
US-08-118-270-22
/ Sequence 22, Application US/08118270
/ Patent No. 5508384
/ GENERAL INFORMATION:
/ APPLICANT: Murphy, Randall B.
/ APPLICANT: Schuster, David I.
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/118,270
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY-2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 334 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US93-08528-22

Query Match 51.4%; Score 37; DB 1; Length 334;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 55 IPFSLANEVMYWYFG 69

RESULT 33
PCT-US93-08528-22
/ Sequence 22, Application PC/TUS9308528
/ GENERAL INFORMATION:
/ APPLICANT: New York University
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08528
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 334 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US93-08528-22

Query Match 51.4%; Score 37; DB 5; Length 334;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 55 IPFSLANEVMYWYFG 69

RESULT 34
US-09-248-796A-17702
/ Sequence 17702, Application US/09248796A
/ Patent No. 6747137
/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstock et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
/ TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
```

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; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17702
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17702

Query Match      51.4%; Score 37; DB 4; Length 729;
Best Local Similarity 42.9%; Pred. No. 2.7e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLYL 14
DB      158 VPYSEMKNIQNLF 171
      ||:| |::|:|
      ||:| |::|:|

RESULT 35
US-09-949-016-11563
; Sequence 11563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11563
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11563

Query Match      50.7%; Score 36.5; DB 4; Length 974;
Best Local Similarity 60.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      2 PFSVAKSVKS-LYL 15
DB      661 PFNIIPSPKSFYL 675
      ||::| |::| |::|
      ||::| |::| |::|

RESULT 36
US-09-185-501B-6
; Sequence 6, Application US/09185501B
; Patent No. 6331428
; GENERAL INFORMATION:
; APPLICANT: KATO, NOBUO
; TITLE OF INVENTION: HEXULOSE PHOSPHATE ISOMERASE GENE
; FILE REFERENCE: 0010-0953-OCIP
; CURRENT APPLICATION NUMBER: US/09/185,501B
; CURRENT FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 09/033,647
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: JP9-233131
; PRIOR FILING DATE: 1997-08-28
; PRIOR APPLICATION NUMBER: JP10-194808
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mycobacterium gastri
US-09-185-501B-14

Query Match      50.0%; Score 36; DB 3; Length 207;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 VPFSVAKSVK 10
DB      159 VPFSVAGGVK 168
      ||||| |
      ||||| |

; ORGANISM: Mycobacterium gastri
US-09-185-501B-6

Query Match      50.0%; Score 36; DB 3; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 VPFSVAKSVK 10
DB      3 VPFSVAGGVK 12
      ||||| |
      ||||| |

RESULT 37
US-09-489-039A-8829
; Sequence 8829, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8829
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8829

Query Match      50.0%; Score 36; DB 4; Length 74;
Best Local Similarity 57.1%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 PFSVAKSVKSLYL 15
DB      15 PLQVAKYVKILFRG 28
      | | | | | | | |
      | | | | | | | |

RESULT 38
US-09-185-501B-14
; Sequence 14, Application US/09185501B
; Patent No. 6331428
; GENERAL INFORMATION:
; APPLICANT: KATO, NOBUO
; TITLE OF INVENTION: HEXULOSE PHOSPHATE ISOMERASE GENE
; FILE REFERENCE: 0010-0953-OCIP
; CURRENT APPLICATION NUMBER: US/09/185,501B
; CURRENT FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 09/033,647
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: JP9-233131
; PRIOR FILING DATE: 1997-08-28
; PRIOR APPLICATION NUMBER: JP10-194808
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Mycobacterium gastri
US-09-185-501B-14

Query Match      50.0%; Score 36; DB 3; Length 207;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 VPFSVAKSVK 10
DB      159 VPFSVAGGVK 168
      ||||| |
      ||||| |
```

```

RESULT 39
US-09-632-947B-4
; Sequence 4, Application US/09632947B
; Patent No. 6356845
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: UDP-N-ACETYLENOUPYRVYLGLUCOSAMINE REDUCTASE (S. aureus)
; TITLE OF INVENTION: MuFB
; FILE REFERENCE: 268.6241 0101
; CURRENT APPLICATION NUMBER: US/09/632,947B
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-09-632-947B-4

```

```

Query Match 50.0%; Score 36; DB 3; Length 297;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

QY 1 VPFSVAKSVKSLY 13
: ||| :|||
DB 97 IRFSVKENKVSFY 109

```

```

RESULT 40
US-09-503-391-2
; Sequence 2, Application US/09503391
; Patent No. 6300091
; GENERAL INFORMATION:
; APPLICANT: Patton, David A.
; APPLICANT: Ashby, Carl S.
; APPLICANT: Thomas, Carla R.
; APPLICANT: McElver, John A.
; APPLICANT: Budziszewski, Gregory J.
; APPLICANT: Levin, Joshua Z.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30852A
; CURRENT APPLICATION NUMBER: US/09/503,391
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-503-391-2

```

```

Query Match 50.0%; Score 36; DB 3; Length 551;
Best Local Similarity 63.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 VPFSVAKSVKS 11
: ||| :|||
DB 322 VPFSVIRAKS 332

```

```

RESULT 41
US-09-503-391-4
; Sequence 4, Application US/09503391
; Patent No. 6300091
; GENERAL INFORMATION:
; APPLICANT: Patton, David A.
; APPLICANT: Ashby, Carl S.
; APPLICANT: Thomas, Carla R.

```

```

; APPLICANT: McElver, John A.
; APPLICANT: Budziszewski, Gregory J.
; APPLICANT: Levin, Joshua Z.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30852A
; CURRENT APPLICATION NUMBER: US/09/503,391
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-503-391-4

```

```

Query Match 50.0%; Score 36; DB 3; Length 551;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 VPFSVAKSVKS 11
: ||| :|||
DB 322 VPFSVIRAKS 332

```

```

RESULT 42
US-08-471-119A-2
; Sequence 2, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Leitner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoergendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoiff, Melvyn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tolypocladium niveum
; STRAIN: ATCC 34921
US-08-471-119A-2

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Query Match 50.0%; Score 36; DB 2; Length 15281;

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Best Local Similarity 58.3%; Pred. No. 1.2e+04;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SVAKSVKSLYLIG 15
Db 12922 SVLSLESYLIG 12933

RESULT 43

US-09-902-540-13147
; Sequence 13147, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13147
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13147

Query Match 48.6%; Score 35; DB 4; Length 148;
Best Local Similarity 46.7%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
Db 6 LPMLVALGLELYIG 20

RESULT 44

US-09-252-991A-32921
; Sequence 32921, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32921
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (7)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-32921

Query Match 48.6%; Score 35; DB 4; Length 279;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKS 11
Db 142 IPFSEIKSIKN 152

RESULT 45

US-09-328-352-4879
; Sequence 4879, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4879
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4879

Query Match 48.6%; Score 35; DB 4; Length 303;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AKSVKSLYLIG 15
Db 74 ARHVKEVYLIG 83

RESULT 46

US-09-489-039A-7261
; Sequence 7261, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7261
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7261

Query Match 48.6%; Score 35; DB 4; Length 332;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSLYL 14
Db 187 PFSVAKGGQPFYV 199

RESULT 47

US-08-121-714-4
; Sequence 4, Application US/08121714
; Patent No. 5470970
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,714
; FILING DATE: 02/28/92
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00510/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-121-714-4

Query Match 48.6%; Score 35; DB 1; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 PFSVAKSVKSLYLG 15
|||::: :||
Db 32 PFSISSAMWVFLG 45

RESULT 48
US-08-477-108A-4
; Sequence 4, Application US/08477108A
; Patent No. 5801001
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; APPLICANT: Zou, Zhiqiang
; APPLICANT: Anisowicz, Anthony
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,108A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92

; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-477-108A-4

Query Match 48.6%; Score 35; DB 1; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 PFSVAKSVKSLYLG 15
|||::: :||
Db 32 PFSISSAMWVFLG 45

RESULT 49
US-08-477-112-4
; Sequence 4, Application US/08477112
; Patent No. 5905023
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,112
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-477-112-4

Query Match 48.6%; Score 35; DB 2; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLIG 15
DB 32 PFSISSAMAMVFLG 45

RESULT 50

PCT-US93-08322-4
; Sequence 4, Application PC/TUS9308322
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08322
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/072001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-08322-4

Query Match 48.6%; Score 35; DB 5; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLIG 15
DB 32 PFSISSAMAMVFLG 45

Search completed: July 7, 2005, 09:40:17
Job time : 21.0121 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:49:00 ; Search time 390.39 Seconds
(without alignments)
224.889 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PRLDCINKYSGPYTNSGF.....LGRMFSGTPIRLRFKRLQP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1297	100.0	678	2	AAR99414 Human gas
2	1297	100.0	678	2	AAR99414 Human gas
3	1297	100.0	678	2	AAR99414 Human gas
4	1297	100.0	678	3	AAY29794 Human gro
5	1297	100.0	678	3	AAY29794 Human gro
6	1297	100.0	678	8	ADL83231 Amino aci
7	1297	100.0	678	8	ADL83231 Amino aci
8	1297	100.0	678	8	ADM40825 Human PRO
9	1297	100.0	678	8	ADM40825 Human PRO
10	1269	97.8	624	8	ADM40823 Human PRO
11	1113	85.8	673	2	AAW46462 Murine gr
12	1113	85.8	673	2	AAW46462 Murine gr
13	1113	85.8	673	3	AAB33459 Human PRO
14	1113	85.8	673	3	AAB33459 Human PRO
15	1113	85.8	673	5	AAY57382 Amino aci
16	1113	85.8	673	5	ABB84840 Human PRO
17	1113	85.8	673	5	ABB84840 Human PRO
18	1113	85.8	673	7	ADD10337 Human sec
19	1113	85.8	673	7	ADD10337 Human sec
20	1113	85.8	673	7	ADD10337 Human sec
21	1113	85.8	673	8	ADH41298 Human PRO
22	1113	85.8	673	8	ADH41298 Human PRO
23	1113	85.8	703	8	ADK82826 Human PRO
24	602.5	46.5	635	2	ABO84420 Mouse can
25	601.5	46.4	635	2	AAR72350 Mature hu
26	601.5	46.4	635	2	AAR72350 Mature hu
27	601.5	46.4	635	2	AAR72350 Mature hu
28	601.5	46.4	635	2	AAR72350 Mature hu
29	601.5	46.4	635	2	AAR72350 Mature hu
30	601.5	46.4	635	2	AAR72350 Mature hu
31	601.5	46.4	635	2	AAR72350 Mature hu
32	601.5	46.4	635	2	AAR72350 Mature hu
33	596.5	46.0	635	2	AAR72350 Mature hu
34	587.5	45.3	635	2	AAR72350 Mature hu
35	587.5	45.3	635	2	AAR72350 Mature hu
36	587.5	45.3	635	2	AAR72350 Mature hu
37	586.5	45.2	635	2	AAR72350 Mature hu
38	586.5	45.2	635	2	AAR72350 Mature hu
39	585.5	45.1	635	2	AAR72350 Mature hu
40	577.5	44.5	635	2	AAR72350 Mature hu
41	418	32.2	244	2	AAR70731 Human pro
42	418	32.2	244	2	AAR70731 Human pro
43	418	32.2	244	2	AAR70731 Human pro
44	365.5	28.2	397	8	ADT49855 Murine FB
45	363	28.0	705	8	ADT49855 Murine FB
46	362	27.9	705	8	ADT49855 Murine FB
47	361	27.8	518	8	ABO84421 Human can
48	359	27.7	258	8	ADT49854 Murine FB
49	357.5	27.6	911	6	ABP56756 Mouse EGF
50	357.5	27.6	911	6	ABP56756 Mouse EGF
51	356	27.4	1598	8	ADT49820 Murine BC
52	354.5	27.3	1394	8	ABE61170 Drosophi
53	354.5	27.3	1587	8	ADT49907 Human LTB
54	353.5	27.3	957	6	ABP56758 Mouse CSG
55	353.5	27.3	997	5	ABB80927 Mouse BCO
56	353.5	27.3	1354	5	ABG79183 Human TGF
57	353.5	27.3	1356	5	ABG79183 Human TGF
58	353.5	27.3	1425	8	ADM87222 Human pro
59	353.5	27.3	1448	8	ADP29294 Human sec
60	353.5	27.3	1467	5	ABG79181 Human TGF
61	353.5	27.3	1469	5	ABG79181 Human TGF
62	353.5	27.3	1474	5	ABG79180 Human TGF
63	350.5	27.0	2873	8	AAO30814 Human cel
64	350	27.0	2873	8	AAO30814 Human cel
65	349	26.9	764	8	ADT49886 Murine FB
66	349	26.9	764	8	ADT49886 Murine FB
67	349	26.9	988	5	ABJ04648 Protein o
68	348.5	26.9	386	8	ADT27624 Human SCU
69	348.5	26.9	2871	8	ADM81619 Tumour-as
70	348.5	26.9	3002	6	AAE34399 Human fib
71	348.5	26.9	3002	6	ABO07260 Human p53
72	348.5	26.9	3002	7	ADJ68389 Human hea
73	348.5	26.9	3002	8	ADQ17682 Human sof
74	348	26.8	387	4	AAG65909 Amino aci
75	346	26.7	286	7	ABU62820 Human LTB
76	346	26.7	339	7	ABU62816 Human LTB
77	346	26.7	594	7	ABU62819 Human LTB
78	346	26.7	785	7	ABU62818 Human LTB
79	346	26.7	964	4	AAG65510 Amino aci
80	346	26.7	964	5	ABU04647 Protein o
81	346	26.7	965	4	AAG67529 Human EGF
82	346	26.7	965	5	ABG70382 Human EGF
83	346	26.7	988	6	ABP56755 Human epi
84	346	26.7	988	7	ABU62815 Human LTB
85	345	26.6	964	6	ADP56757 Human CSG
86	345	26.6	971	8	ADP66056 Novel hum
87	345	26.6	997	6	ABJ37049 Human bre
88	345	26.6	999	5	ABP69329 Human pol
89	345	26.6	999	5	ABG61893 Prostate
90	345	26.6	999	5	ABB80926 Human bre
91	345	26.6	999	5	ABJ05567 Breast ca
92	345	26.6	999	6	ABU19815 Androgen-
93	345	26.6	999	6	ABR47407 Breast ca
94	345	26.6	999	7	ADN39416 Cancer/an
95	345	26.6	999	7	ADN38734 Cancer/an
96	345	26.6	999	7	ADN39569 Cancer/an
97	345	26.6	999	8	ADN27636 SCUBE2 no
98	344.5	26.6	798	8	ADN23443 Bacterial

99	344.5	26.6	798	8	ADN23442	Adn23442 Bacterial	172	330.5	25.5	845	2	AAR53089	Aar53089 Human mas
100	344.5	26.6	957	5	AD128028	Ad128028 ECMCAD pr	173	330.5	25.5	961	6	ABR41625	Abr41625 Human DIT
101	344.5	26.6	2695	5	ABG294632	Abg294632 Human fib	174	330.5	25.5	1118	4	AAW50209	Aaw50209 Human fib
102	344.5	26.6	2695	7	ADL35969	Adl35969 Human NOV	175	330.5	25.5	1342	6	AAO16655	Aao16655 Human ext
103	342.5	26.4	2809	5	AAAG66169	Aag66169 Human fib	176	330.5	25.5	1590	8	ABM82596	Abm82596 Human dia
104	341	26.3	653	7	ADD26679	Add26679 Human adi	177	330.5	25.5	1631	8	ABM82598	Abm82598 Human dia
105	339.5	26.2	1018	7	AD078255	Ad078255 Human CGD	178	330.5	25.5	1642	8	ABM82597	Abm82597 Human dia
106	339	26.1	524	8	ABO84713	Ab084713 Human can	179	330.5	25.5	1668	6	AAO16647	Aao16647 Human ext
107	339	26.1	556	2	AAW27598	Aaw27598 Human fib	180	330.5	25.5	1668	6	ABU52394	Abu52394 Human GPC
108	339	26.1	559	8	ABO84709	Ab084709 Human can	181	330.5	25.5	1668	6	ADL24123	Adl24123 Human NOV
109	339	26.1	566	2	AAK11148	Aak11148 Fibulin A	182	330.5	25.5	1720	6	ABU52393	Abu52393 Human GPC
110	339	26.1	566	5	AAE15574	Aae15574 Human fib	183	330.5	25.5	1721	6	AAO16650	Aao16650 Human ext
111	339	26.1	566	8	ADN03779	Adn03779 Antipsori	184	330.5	25.5	1721	6	ADL24121	Adl24121 Human NOV
112	339	26.1	566	8	ABO84714	Ab084714 Human can	185	330.5	25.5	1722	8	ADSI10847	Adsi10847 Human the
113	339	26.1	581	8	ABO84710	Ab084710 Human can	186	330.5	25.5	2844	5	ABG94629	Abg94629 Human NOV
114	339	26.1	601	2	AAK11149	Aak11149 Fibulin B	187	330.5	25.5	2844	7	ADL35963	Adl35963 Human NOV
115	339	26.1	601	2	AAW27599	Aaw27599 Human fib	188	330.5	25.5	2845	5	ABG94631	Abg94631 Human NOV
116	339	26.1	601	5	AAE15575	Aae15575 Human fib	189	330.5	25.5	2877	5	ABG94630	Abg94630 Human NOV
117	339	26.1	601	8	ABO84717	Ab084717 Human can	190	330.5	25.5	2877	7	ADL35965	Adl35965 Human NOV
118	339	26.1	641	8	ABO84712	Ab084712 Human can	191	330.5	25.5	2995	7	ADL35961	Adl35961 Human NOV
119	339	26.1	661	8	ABO84708	Ab084708 Human can	192	330.5	25.5	2995	7	ADL35961	Adl35961 Human NOV
120	339	26.1	683	2	AAK11150	Aak11150 Fibulin C	193	329.5	25.4	2910	8	ADQ97206	Adq97206 Mouse can
121	339	26.1	683	2	AAW27600	Aaw27600 Human fib	194	328.5	25.3	1253	3	AAAB12271	Aab12271 Mouse lat
122	339	26.1	683	5	AAE15576	Aae15576 Human fib	195	328.5	25.3	1253	4	AAAB61420	Aab61420 Murine TA
123	339	26.1	683	8	ABO84716	Ab084716 Human can	196	328.5	25.3	1253	4	AAAB61420	Aab61420 Murine la
124	339	26.1	686	4	ABG19385	Abg19385 Novel hum	197	327.5	25.3	333	3	AAAY84709	Aay84709 Amino aci
125	339	26.1	698	8	ABO84711	Ab084711 Human can	198	327	25.2	448	6	ABR59720	Abr59720 Human fib
126	339	26.1	703	2	AAW27601	Aaw27601 Human fib	199	327	25.2	448	7	ADD14954	Add14954 Human UP
127	339	26.1	703	5	AAE15577	Aae15577 Human fib	200	327	25.2	448	7	ADF90891	Adf90891 Human hep
128	339	26.1	703	8	ADN03922	Adn03922 Antipsori	201	327	25.2	448	8	ADL13450	Adl13450 Human UP5
129	339	26.1	703	8	ABO84715	Ab084715 Human can	202	327	25.2	448	8	ADQ67955	Adq67955 Human hep
130	339	26.1	703	8	ADT49905	Adt49905 Human FBL	203	327	25.2	897	4	AAAG65887	Aag65887 Amino aci
131	339	26.1	706	4	ABG19386	Abg19386 Novel hum	204	327	25.2	897	4	ABG06309	Abg06309 Novel hum
132	339	26.1	1221	8	ADT49892	Adt49892 Murine FB	205	327	25.2	897	5	ABG91402	Abg91402 Primate L
133	338	26.1	576	4	AAW80175	Aaw80175 Human pro	206	327	25.2	897	5	ABG07852	Abg07852 Novel pro
134	338	26.1	576	4	AAW80174	Aaw80174 Human pro	207	327	25.2	897	7	ADE08940	Ade08940 Novel pro
135	338	26.1	576	4	AAW41932	Aaw41932 Human pol	208	327	25.2	914	8	ADL27628	Adl27628 Human SCU
136	338	26.1	603	4	AAW79191	Aaw79191 Human pro	209	327	25.2	939	6	AAE29932	Aae29932 Human LP2
137	338	26.1	636	4	AAW40146	Aaw40146 Human pro	210	327	25.2	991	6	AAO16645	Aao16645 Human ext
138	338	26.1	650	4	AAW79190	Aaw79190 Human pro	211	327	25.2	993	4	AAAG65888	Aag65888 Amino aci
139	337	26.0	1184	7	ADE95474	Ade95474 Human NOV	212	327	25.2	993	6	AAE29931	Aae29931 Human LP2
140	337	26.0	1231	5	ABP63045	Abp63045 Human pol	213	327	25.2	993	8	ADL27630	Adl27630 Human SCU
141	336	25.9	974	6	ABU12093	Abu12093 Novel hum	214	327	25.2	993	7	ADL27637	Adl27637 SCUBEB3-2
142	335.5	25.9	505	8	ADT49801	Adt49801 Murine BC	215	326.5	25.2	737	7	AAE38806	Aae38806 Human POL
143	334.5	25.8	733	8	ADQ65159	Adq65159 Novel hum	216	326.5	25.2	1288	8	ADQ59379	Adq59379 Human can
144	334.5	25.8	1121	4	AAW78887	Aaw78887 Human fib	217	326.5	25.2	1300	6	AAO16653	Aao16653 Human ext
145	334.5	25.8	1208	3	AAW70551	Aaw70551 Human lat	218	326.5	25.2	1353	6	AAO16654	Aao16654 Human ext
146	334.5	25.8	1256	8	ADR14553	Adr14553 Human NF-	219	326.5	25.2	1626	6	AAO16652	Aao16652 Human ext
147	334.5	25.8	1257	3	AAW70554	Aaw70554 Human lat	220	326.5	25.2	1679	6	AAO16651	Aao16651 Human ext
148	334.5	25.8	1260	4	AAAB61420	Aab61420 TANGO 275	221	326.5	25.2	2676	7	ADL35971	Adl35971 Human NOV
149	334.5	25.8	1289	4	AAAB61419	Aab61419 Human TAN	222	325	25.1	735	5	AAAG68258	Aag68258 Human POL
150	333	25.7	596	7	AAO30833	Aao30833 Human cel	223	325	25.1	735	6	ABU12091	Abu12091 Novel hum
151	333	25.7	845	5	AAW68259	Aaw68259 Human POL	224	324	25.0	349	7	ADB65110	Adb65110 Human pro
152	333	25.7	845	6	ABU12092	Abu12092 Novel hum	225	324	25.0	974	7	AAE38808	Aae38808 Human POL
153	333	25.7	845	7	AAE38807	Aae38807 Human POL	226	323.5	24.9	682	8	ADR10465	Adr10465 Human pro
154	333	25.7	880	7	ADB64680	Adb64680 Human pro	227	323.5	24.9	1355	2	AAAR14584	Aar14584 TGF beta
155	333	25.7	973	5	AAAG68260	Aag68260 Human POL	228	323	24.9	335	3	AAAY76008	Aay76008 Rat EGF e
156	333	25.7	989	6	AAE30306	Aae30306 Human LP2	229	323	24.9	335	4	AAAB55947	Aab55947 Skin cell
157	333	25.7	1006	5	AAU79172	Aau79172 Human MEG	230	323	24.9	335	5	ABB72147	Abb72147 Rat prote
158	333	25.7	1009	6	AAE29930	Aae29930 Human LP2	231	323	24.9	392	2	AAAW31705	Aaw31705 Human ext
159	332.5	25.6	1218	6	ABJ19368	Abj19368 NOX rela	232	323	24.9	448	2	AAW79739	Aaw79739 Human EEG
160	332.5	25.6	1218	8	ADO41736	Ado41736 Novel hum	233	323	24.9	448	2	AAW95709	Aaw95709 Homo sapi
161	331.5	25.6	2000	8	ADP23488	Adp23488 PRO polyyp	234	323	24.9	448	2	AAW94281	Aaw94281 Human ext
162	331.5	25.6	2911	6	ABU56630	Abu56630 Lung canc	235	323	24.9	448	3	AAAY54989	Aay54989 Full leng
163	331.5	25.6	2911	6	ABO07259	Ab007259 Human p53	236	323	24.9	448	3	AAAY57058	Aay57058 Amino aci
164	331.5	25.6	2911	7	ADJ68615	Adj68615 Human hea	237	323	24.9	448	3	AAAM93573	Aam93573 Human pol
165	331.5	25.6	2911	7	ADN38844	Adn38844 Cancer/an	238	323	24.9	448	5	AAAU75494	Aau75494 Human ext
166	331.5	25.6	2911	8	ADQ18204	Adq18204 Human sof	239	323	24.9	448	6	ABR59721	Abr59721 Human fib
167	331.5	25.6	2912	4	ABG06402	Abg06402 Novel hum	240	323	24.9	448	7	ADE59306	Ade59306 Human Pro
168	330.5	25.5	315	6	ABR41616	Ab41616 Human DIT	241	323	24.9	448	7	ADE59310	Ade59310 Human Pro
169	330.5	25.5	751	2	AAAR53088	Aar53088 Human mas	242	323	24.9	448	7	ADE59304	Ade59304 Rat Prote
170	330.5	25.5	752	2	AAAR53087	Aar53087 Human mas	243	323	24.9	448	7	ADE59308	Ade59308 Rat Prote
171	330.5	25.5	756	2	AAAR53086	Aar53086 Human mas	244	323	24.9	448	8	ADL31324	Adl31324 Human pro

391	319	24.6	448	6	ABR60239	ABr60239	Human	sec	464	319	24.6	448	6	ABO31673	ABO31673	Human	sec
392	319	24.6	448	6	ABR67974	ABr67974	Human	sec	465	319	24.6	448	6	ABM08090	ABm08090	Human	sec
393	319	24.6	448	6	ABR65362	ABr65362	Human	sec	466	319	24.6	448	6	ABO40570	ABo40570	Human	sec
394	319	24.6	448	6	ABR68584	ABr68584	Human	sec	467	319	24.6	448	6	ABO35995	ABo35995	Human	PRO
395	319	24.6	448	6	ABR71996	ABr71996	Human	sec	468	319	24.6	448	6	ABO44134	ABo44134	Human	PRO
396	319	24.6	448	6	ABU85476	ABu85476	Human	PRO	469	319	24.6	448	6	ADA78160	ADa78160	Human	sec
397	319	24.6	448	6	ABU89166	ABu89166	Human	sec	470	319	24.6	448	6	ABM24929	ABm24929	Human	sec
398	319	24.6	448	6	ABU83246	ABu83246	Human	sec	471	319	24.6	448	6	ABO03197	ABo03197	Human	sec
399	319	24.6	448	6	ABU95102	ABu95102	Novel	hum	472	319	24.6	448	6	ABR90453	ABr90453	Human	sec
400	319	24.6	448	6	ABU90850	ABu90850	Novel	hum	473	319	24.6	448	6	ABM17367	ABm17367	Human	sec
401	319	24.6	448	6	ABU84161	ABu84161	Human	sec	474	319	24.6	448	6	ABR95113	ABr95113	Human	sec
402	319	24.6	448	6	ABU93812	ABu93812	Novel	hum	475	319	24.6	448	6	ABR95418	ABr95418	Human	sec
403	319	24.6	448	6	ABR65057	ABr65057	Human	sec	476	319	24.6	448	6	ABO21656	ABo21656	Human	sec
404	319	24.6	448	6	ABR68889	ABr68889	Human	sec	477	319	24.6	448	6	ABR97920	ABr97920	Human	sec
405	319	24.6	448	6	ABO06705	ABo06705	Human	sec	478	319	24.6	448	6	ABR87708	ABr87708	Human	sec
406	319	24.6	448	6	ABR99250	ABr99250	Human	sec	479	319	24.6	448	6	ABM77749	ABm77749	Human	sec
407	319	24.6	448	6	ABU57134	ABu57134	Human	PRO	480	319	24.6	448	6	ABM27979	ABm27979	Human	sec
408	319	24.6	448	6	ABU72040	ABu72040	Novel	hum	481	319	24.6	448	6	ABM06260	ABm06260	Human	sec
409	319	24.6	448	6	ABU86086	ABu86086	Novel	hum	482	319	24.6	448	6	ABM03766	ABm03766	Human	sec
410	319	24.6	448	6	ABU82373	ABu82373	Novel	hum	483	319	24.6	448	6	ABM35217	ABm35217	Human	sec
411	319	24.6	448	6	ABU87384	ABu87384	Human	PRO	484	319	24.6	448	6	ABM26454	ABm26454	Human	sec
412	319	24.6	448	6	ABU67141	ABu67141	Novel	hum	485	319	24.6	448	6	ABO48236	ABo48236	Human	sec
413	319	24.6	448	6	ABU83856	ABu83856	Human	sec	486	319	24.6	448	6	ABR92978	ABr92978	Human	sec
414	319	24.6	448	6	ABO08230	ABo08230	Human	PRO	487	319	24.6	448	6	ABO24739	ABo24739	Human	sec
415	319	24.6	448	6	ABU81941	ABu81941	Novel	hum	488	319	24.6	448	6	ABM11750	ABm11750	Human	sec
416	319	24.6	448	6	ABU66105	ABu66105	Novel	hum	489	319	24.6	448	6	ABM02851	ABm02851	Human	sec
417	319	24.6	448	6	ABR59934	ABr59934	Human	sec	490	319	24.6	448	6	ABM16147	ABm16147	Human	sec
418	319	24.6	448	6	ABU94122	ABu94122	Novel	hum	491	319	24.6	448	6	ABO27708	ABo27708	Human	sec
419	319	24.6	448	6	ABU99975	ABu99975	Novel	hum	492	319	24.6	448	6	ABM39199	ABm39199	Human	sec
420	319	24.6	448	6	ABR66645	ABr66645	Human	sec	493	319	24.6	448	6	ABM07175	ABm07175	Human	sec
421	319	24.6	448	6	ABR91063	ABr91063	Human	sec	494	319	24.6	448	6	ABM21269	ABm21269	Human	sec
422	319	24.6	448	6	ABU94490	ABu94490	Human	PRO	495	319	24.6	448	6	ABM09615	ABm09615	Human	sec
423	319	24.6	448	6	ABU79372	ABu79372	Human	PRO	496	319	24.6	448	6	ABO41485	ABo41485	Human	sec
424	319	24.6	448	6	ABU86701	ABu86701	Human	sec	497	319	24.6	448	6	ABO36300	ABo36300	Human	PRO
425	319	24.6	448	6	ABU87006	ABu87006	Novel	hum	498	319	24.6	448	6	ABO43829	ABo43829	Human	PRO
426	319	24.6	448	6	ABU94795	ABu94795	Human	PRO	499	319	24.6	448	6	ABM76529	ABm76529	Human	sec
427	319	24.6	448	6	ABO04722	ABo04722	Human	PRO	500	319	24.6	448	6	ABM76225	ABm76225	Human	sec
428	319	24.6	448	6	ABR70471	ABr70471	Human	sec	501	319	24.6	448	6	ABM25844	ABm25844	Human	sec
429	319	24.6	448	6	ABU98636	ABu98636	Human	PRO	502	319	24.6	448	6	ABM26149	ABm26149	Human	sec
430	319	24.6	448	6	ABR66035	ABr66035	Human	sec	503	319	24.6	448	6	ABO03502	ABo03502	Human	sec
431	319	24.6	448	6	ABR64752	ABr64752	Human	sec	504	319	24.6	448	6	ABO02587	ABo02587	Human	sec
432	319	24.6	448	6	ABU79677	ABu79677	Human	PRO	505	319	24.6	448	6	ABR90758	ABr90758	Human	sec
433	319	24.6	448	6	ABU93068	ABu93068	Human	sec	506	319	24.6	448	6	ABR73826	ABr73826	Human	sec
434	319	24.6	448	6	ABU96027	ABu96027	Human	PRO	507	319	24.6	448	6	ABO17078	ABo17078	Human	sec
435	319	24.6	448	6	ABU91247	ABu91247	Novel	hum	508	319	24.6	448	6	ABR94503	ABr94503	Human	sec
436	319	24.6	448	6	ABU90340	ABu90340	Novel	hum	509	319	24.6	448	6	ABR76010	ABr76010	Human	sec
437	319	24.6	448	6	ABO09755	ABo09755	Human	sec	510	319	24.6	448	6	ABR71386	ABr71386	Human	sec
438	319	24.6	448	6	ABO11027	ABo11027	Human	sec	511	319	24.6	448	6	ABR93283	ABr93283	Human	sec
439	319	24.6	448	6	ABR71081	ABr71081	Human	sec	512	319	24.6	448	6	ABR93588	ABr93588	Human	sec
440	319	24.6	448	6	ABU87689	ABu87689	Human	PRO	513	319	24.6	448	6	ABR88013	ABr88013	Human	sec
441	319	24.6	448	6	ABU91557	ABu91557	Human	PRO	514	319	24.6	448	6	ABO28013	ABo28013	Human	sec
442	319	24.6	448	6	ABU84771	ABu84771	Human	sec	515	319	24.6	448	6	ABO30148	ABo30148	Human	sec
443	319	24.6	448	6	ABR69861	ABr69861	Human	sec	516	319	24.6	448	6	ABO33357	ABo33357	Human	PRO
444	319	24.6	448	6	ABU80238	ABu80238	Human	PRO	517	319	24.6	448	6	ABM05045	ABm05045	Human	sec
445	319	24.6	448	6	ABU93507	ABu93507	Human	PRO	518	319	24.6	448	6	ABM09005	ABm09005	Human	sec
446	319	24.6	448	6	ABO10060	ABo10060	Human	sec	519	319	24.6	448	6	ABO36605	ABo36605	Human	sec
447	319	24.6	448	6	ABO09145	ABo09145	Human	sec	520	319	24.6	448	6	ABO35690	ABo35690	Human	PRO
448	319	24.6	448	6	ABU10713	ABu10713	Human	sec	521	319	24.6	448	6	ABO39655	ABo39655	Human	sec
449	319	24.6	448	6	ABU95722	ABu95722	Human	PRO	522	319	24.6	448	6	ABM10530	ABm10530	Human	sec
450	319	24.6	448	6	ABU79783	ABu79783	Human	sec	523	319	24.6	448	6	ABM12055	ABm12055	Human	sec
451	319	24.6	448	6	ABU96931	ABu96931	Novel	hum	524	319	24.6	448	6	ABO52201	ABo52201	Human	PRO
452	319	24.6	448	6	ABR70776	ABr70776	Human	sec	525	319	24.6	448	6	ABO52506	ABo52506	Human	PRO
453	319	24.6	448	6	ABO05127	ABo05127	Novel	hum	526	319	24.6	448	6	ABO23824	ABo23824	Human	sec
454	319	24.6	448	6	ABO08535	ABo08535	Human	sec	527	319	24.6	448	6	ABR97310	ABr97310	Human	sec
455	319	24.6	448	6	ABO05742	ABo05742	Human	sec	528	319	24.6	448	6	ABR87098	ABr87098	Human	sec
456	319	24.6	448	6	ABR74131	ABr74131	Human	sec	529	319	24.6	448	6	ABM11140	ABm11140	Human	sec
457	319	24.6	448	6	ABR95723	ABr95723	Human	sec	530	319	24.6	448	6	ABM28284	ABm28284	Human	sec
458	319	24.6	448	6	ABR81020	ABr81020	Human	sec	531	319	24.6	448	6	ABO32283	ABo32283	Human	sec
459	319	24.6	448	6	ABR81325	ABr81325	Human	sec	532	319	24.6	448	6	ABM15410	ABm15410	Human	sec
460	319	24.6	448	6	ABM01021	ABm01021	Human	sec	533	319	24.6	448	6	ABM05565	ABm05565	Human	sec
461	319	24.6	448	6	ABR88623	ABr88623	Human	sec	534	319	24.6	448	6	ABM04376	ABm04376	Human	sec
462	319	24.6	448	6	ABM77444	ABm77444	Human	sec	535	319	24.6	448	6	ABM22489	ABm22489	Human	sec
463	319	24.6	448	6	ABO28928	ABo28928	Human	sec	536	319	24.6	448	6	ABM07785	ABm07785	Human	sec

537	319	24.6	448	6	ABO40875	Human sec	610	319	24.6	448	6	ABM25234	Human sec
538	319	24.6	448	6	ABM35522	Human sec	611	319	24.6	448	6	ABO47626	Human sec
539	319	24.6	448	6	ABM33285	Human sec	612	319	24.6	448	6	ABO47931	Human sec
540	319	24.6	448	6	ABO52811	Human PRO	613	319	24.6	448	6	ABO48541	Human sec
541	319	24.6	448	6	ABO50371	Human sec	614	319	24.6	448	6	ABO51591	Human PRO
542	319	24.6	448	6	ABU99365	Human sec	615	319	24.6	448	6	ABO51896	Human PRO
543	319	24.6	448	6	ABO04417	Human sec	616	319	24.6	448	6	ABO50676	Human sec
544	319	24.6	448	6	ABO06047	Human sec	617	319	24.6	448	6	ABR79800	Human sec
545	319	24.6	448	6	ABM18587	Human sec	618	319	24.6	448	6	ABM17062	Human sec
546	319	24.6	448	6	ABR97615	Human sec	619	319	24.6	448	6	ABM18094	Human sec
547	319	24.6	448	6	ABR80715	Human sec	620	319	24.6	448	6	ABO21046	Human sec
548	319	24.6	448	6	ABM01326	Human sec	621	319	24.6	448	6	ABR97005	Human sec
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550	319	24.6	448	6	ABM13580	Human sec	623	319	24.6	448	6	ABM16452	Human sec
551	319	24.6	448	6	ABM20364	Human sec	624	319	24.6	448	6	ABM24319	Human sec
552	319	24.6	448	6	ABO42095	Human sec	625	319	24.6	448	6	ABM14800	Human sec
553	319	24.6	448	6	ABO42705	Human sec	626	319	24.6	448	6	ABM04681	Human sec
554	319	24.6	448	6	ABM10225	Human sec	627	319	24.6	448	6	ABM06870	Human sec
555	319	24.6	448	6	ABO38740	Human sec	628	319	24.6	448	6	ABM09310	Human sec
556	319	24.6	448	6	ABM32980	Human sec	629	319	24.6	448	6	ABO39350	Human sec
557	319	24.6	448	6	ABM22794	Human sec	630	319	24.6	448	6	ABM75615	Human sec
558	319	24.6	448	6	ABM75005	Human sec	631	319	24.6	448	6	ABM25539	Human sec
559	319	24.6	448	6	ADA79952	Human sec	632	319	24.6	448	6	ABM20049	Human sec
560	319	24.6	448	6	ABR96395	Human sec	633	319	24.6	448	6	ABO46955	Human PRO
561	319	24.6	448	6	ABM02546	Human sec	634	319	24.6	448	6	ABO47260	Human PRO
562	319	24.6	448	6	ABR86488	Human sec	635	319	24.6	448	6	ADA83477	Human sec
563	319	24.6	448	6	ABR86793	Human sec	636	319	24.6	448	6	ABR71691	Human sec
564	319	24.6	448	6	ABM16757	Human sec	637	319	24.6	448	6	ABR72301	Human sec
565	319	24.6	448	6	ABM29809	Human sec	638	319	24.6	448	6	ABR98640	Human sec
566	319	24.6	448	6	ABO29233	Human sec	639	319	24.6	448	6	ABO07010	Human sec
567	319	24.6	448	6	ABM24014	Human sec	640	319	24.6	448	6	ABR84963	Human sec
568	319	24.6	448	6	ABM23404	Human sec	641	319	24.6	448	6	ABR73521	Human sec
569	319	24.6	448	6	ADA47187	Human sec	642	319	24.6	448	6	ABR76615	Human sec
570	319	24.6	448	6	ABM22184	Human sec	643	319	24.6	448	6	ABR73216	Human sec
571	319	24.6	448	6	ABO37825	Human sec	644	319	24.6	448	6	ABM18282	Human sec
572	319	24.6	448	6	ABM28589	Human sec	645	319	24.6	448	6	ABO20741	Human sec
573	319	24.6	448	6	ABM28894	Human sec	646	319	24.6	448	6	ABO25484	Human PRO
574	319	24.6	448	6	ABM66538	Human sec	647	319	24.6	448	6	ABO25789	Human PRO
575	319	24.6	448	6	ABM75920	Human sec	648	319	24.6	448	6	ABR94198	Human sec
576	319	24.6	448	6	ABM34200	Human sec	649	319	24.6	448	6	ABR80105	Human sec
577	319	24.6	448	6	ABM34505	Human sec	650	319	24.6	448	6	ABM11445	Human sec
578	319	24.6	448	6	ABO20436	Human sec	651	319	24.6	448	6	ABO33052	Human PRO
579	319	24.6	448	6	ABO221351	Human sec	652	319	24.6	448	6	ABO30758	Human sec
580	319	24.6	448	6	ABO22266	Human sec	653	319	24.6	448	6	ABO31063	Human sec
581	319	24.6	448	6	ABR96700	Human sec	654	319	24.6	448	6	ABM27369	Human sec
582	319	24.6	448	6	ABR85878	Human sec	655	319	24.6	448	6	ABM30114	Human sec
583	319	24.6	448	6	ABR99860	Human sec	656	319	24.6	448	6	ABM05650	Human sec
584	319	24.6	448	6	ABM00411	Human sec	657	319	24.6	448	6	ABM15715	Human sec
585	319	24.6	448	6	ABM00716	Human sec	658	319	24.6	448	6	ABM08700	Human sec
586	319	24.6	448	6	ABO29843	Human sec	659	319	24.6	448	6	ABO42400	Human sec
587	319	24.6	448	6	ABM23709	Human sec	660	319	24.6	448	6	ABO38130	Human sec
588	319	24.6	448	6	ABM29504	Human sec	661	319	24.6	448	6	ABO46040	Human PRO
589	319	24.6	448	6	ABO38435	Human sec	662	319	24.6	448	6	ABM66843	Human sec
590	319	24.6	448	6	ABO45735	Human sec	663	319	24.6	448	6	ABD20520	Human sec
591	319	24.6	448	6	ABM20659	Human sec	664	319	24.6	448	6	ABM19744	Human sec
592	319	24.6	448	6	ADA81679	Human sec	665	319	24.6	448	6	ABO49456	Human sec
593	319	24.6	448	6	ABO16773	Human sec	666	319	24.6	448	6	ABO49761	Human sec
594	319	24.6	448	6	ABO18399	Human sec	667	319	24.6	448	6	ADA78772	Human sec
595	319	24.6	448	6	ABO22826	Human PRO	668	319	24.6	448	6	ABR88318	Human sec
596	319	24.6	448	6	ABO23131	Human PRO	669	319	24.6	448	6	ABM27064	Human sec
597	319	24.6	448	6	ABR92673	Human sec	670	319	24.6	448	6	ABM03461	Human sec
598	319	24.6	448	6	ABR81630	Human sec	671	319	24.6	448	6	ABO39960	Human sec
599	319	24.6	448	6	ABM78054	Human sec	672	319	24.6	448	6	ABO50066	Human sec
600	319	24.6	448	6	ABR89843	Human sec	673	319	24.6	448	7	ABO50981	Human sec
601	319	24.6	448	6	ABM26759	Human sec	674	319	24.6	448	7	ABO5437	Human sec
602	319	24.6	448	6	ABM13885	Human sec	675	319	24.6	448	7	ABR74741	Human sec
603	319	24.6	448	6	ABO28623	Human sec	676	319	24.6	448	7	ABR77220	Human sec
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605	319	24.6	448	6	ABM07480	Human sec	678	319	24.6	448	7	ABR96028	Human sec
606	319	24.6	448	6	ABM04071	Human sec	679	319	24.6	448	7	ABO21961	Human sec
607	319	24.6	448	6	ABO37215	Human sec	680	319	24.6	448	7	ABO20131	Human sec
608	319	24.6	448	6	ABO41790	Human sec	681	319	24.6	448	7	ABO24434	Human sec
609	319	24.6	448	6	ABO35385	Human PRO	682	319	24.6	448	7	ABR86183	Human sec

683	319	24.6	448	7	ABM10835	Abm10835 Human sec	756	319	24.6	448	7	ADB86151	Adb86151 Human sec
684	319	24.6	448	7	ABM76834	Abm76834 Human sec	757	319	24.6	448	7	ABM32249	Abm32249 Human sec
685	319	24.6	448	7	ABR89538	AbR89538 Human sec	758	319	24.6	448	7	ABM32554	Abm32554 Human sec
686	319	24.6	448	7	ABM12865	Abm12865 Human sec	759	319	24.6	448	7	ABM31639	Abm31639 Human sec
687	319	24.6	448	7	ABM05955	Abm05955 Human sec	760	319	24.6	448	7	ABM31029	Abm31029 Human sec
688	319	24.6	448	7	ABO35080	AbO35080 Human PRO	761	319	24.6	448	7	ADD05881	Add05881 Human sec
689	319	24.6	448	7	ABM03156	Abm03156 Human sec	762	319	24.6	448	7	ADC78773	Adc78773 Human PRO
690	319	24.6	448	7	ABM19134	Abm19134 Human sec	763	319	24.6	448	7	ADG02876	Adg02876 Novel hum
691	319	24.6	448	7	ABM19439	Abm19439 Human sec	764	319	24.6	448	7	ADG01583	Adg01583 Novel hum
692	319	24.6	448	7	ABO46650	AbO46650 Human PRO	765	319	24.6	448	7	ADP95758	Adp95758 Novel hum
693	319	24.6	448	7	ABO49151	AbO49151 Human sec	766	319	24.6	448	7	ADG12573	Adg12573 Novel hum
694	319	24.6	448	7	ABR69194	AbR69194 Human sec	767	319	24.6	448	7	ADH09233	Adh09233 Human PRO
695	319	24.6	448	7	ABR89233	AbR89233 Human sec	768	319	24.6	448	7	ADG63696	Adg63696 Human sec
696	319	24.6	448	7	ABR72606	AbR72606 Human sec	769	319	24.6	448	7	ADL33014	Adl33014 Novel hum
697	319	24.6	448	7	ABR74436	AbR74436 Human sec	770	319	24.6	448	7	ADL33014	Adl33014 Novel hum
698	319	24.6	448	7	ABO18704	AbO18704 Human sec	771	319	24.6	448	8	ADL33014	Adl33014 Novel hum
699	319	24.6	448	7	ABR80410	AbR80410 Human sec	772	319	24.6	448	8	ADL33014	Adl33014 Novel hum
700	319	24.6	448	7	ABM01631	Abm01631 Human sec	773	319	24.6	448	8	ADL33014	Adl33014 Novel hum
701	319	24.6	448	7	ABM02241	Abm02241 Human sec	774	319	24.6	448	8	ADL33014	Adl33014 Novel hum
702	319	24.6	448	7	ABR87403	AbR87403 Human sec	775	319	24.6	448	8	ADL33014	Adl33014 Novel hum
703	319	24.6	448	7	ABM12970	Abm12970 Human sec	776	319	24.6	448	8	ADL33014	Adl33014 Novel hum
704	319	24.6	448	7	ABM30724	Abm30724 Human sec	777	319	24.6	448	8	ADL33014	Adl33014 Novel hum
705	319	24.6	448	7	ABM24624	Abm24624 Human sec	778	319	24.6	448	8	ADL33014	Adl33014 Novel hum
706	319	24.6	448	7	ABO29538	AbO29538 Human sec	779	319	24.6	448	8	ADL33014	Adl33014 Novel hum
707	319	24.6	448	7	ABO31368	AbO31368 Human sec	780	319	24.6	448	8	ADL33014	Adl33014 Novel hum
708	319	24.6	448	7	ABM14495	Abm14495 Human sec	781	319	24.6	448	8	ADL33014	Adl33014 Novel hum
709	319	24.6	448	7	ABM09920	Abm09920 Human sec	782	319	24.6	448	8	ADL33014	Adl33014 Novel hum
710	319	24.6	448	7	ABO39045	AbO39045 Human sec	783	319	24.6	448	8	ADL33014	Adl33014 Novel hum
711	319	24.6	448	7	ABM34810	Abm34810 Human sec	784	319	24.6	448	8	ADL33014	Adl33014 Novel hum
712	319	24.6	448	7	ABO51286	AbO51286 Human sec	785	319	24.6	448	8	ADL33014	Adl33014 Novel hum
713	319	24.6	448	7	ABO04112	AbO04112 Human sec	786	319	24.6	448	8	ADL33014	Adl33014 Novel hum
714	319	24.6	448	7	ABO10582	AbO10582 Human PRO	787	319	24.6	448	8	ADL33014	Adl33014 Novel hum
715	319	24.6	448	7	ABR77825	AbR77825 Human sec	788	319	24.6	448	8	ADL33014	Adl33014 Novel hum
716	319	24.6	448	7	ABR79035	AbR79035 Human sec	789	319	24.6	448	8	ADL33014	Adl33014 Novel hum
717	319	24.6	448	7	ABO24129	AbO24129 Human sec	790	319	24.6	448	8	ADL33014	Adl33014 Novel hum
718	319	24.6	448	7	ABR93893	AbR93893 Human sec	791	319	24.6	448	8	ADL33014	Adl33014 Novel hum
719	319	24.6	448	7	ABM01936	Abm01936 Human sec	792	319	24.6	448	8	ADL33014	Adl33014 Novel hum
720	319	24.6	448	7	ABM78359	Abm78359 Human sec	793	319	24.6	448	8	ADL33014	Adl33014 Novel hum
721	319	24.6	448	7	ABR90148	AbR90148 Human sec	794	319	24.6	448	8	ADL33014	Adl33014 Novel hum
722	319	24.6	448	7	ABM27674	Abm27674 Human sec	795	319	24.6	448	8	ADL33014	Adl33014 Novel hum
723	319	24.6	448	7	ABM13275	Abm13275 Human sec	796	319	24.6	448	8	ADL33014	Adl33014 Novel hum
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725	319	24.6	448	7	ABM14190	Abm14190 Human sec	798	319	24.6	448	8	ADL33014	Adl33014 Novel hum
726	319	24.6	448	7	ABM08395	Abm08395 Human sec	799	319	24.6	448	8	ADL33014	Adl33014 Novel hum
727	319	24.6	448	7	ABO40265	AbO40265 Human sec	800	319	24.6	448	8	ADL33014	Adl33014 Novel hum
728	319	24.6	448	7	ABM74700	Abm74700 Human sec	801	319	24.6	448	8	ADL33014	Adl33014 Novel hum
729	319	24.6	448	7	ABM33895	Abm33895 Human sec	802	319	24.6	448	8	ADL33014	Adl33014 Novel hum
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732	319	24.6	448	7	ABR72911	AbR72911 Human sec	805	319	24.6	448	8	ADL33014	Adl33014 Novel hum
733	319	24.6	448	7	ABO15553	AbO15553 Human sec	806	319	24.6	448	8	ADL33014	Adl33014 Novel hum
734	319	24.6	448	7	ABR85268	AbR85268 Human sec	807	319	24.6	448	8	ADL33014	Adl33014 Novel hum
735	319	24.6	448	7	ABO15248	AbO15248 Human sec	808	319	24.6	448	8	ADL33014	Adl33014 Novel hum
736	319	24.6	448	7	ABO17383	AbO17383 Human sec	809	319	24.6	448	8	ADL33014	Adl33014 Novel hum
737	319	24.6	448	7	ABO19841	AbO19841 Human sec	810	319	24.6	448	8	ADL33014	Adl33014 Novel hum
738	319	24.6	448	7	ABM17672	Abm17672 Human sec	811	319	24.6	448	8	ADL33014	Adl33014 Novel hum
739	319	24.6	448	7	ABR85573	AbR85573 Human sec	812	319	24.6	448	8	ADL33014	Adl33014 Novel hum
740	319	24.6	448	7	ABM77139	Abm77139 Human sec	813	319	24.6	448	8	ADL33014	Adl33014 Novel hum
741	319	24.6	448	7	ABO28318	AbO28318 Human sec	814	319	24.6	448	8	ADL33014	Adl33014 Novel hum
742	319	24.6	448	7	ABM23099	Abm23099 Human sec	815	319	24.6	448	8	ADL33014	Adl33014 Novel hum
743	319	24.6	448	7	ABM30419	Abm30419 Human sec	816	319	24.6	448	8	ADL33014	Adl33014 Novel hum
744	319	24.6	448	7	ABM21879	Abm21879 Human sec	817	319	24.6	448	8	ADL33014	Adl33014 Novel hum
745	319	24.6	448	7	ABM21574	Abm21574 Human sec	818	319	24.6	448	8	ADL33014	Adl33014 Novel hum
746	319	24.6	448	7	ABM15105	Abm15105 Human sec	819	319	24.6	448	8	ADL33014	Adl33014 Novel hum
747	319	24.6	448	7	ABO41180	AbO41180 Human sec	820	319	24.6	448	8	ADL33014	Adl33014 Novel hum
748	319	24.6	448	7	ABO36910	AbO36910 Human sec	821	319	24.6	448	8	ADL33014	Adl33014 Novel hum
749	319	24.6	448	7	ABO37520	AbO37520 Human sec	822	319	24.6	448	8	ADL33014	Adl33014 Novel hum
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751	319	24.6	448	7	ABM33590	Abm33590 Human sec	824	319	24.6	448	8	ADL33014	Adl33014 Novel hum
752	319	24.6	448	7	ABO46345	AbO46345 Human PRO	825	319	24.6	448	8	ADL33014	Adl33014 Novel hum
753	319	24.6	448	7	ADA82843	Ada82843 Human sec	826	319	24.6	448	8	ADL33014	Adl33014 Novel hum
754	319	24.6	448	7	ABM31944	Abm31944 Human sec	827	319	24.6	448	8	ADL33014	Adl33014 Novel hum
755	319	24.6	448	7	ABM31334	Abm31334 Human sec	828	319	24.6	448	8	ADL33014	Adl33014 Novel hum

829	318	24.5	915	6	ADA67467	Ada67467 Human PRO	902	318	24.5	915	7	ADB34411	ADB34411 Human PRO
830	318	24.5	915	6	ADB30474	ADB30474 Human PRO	903	318	24.5	915	7	ADB35515	ADB35515 Human PRO
831	318	24.5	915	6	ADA85770	ADA85770 Novel hum	904	318	24.5	915	7	ADB33859	ADB33859 Human PRO
832	318	24.5	915	6	ADA96982	ADA96982 Human PRO	905	318	24.5	915	7	ADB34963	ADB34963 Human PRO
833	318	24.5	915	6	ADA79286	ADA79286 Human PRO	906	318	24.5	915	7	ADB36067	ADB36067 Human PRO
834	318	24.5	915	6	ADA87425	ADA87425 Novel hum	907	318	24.5	915	7	ADB46462	ADB46462 Novel hum
835	318	24.5	915	6	ADB16627	ADB16627 Human PRO	908	318	24.5	915	7	ADC28342	ADC28342 Human sec
836	318	24.5	915	6	ABO34822	ABO34822 Human PRO	909	318	24.5	915	7	ADC39542	ADC39542 Human sec
837	318	24.5	915	6	ADA16070	ADA16070 Human sec	910	318	24.5	915	7	ADC40056	ADC40056 Human sec
838	318	24.5	915	6	ADA91719	ADA91719 Novel hum	911	318	24.5	915	7	ADC18884	ADC18884 Human sec
839	318	24.5	915	6	ADB14782	ADB14782 Human PRO	912	318	24.5	915	7	ADC34180	ADC34180 Human sec
840	318	24.5	915	6	ADB18743	ADB18743 Novel hum	913	318	24.5	915	7	ADC29235	ADC29235 Human sec
841	318	24.5	915	6	ADA93958	ADA93958 Human PRO	914	318	24.5	915	7	ADC28766	ADC28766 Human sec
842	318	24.5	915	6	ADB19854	ADB19854 Novel hum	915	318	24.5	915	7	ADC40651	ADC40651 Human sec
843	318	24.5	915	6	ADB13166	ADB13166 Human PRO	916	318	24.5	915	7	ADC19308	ADC19308 Human sec
844	318	24.5	915	6	ABO43295	ABO43295 Novel hum	917	318	24.5	915	7	ADC33756	ADC33756 Human sec
845	318	24.5	915	6	ADA74420	ADA74420 Human PRO	918	318	24.5	915	7	ADC12826	ADC12826 Human sec
846	318	24.5	915	6	ADA42215	ADA42215 Human sec	919	318	24.5	915	7	ADC50335	ADC50335 Novel hum
847	318	24.5	915	6	ADB24653	ADB24653 Human PRO	920	318	24.5	915	7	ADC71882	ADC71882 Novel hum
848	318	24.5	915	6	ADA82177	ADA82177 Human PRO	921	318	24.5	915	7	ADC59861	ADC59861 Novel hum
849	318	24.5	915	6	ADA75140	ADA75140 Human PRO	922	318	24.5	915	7	ADC52868	ADC52868 Novel hum
850	318	24.5	915	6	ADA85218	ADA85218 Novel hum	923	318	24.5	915	7	ADC57222	ADC57222 Novel hum
851	318	24.5	915	6	ADA84666	ADA84666 Novel hum	924	318	24.5	915	7	ADC60413	ADC60413 Novel hum
852	318	24.5	915	6	ABO17500	ABO17500 Human PRO	925	318	24.5	915	7	ADC50888	ADC50888 Novel hum
853	318	24.5	915	6	ADB29922	ADB29922 Human PRO	926	318	24.5	915	7	ADC65415	ADC65415 Human PRO
854	318	24.5	915	6	ADA80450	ADA80450 Human PRO	927	318	24.5	915	7	ADC54513	ADC54513 Novel hum
855	318	24.5	915	6	ADA75692	ADA75692 Human PRO	928	318	24.5	915	7	ADC53474	ADC53474 Novel hum
856	318	24.5	915	6	ADA46917	ADA46917 Human PRO	929	318	24.5	915	7	ADC58997	ADC58997 Novel hum
857	318	24.5	915	6	ADB25213	ADB25213 Human PRO	930	318	24.5	915	7	ADC55875	ADC55875 Novel hum
858	318	24.5	915	6	ADA93389	ADA93389 Human PRO	931	318	24.5	915	7	ADC58445	ADC58445 Novel hum
859	318	24.5	915	6	ADB26739	ADB26739 Human PRO	932	318	24.5	915	7	ADC12278	ADC12278 Human sec
860	318	24.5	915	6	ADB31026	ADB31026 Human PRO	933	318	24.5	915	7	ADC90111	ADC90111 Novel hum
861	318	24.5	915	6	ADA60954	ADA60954 Homo sapi	934	318	24.5	915	7	ADC69530	ADC69530 Human PRO
862	318	24.5	915	6	ADB24101	ADB24101 Human PRO	935	318	24.5	915	7	ADC48419	ADC48419 Human PRO
863	318	24.5	915	6	ADA96430	ADA96430 Human PRO	936	318	24.5	915	7	ADC40948	ADC40948 Human PRO
864	318	24.5	915	6	ADA81002	ADA81002 Human PRO	937	318	24.5	915	7	ADC09948	ADC09948 Novel hum
865	318	24.5	915	6	ADA95878	ADA95878 Human PRO	938	318	24.5	915	7	ADC04523	ADC04523 Novel hum
866	318	24.5	915	6	ADB26187	ADB26187 Human PRO	939	318	24.5	915	7	ADC80479	ADC80479 Novel hum
867	318	24.5	915	6	ADB21672	ADB21672 Novel hum	940	318	24.5	915	7	ADC10986	ADC10986 Human PRO
868	318	24.5	915	7	ADA77451	ADA77451 Human PRO	941	318	24.5	915	7	ADC47867	ADC47867 Human PRO
869	318	24.5	915	7	ADB18191	ADB18191 Human PRO	942	318	24.5	915	7	ADC04833	ADC04833 Human sec
870	318	24.5	915	7	ADA86874	ADA86874 Novel hum	943	318	24.5	915	7	ADC79927	ADC79927 Novel hum
871	318	24.5	915	7	ADA16494	ADA16494 Human sec	944	318	24.5	915	7	ADC09396	ADC09396 Human PRO
872	318	24.5	915	7	ADA12923	ADA12923 Human sec	945	318	24.5	915	7	ADC03839	ADC03839 Human sec
873	318	24.5	915	7	ADA41791	ADA41791 Human sec	946	318	24.5	915	7	ADC03415	ADC03415 Human sec
874	318	24.5	915	7	ADA87977	ADA87977 Novel hum	947	318	24.5	915	7	ADC41109	ADC41109 Novel hum
875	318	24.5	915	7	ADA46365	ADA46365 Novel hum	948	318	24.5	915	7	ADC52248	ADC52248 Human PRO
876	318	24.5	915	7	ADA17138	ADA17138 Human sec	949	318	24.5	915	7	ADC52988	ADC52988 Human PRO
877	318	24.5	915	7	ADA42641	ADA42641 Human sec	950	318	24.5	915	7	ADC53540	ADC53540 Novel hum
878	318	24.5	915	7	ADB28395	ADB28395 Human PRO	951	318	24.5	915	7	ADC51696	ADC51696 Human PRO
879	318	24.5	915	7	ADB28947	ADB28947 Human PRO	952	318	24.5	915	7	ADC02495	ADC02495 Human PRO
880	318	24.5	915	7	ADA76899	ADA76899 Human PRO	953	318	24.5	915	7	ADC01929	ADC01929 Human PRO
881	318	24.5	915	7	ADA88529	ADA88529 Novel hum	954	318	24.5	915	7	ADC54111	ADC54111 Novel hum
882	318	24.5	915	7	ADA97534	ADA97534 Human PRO	955	318	24.5	915	7	ADC92428	ADC92428 Human PRO
883	318	24.5	915	7	ADB27291	ADB27291 Human PRO	956	318	24.5	915	7	ADC91324	ADC91324 Human PRO
884	318	24.5	915	7	ADB22224	ADB22224 Novel hum	957	318	24.5	915	7	ADC03938	ADC03938 Human PRO
885	318	24.5	915	7	ABO17561	ABO17561 Human PRO	958	318	24.5	915	7	ADC32235	ADC32235 Novel hum
886	318	24.5	915	7	ADA66915	ADA66915 Human PRO	959	318	24.5	915	7	ADC22167	ADC22167 Human PRO
887	318	24.5	915	7	ADB22776	ADB22776 Human PRO	960	318	24.5	915	7	ADC79391	ADC79391 Human PRO
888	318	24.5	915	7	ADB23549	ADB23549 Human PRO	961	318	24.5	915	7	ADC41927	ADC41927 Human PRO
889	318	24.5	915	7	ADA92271	ADA92271 Novel hum	962	318	24.5	915	7	ADC17744	ADC17744 Human PRO
890	318	24.5	915	7	ADB15334	ADB15334 Human PRO	963	318	24.5	915	7	ADC91876	ADC91876 Human PRO
891	318	24.5	915	7	ADB38586	ADB38586 Novel hum	964	318	24.5	915	7	ADC33339	ADC33339 Novel hum
892	318	24.5	915	7	ADB38034	ADB38034 Novel hum	965	318	24.5	915	7	ADC33891	ADC33891 Novel hum
893	318	24.5	915	7	ADB66506	ADB66506 Novel hum	966	318	24.5	915	7	ADC79943	ADC79943 Human PRO
894	318	24.5	915	7	ADB89586	ADB89586 Human PRO	967	318	24.5	915	7	ADC92980	ADC92980 Human PRO
895	318	24.5	915	7	ADB90318	ADB90318 Human PRO	968	318	24.5	915	7	ADC19400	ADC19400 Human PRO
896	318	24.5	915	7	ADB77560	ADB77560 Human sec	969	318	24.5	915	7	ADC34667	ADC34667 Human sec
897	318	24.5	915	7	ADB39419	ADB39419 Novel hum	970	318	24.5	915	7	ADC18848	ADC18848 Human PRO
898	318	24.5	915	7	ADB74696	ADB74696 Human sec	971	318	24.5	915	7	ADC43044	ADC43044 Human PRO
899	318	24.5	915	7	ADB47042	ADB47042 Novel hum	972	318	24.5	915	7	ADC95833	ADC95833 Human PRO
900	318	24.5	915	7	ADB86649	ADB86649 Human PRO	973	318	24.5	915	7	ADC22719	ADC22719 Human PRO
901	318	24.5	915	7	ADB77254	ADB77254 Novel hum	974	318	24.5	915	7	ADC78837	ADC78837 Human PRO

975 318 24.5 915 7 ADE32787
976 318 24.5 915 7 ADE42479
977 318 24.5 915 7 AD80495
978 318 24.5 915 7 AD80495
979 318 24.5 915 7 AD89523
980 318 24.5 915 7 ADE40807
981 318 24.5 915 7 ADE04606
982 318 24.5 915 7 ADE92735
983 318 24.5 915 7 ADG21444
984 318 24.5 915 7 ADG23085
985 318 24.5 915 7 ADG97420
986 318 24.5 915 7 ADG80484
987 318 24.5 915 7 ADG79932
988 318 24.5 915 7 ADH59150
989 318 24.5 915 7 ADH55224
990 318 24.5 915 7 ADH55776
991 318 24.5 915 7 ADI37929
992 318 24.5 915 7 ADI63995
993 318 24.5 915 7 ADI64944
994 318 24.5 915 7 ADI63443
995 318 24.5 915 7 ADH81857
996 318 24.5 915 7 ADH81305
997 318 24.5 915 7 ADJ26197
998 318 24.5 915 7 ADM82474
999 318 24.5 915 7 ADN15873
1000 318 24.5 915 7 ADN16502
ADN15321

ALIGNMENTS

RESULT 1
AAR99414
ID AAR99414 standard; protein; 678 AA.
XX
AC AAR99414;
XX
XX
DT 04-DEC-1996 (first entry)
XX
DE Human gas6 protein, an S protein homologue and axl receptor ligand.
XX
KW Axl receptor ligand; human protein S homologue; growth factor;
KW myeloid cell proliferation; myeloid malignancy; regulation; prevention;
KW recombinant production.
XX
OS Homo sapiens.
XX
PN US5538861-A.
XX
PD 23-JUL-1996.
XX
PF 29-JUL-1994; 94US-00282141.
XX
PR 29-JUL-1994; 94US-00282141.
XX
PA (AMGE-) AMGEN INC.
PA (SCHN/) SCHNEIDER C.
XX
PI Manfioletti G, Varnum BC, Schneider C, Avanzi G, Brancolini C;
XX
DR WPI; 1996-353825/35.
DR N-PSDB; AAT41544.
XX
PT DNA encoding gas6, the axl receptor ligand - useful to regulate growth of
PT myeloid cells and malignancies.
PS Claim 1; Col 19-22; 36pp; English.
XX
CC AAR99414 is the gas6 protein [from the growth arrest specific gene number
CC 6]. The gas6 protein has homology to human protein S which functions as a
CC cofactor in a protease cascade that regulates coagulation. Gas6
CC expression, as with gas1 and gas2, is associated with cell growth arrest
CC which suggests a possible role of gas6 in the regulation of cell growth.

CC In fact the gas6 protein is an axl receptor (axlr) ligand and a growth
CC factor for any cells expressing axlr e.g. bone marrow, spleen, thymus,
CC ovary, heart, intestine and lung cells. The axl receptor is involved in
CC myeloid cell proliferation and myeloid malignancies, so gas6 may regulate
CC growth of such cells
XX
SQ Sequence 678 AA;

Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.6e-83; Indels 0; Gaps 0;
Matches 227; Conservative 0; Mismatches 0;
QY 1 PRYLDCKNKYKSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDCKNKYKSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY 61 GRLCDKDVNECSQNGGCLQICHNKPGSFHCSHSGFELSDGRTQCIDDECAUSEACGE 120
DB 150 GRLCDKDVNECSQNGGCLQICHNKPGSFHCSHSGFELSDGRTQCIDDECAUSEACGE 209
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269
QY 181 LSQDMDCEDILPCVPFSAKSVKSLYLGRMFSGTPVIRLRFKELQP 227
DB 270 LSQDMDCEDILPCVPFSAKSVKSLYLGRMFSGTPVIRLRFKELQP 316

RESULT 2

AAW46463
ID AAW46463 standard; protein; 678 AA.
XX
AC AAW46463;
XX
DT 15-MAY-1998 (first entry)
XX
DE Human growth arrest specific-gene 6 (gas6) protein.
XX
KW Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
KW receptor tyrosine kinase; regulation; protease cascade; insulin;
KW growth regulation; serum-free culture medium; human; Schwann cell;
KW receptor activator; erbB receptor; heregulin; CAMP level; proliferation;
KW treatment; nervous system injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 49..89
FT FT /note= "A domain of gas6"
FT Domain 90..117
FT FT /note= "B domain of gas6 comprising a thrombin sensitive
FT FT loop"
FT Domain 118..278
FT FT /note= "C domain of gas6, contains 4 epidermal growth
FT FT factor-like repeats"
FT Domain 279..678
FT FT /note= "D domain of gas6, homologous to steroid binding
FT FT hormone"
FT Domain 314..471
FT FT /note= "G domain 1"
FT Domain 503..671
FT FT /note= "G domain 2"
XX US5714385-A.
PN
XX
PD 03-FEB-1998.
XX
PF 10-MAY-1995; 95US-00435434.
XX
PR 10-MAY-1995; 95US-00435434.
XX
PA (GETH) GENENTECH INC.

XX Chen J, Mather JP, Li R;
 XX WPI; 1998-129864/12.
 XX Medium for culturing human Schwann cells - is serum-free and contains Rse
 XX receptor activator and other mitogens.
 XX Disclosure; Fig 2; Sipp; English.
 XX
 CC The present sequence represents a human growth arrest specific-gene 6
 CC (gas6) protein which is able to activate the Rse and Axl receptor. Rse is
 CC a receptor tyrosine kinase that is preferentially expressed in the adult
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise cAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries
 XX
 XX Sequence 678 AA;
 Query Match 100.0%; Score 1297; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.6e-83;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRLDCINKYGPYTKNSGFATCVNLPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 60
 DB 90 PRLDCINKYGPYTKNSGFATCVNLPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 149
 QY 61 GRLCDKDVNECSQENGCGCLQICHNKPFSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 120
 DB 150 GRLCDKDVNECSQENGCGCLQICHNKPFSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 209
 QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCEQVNSPGSYTCHDGRGGLK 180
 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCEQVNSPGSYTCHDGRGGLK 269
 QY 181 LSQMDTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 227
 DB 270 LSQMDTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 316
 RESULT 3
 AAY29794
 ID AAY29794 standard; protein; 678 AA.
 XX AAY29794;
 XX
 DT 15-NOV-1999 (first entry)
 DE Human growth arrest-specific gene 6 protein.
 XX
 KW Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; gas6;
 KW growth arrest-specific gene 6; proliferation; differentiation;
 KW Gli3 cell; Schwann cell; fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN US5955420-A.
 XX
 PD 21-SEP-1999.
 XX
 PF 10-MAY-1995; 95US-00438864.
 XX
 PR 10-MAR-1995; 95US-00402253.
 XX
 PA (GETH) GENENTECH INC.

XX Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
 XX WPI; 1999-539585/45.
 XX Activation of the Rse receptor on a cell, useful for promoting cell
 XX proliferation and differentiation.
 XX Disclosure; Fig 2; 48pp; English.
 XX
 CC A method has been developed for activating the Rse receptor on a cell.
 CC The method comprises exposing the receptor to the exogenous growth arrest
 CC specific gene 6 (gas6) polypeptide. The method is useful for enhancing
 CC cell proliferation and cell differentiation. The present sequence
 CC represents human gas6 given in the present invention
 XX
 XX Sequence 678 AA;
 Query Match 100.0%; Score 1297; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.6e-83;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRLDCINKYGPYTKNSGFATCVNLPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 60
 DB 90 PRLDCINKYGPYTKNSGFATCVNLPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 149
 QY 61 GRLCDKDVNECSQENGCGCLQICHNKPFSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 120
 DB 150 GRLCDKDVNECSQENGCGCLQICHNKPFSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 209
 QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCEQVNSPGSYTCHDGRGGLK 180
 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCEQVNSPGSYTCHDGRGGLK 269
 QY 181 LSQMDTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 227
 DB 270 LSQMDTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 316
 RESULT 4
 AAY57383
 ID AAY57383 standard; protein; 678 AA.
 XX AAY57383;
 XX
 DT 19-JUN-2000 (first entry)
 DE Amino acid sequence of human gas6 (h gas6) protein.
 XX
 KW Nervous system; Schwann cell; mitogen; Rse/Axl receptor activator;
 KW central nervous system; peripheral nervous system; injury; trauma;
 KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 KW protein S.
 XX
 OS Homo sapiens.
 XX
 PN US6033660-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 10-MAY-1995; 95US-00438862.
 XX
 PR 10-MAY-1995; 95US-00438862.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Mather JP, Chen J, Li R;
 XX WPI; 2000-246046/21.
 XX Repairing nervous system injuries in mammals, by administering human
 XX Schwann cells that have been propagated in medium supplemented with
 XX mitogens.

XX Disclosure; Fig 2; 52pp; English.

XX The invention relates to a method for treating nervous system injuries in

CC mammals by administering human Schwann cells (SC) that have been cultured

CC in serum-free medium. The serum-free medium is a nutrient solution

CC supplemented with two mitogens, one of which, is a Ret/Axl receptor

CC activator, to increase survival and proliferation of SC. The method is

CC used to treat (or prevent) central or peripheral nervous system injury,

CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,

CC or lesions associated with nutritional deficiencies, systemic disease,

CC toxins or demyelination. Culturing cells in the specified medium allows

CC proliferation of adult SC for use in autologous transplants. The present

CC sequence represents a human gas6 (h gas6) protein, having 44% sequence

CC identity to human protein S. Gas6 is demonstrated to be a potent growth/

CC survival factor for SCs in defined serum-free culture

XX

SQ Sequence 678 AA;

Query Match 100.0%; Score 1297; DB 3; Length 678;

Best Local Similarity 100.0%; Pred. No. 2.6e-83;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60

DB 90 PRYLDCKINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149

QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFHCSHSGFELSSDGRTCQDIDECADSEACGE 120

DB 150 GRLCDKDVNECSQENGGLQICHNKPFSFHCSHSGFELSSDGRTCQDIDECADSEACGE 209

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180

DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269

QY 181 LSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGTGPVIRLRFKRLQ 227

DB 270 LSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGTGPVIRLRFKRLQ 316

RESULT 5

ADL83231

ID ADL83231 standard; protein; 678 AA.

XX

AC ADL83231;

XX

DT 17-JUN-2004 (first entry)

DE Human PRO12613, SEQ ID 433.

XX

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;

KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;

KW Gene Therapy; PRO; B cell related disorder; cancer;

KW immune-mediated inflammatory disease; human.

XX

OS Homo sapiens.

XX

XX WO2004024097-A2.

PN

XX

PD 25-MAR-2004.

XX

PF 15-SEP-2003; 2003WO-US029097.

XX

XX 16-SEP-2002; 2002US-0411392P.

PR

XX (GETH) GENENTECH INC.

XX

XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;

PI Wu TD;

XX

XX WPI; 2004-329389/30.

DR N-PSDB; ADL83230.

XX

PT New PRO polypeptide, useful for diagnosing and treating a B cell related

PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune

PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX

PS Claim 10; Fig 433; 695pp; English.

XX

CC The present invention relates to PRO proteins and their coding sequences.

CC The PRO proteins are useful for diagnosing and treating a B cell related

CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyasaccharide

CC antigen unresponsiveness, selective IGA deficiency, selective IgM

CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with

CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's

CC lymphoma, intermediate lymphoma, follicular lymphoma, type II

CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic

CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or

CC ankylosing spondylitis. The PRO proteins are also useful for preparing a

CC medicament for treating a condition that is responsive to the PRO

CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO

CC coding sequences are useful as hybridization probes in chromosome and

CC gene mapping, in preparing PRO proteins, or in generating transgenic

CC animals or knockout animals, which in turn are useful in the development

CC and screening of therapeutically useful reagents.

XX

SQ Sequence 678 AA;

Query Match 100.0%; Score 1297; DB 8; Length 678;

Best Local Similarity 100.0%; Pred. No. 2.6e-83;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60

DB 90 PRYLDCKINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149

QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFHCSHSGFELSSDGRTCQDIDECADSEACGE 120

DB 150 GRLCDKDVNECSQENGGLQICHNKPFSFHCSHSGFELSSDGRTCQDIDECADSEACGE 209

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180

DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269

QY 181 LSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGTGPVIRLRFKRLQ 227

DB 270 LSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGTGPVIRLRFKRLQ 316

RESULT 6

ADM40825

ID ADM40825 standard; protein; 678 AA.

XX

AC ADM40825;

XX

DT 01-JUL-2004 (first entry)

XX

DE Human Gas6 protein SEQ ID NO:3.

XX

XX growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;

KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;

KW receptor internalisation; cell proliferation; cell apoptosis prevention;

KW signaling molecule; cell marker; human.

XX

OS Homo sapiens.

XX

XX WO2004029209-A2.

PN

XX

PD 08-APR-2004.

XX

XX 24-SEP-2003; 2003WO-US030330.

PF

XX 24-SEP-2002; 2002US-0413157P.

PR

XX (CENZ) CENTOCOR INC.

XX

```
PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
XX WPI; 2004-316097/29.
XX
XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
XX manufacturing medicines or for identifying inhibitors of Gas6 and its
XX receptors.
XX
XX Disclosure; SEQ ID NO 3; 28pp; English.
XX
XX The present invention describes an isolated growth arrest specific gene 6
XX (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
XX terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
XX ID NO:2, ADM40824), or a polyhistidine sequence. The variant Gas6
XX polypeptide has 75% identity to native human Gas6 protein. Also
XX described: (1) a recombinant DNA molecule encoding the amino acid
XX sequence of the polypeptide described above; (2) a vector comprising the
XX above nucleic acid; (3) a host cell comprising the vector, where the host
XX cell is of mammalian origin; and (4) a composition comprising the
XX polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
XX activity. The composition is useful for manufacturing medicines or for
XX identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
XX may also be used for Gas6-dependent receptor phosphorylation, receptor
XX internalisation, cell proliferation, prevention of cell apoptosis, or
XX induction of signaling molecules or cell markers. The present sequence
XX represents the human Gas6 protein from the present invention.
XX
XX Sequence 678 AA;
XX
XX Query Match 100.0%; Score 1297; DB 8; Length 678;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-83;
XX Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PRYLDICINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 60
XX Db |||||
XX
XX QY 61 GRLCDKDVNECSQENGGCLQICHNKPFSFHCSCHSFELSDDGRTCDQIDECADSEACGE 120
XX Db |||||
XX
XX QY 150 GRLCDKDVNECSQENGGCLQICHNKPFSFHCSCHSFELSDDGRTCDQIDECADSEACGE 209
XX Db |||||
XX
XX QY 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
XX Db |||||
XX
XX QY 210 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269
XX Db |||||
XX
XX QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227
XX Db |||||
XX
XX QY 270 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 316
XX Db |||||
XX
XX RESULT 7
XX ID ADN60275 standard; protein; 678 AA.
XX
XX AC ADN60275;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human growth arrest-specific 6 (GAS6) protein.
XX
XX KW angiogenesis modulator; tumorigenesis modulator; angiogenesis; Axl;
XX tubulin cofactor D; transglutaminase 2; cytosine deaminase;
XX peptidase M41; paralogin; CD13 aminopeptidase; PPK-1; zip kinase; Gas6;
XX SRM160; non-muscle myosin heavy chain; calmodulin 2; symporter;
XX semaphorin; zinc finger helix; plexin-A2; deoxycytidylate deaminase;
XX sugar transporter; tumorigenesis; antiangiogenic; cytosatic;
XX cerebroprotective; vasotropic; antiinfertility; cardiac;
XX antibody therapy; antisense therapy; RNA interference therapy;
XX RNAi therapy; cancer; stroke; infertility; heart disease; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004039955-A2.
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XX 13-MAY-2004.
XX
XX 29-OCT-2003; 2003WO-US034281.
XX
XX 29-OCT-2002; 2002US-0421989P.
XX 17-OCT-2003; 2003US-0512251P.
XX
XX (RIGE-) RIGEL PHARM INC.
XX
XX Lorens JB, Atchison RE, Frieria A, Holland S;
XX WPI; 2004-376181/35.
XX N-PSDB; ADN60274.
XX
XX Identifying a compound that modulates angiogenesis or tumorigenesis,
XX useful in diagnosing and treating angiogenesis, cancer, stroke,
XX infertility and heart disease, comprises contacting the compound with
XX angiogenesis polypeptide.
XX
XX Disclosure; Page 65; 105pp; English.
XX
XX The present invention describes a method for identifying a compound that
XX modulates angiogenesis or tumorigenesis. The method comprises: (a)
XX contacting the compound with angiogenesis polypeptide, e.g. Axl, tubulin
XX cofactor D, transglutaminase 2, cytosine deaminase, peptidase M41
XX (paralogin), CD13 aminopeptidase, PPK-1, zip kinase, Gas6, SRM160, non-
XX muscle myosin heavy chain, calmodulin 2, novel symporter, novel
XX semaphorin, novel zinc finger helix (FLJ22611), plexin-A2,
XX deoxycytidylate deaminase or novel sugar transporter; (b) determining the
XX functional effector of the compound upon the angiogenesis polypeptide or
XX the physical effect of the compound upon the target polypeptide or its
XX fragment or inactive variant; and (c) determining the chemical or
XX phenotypic effect of the compound upon a cell comprising the target
XX polypeptide or its fragment or inactive variant, thus identifying a
XX compound that modulates cell cycle arrest. Also described is a method of
XX modulating angiogenesis in a subject. The angiogenesis or tumorigenesis
XX modulating compound has antiangiogenic, cytostatic, cerebroprotective,
XX vasotropic, antiinfertility and cardiac activities, and can be used in
XX antibody, antisense and RNA interference (RNAi) therapies. The method is
XX useful in identifying a compound that modulates angiogenesis. The methods
XX and compounds or compositions are useful in diagnosing and treating
XX angiogenesis, cancer, stroke, infertility and heart disease. The present
XX sequence represents a human growth arrest-specific 6 (GAS6) protein,
XX which is used in the exemplification of the present invention.
XX
XX Sequence 678 AA;
XX
XX Query Match 100.0%; Score 1297; DB 8; Length 678;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-83;
XX Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PRYLDICINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 60
XX Db |||||
XX
XX QY 90 PRYLDICINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 149
XX Db |||||
XX
XX QY 61 GRLCDKDVNECSQENGGCLQICHNKPFSFHCSCHSFELSDDGRTCDQIDECADSEACGE 120
XX Db |||||
XX
XX QY 150 GRLCDKDVNECSQENGGCLQICHNKPFSFHCSCHSFELSDDGRTCDQIDECADSEACGE 209
XX Db |||||
XX
XX QY 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
XX Db |||||
XX
XX QY 210 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269
XX Db |||||
XX
XX QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227
XX Db |||||
XX
XX QY 270 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 316
XX Db |||||
XX
XX RESULT 8
XX ID ADD48757
XX ADD48757 standard; protein; 679 AA.
XX
XX
```

AC ADD48757;
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein L13720, SEQ ID NO 14467.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; L13720.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 1297; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.6e-83;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKYKSPYTKNSGFATCVQNLFDQCTPNFCDKGTQACQDLMGNFCCCKAGWG 60
|||||

Db 90 PRYLDCKYKSPYTKNSGFATCVQNLFDQCTPNFCDKGTQACQDLMGNFCCCKAGWG 149
QY 61 GRLCDKDVNECSQENGGCLQICHNKPGSFHCSCHSGFELSDGRTCODIDECADSEACGE 120
|||||
Db 150 GRLCDKDVNECSQENGGCLQICHNKPGSFHCSCHSGFELSDGRTCODIDECADSEACGE 209
|||||
QY 121 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTTCDCGRGLK 180
|||||
Db 210 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTTCDCGRGLK 269
|||||
QY 181 LSQDMTCEBILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
|||||
Db 270 LSQDMTCEBILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 316
|||||

RESULT 9
ADM40823
ID ADM40823 standard; protein; 686 AA.
XX
AC ADM40823;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human Gas6 protein with a C-terminal epitope tag SEQ ID NO:1.
XX
KW growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
KW receptor internalisation; cell proliferation; cell apoptosis prevention;
KW signaling molecule; cell marker; human.
XX
OS Homo sapiens.
OS
PN WO2004029209-A2.
XX
PD 08-APR-2004.
XX
PF 24-SEP-2003; 2003WO-US030330.
XX
PR 24-SEP-2002; 2002US-0413157P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
XX WPI; 2004-316097/29.
XX
PT New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
PT manufacturing medicines or for identifying inhibitors of Gas6 and its
PT receptors.
XX
PS Claim 2; SEQ ID NO 1; 28pp; English.
XX
CC The present invention describes an isolated growth arrest specific gene 6
CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
CC ID NO:2, ADM40824), or a polyhistidine sequence. The variant Gas6
CC polypeptide has 75% identity to native human Gas6 protein. Also
CC described: (1) a recombinant DNA molecule encoding the amino acid
CC sequence of the polypeptide described above; (2) a vector comprising the
CC above nucleic acid; (3) a host cell comprising the vector, where the host
CC cell is of mammalian origin; and (4) a composition comprising the
CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
CC activity. The composition is useful for manufacturing medicines or for
CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
CC may also be used for Gas6-dependent receptor phosphorylation, receptor
CC internalisation, cell proliferation, prevention of cell apoptosis, or
CC induction of signaling molecules or cell markers. The present sequence
CC represents the human Gas6 protein with an epitope tag fused at the C-
CC terminus, from the present invention.
XX
SQ Sequence 686 AA;

Query Match 100.0%; Score 1297; DB 8; Length 686;

Best Local Similarity 100.0%; Pred. No. 2.6e-83; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDICINIKYSGPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDICINIKYSGPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY 61 GRLCDKDVNECSQENGCGCLOICHNKPFSFHCSCHSFELSSDGRTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQENGCGCLOICHNKPFSFHCSCHSFELSSDGRTCQDIDECADSEACGE 209
QY 121 ARCKNLPGSVSLCDRGGFAYSSOEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB 210 ARCKNLPGSVSLCDRGGFAYSSOEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 269
QY 181 LSQDMTDCEDILPCVPFVSVAKSLSYLGRMFSGTPVIRLRFKRLQ 227
DB 270 LSQDMTDCEDILPCVPFVSVAKSLSYLGRMFSGTPVIRLRFKRLQ 316

RESULT 10
ADQ67207
ID ADQ67207 standard; protein; 624 AA.
XX
AC ADQ67207;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human protein sequence #2180.
XX
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
WPI: 2004-535376/52.
DR N-PSDB; ADQ65019.
XX
Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 4368; 2449pp; English.
XX
The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.
XX
SQ Sequence 624 AA;

Query Match 97.8%; Score 1269; DB 8; Length 624;
Best Local Similarity 99.6%; Pred. No. 2.3e-81;

Matches 222; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DCINKYSGPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWGRLC 64
DB 40 NCINKYSGPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWGRLC 99
QY 65 KDVNECSQENGCGCLOICHNKPFSFHCSCHSFELSSDGRTCQDIDECADSEACGEARCK 124
DB 100 KDVNECSQENGCGCLOICHNKPFSFHCSCHSFELSSDGRTCQDIDECADSEACGEARCK 159
QY 125 NLPGSVSLCDRGGFAYSSOEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLKLSQD 184
DB 160 NLPGSVSLCDRGGFAYSSOEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLKLSQD 219
QY 185 MDTCEDILPCVPFVSVAKSLSYLGRMFSGTPVIRLRFKRLQ 227
DB 220 MDTCEDILPCVPFVSVAKSLSYLGRMFSGTPVIRLRFKRLQ 262

RESULT 11
AAW46462
ID AAW46462 standard; protein; 673 AA.
XX
AC AAW46462;
XX
DT 15-MAY-1998 (first entry)
XX
DE Murine growth arrest specific-gene 6 (gas6) protein.
XX
KW Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
KW receptor tyrosine kinase; regulation; protease cascade; insulin;
KW growth regulation; serum-free culture medium; human; Schwann cell;
KW receptor activator; erbB receptor; heregulin; cAMP level; proliferation;
KW treatment; nervous system injury.
XX
OS Mus sp.
XX
PN US5714385-A.
XX
PD 03-FEB-1998.
XX
PF 10-MAY-1995; 95US-00435434.
XX
PR 10-MAY-1995; 95US-00435434.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Mather JP, Li R;
XX
WPI: 1998-129864/12.
XX
Medium for culturing human Schwann cells - is serum-free and contains Rse
PT receptor activator and other mitogens.
XX
PS Disclosure; Fig 2; 51pp; English.
XX
The present sequence represents a murine growth arrest specific-gene 6
CC (gas6) protein which is able to activate the Rsa and Axl receptor. Rse is
CC a receptor tyrosine kinase that is preferentially expressed in the adult
CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
CC regulation of a protease cascade relevant in growth regulation. The
CC protein is used in a serum-free culture medium for culturing human
CC Schwann cells, which does not support fibroblast growth. Gas6 functions
CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
CC mitogenic agent e.g. insulin or an erbB receptor activator such as
CC heregulin, is also required to raise cAMP levels and enhance survival or
CC proliferation of human Schwann cells. The culture medium additionally
CC comprises a molecule or composition that provides Fe ions to the Schwann
CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
CC cells can be used to treat patients with nervous system injuries
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 2; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGGCLQICHNKPFGSFCVCHSGFELSDGRTCDIDECADSEACGE 120
DB 87 PRYQCMRKRYGRPEKNPDPFAKCVQNLDPQCTPNPCDRKGTQACODLMGNFFCVCCTDGGW 146

QY 61 GRLCDKDVNECSQENGGCLQICHNKPFGSFCVCHSGFELSDGRTCDIDECADSEACGE 120
DB 147 GRLCDKDVNECSQENGGCLQICHNKPFGSFCVCHSGFELSDGRTCDIDECADSEACGE 206

QY 121 ARCKNLPGSYSCCLDEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 180
DB 207 ARCKNLPGSYSCCLDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266

QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 267 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 12
AA29793
ID AA29793 standard; protein; 673 AA.
XX
AC AA29793;
DT 15-NOV-1999 (first entry)
XX
DE Murine growth arrest-specific gene 6 protein.
XX
KW Rse receptor protein tyrosine kinase; Rse ligand; Rse-Li; Gas6;
KW growth arrest-specific gene 6; proliferation; differentiation;
KW glial cell; Schwann cell; fusion protein.
XX
OS Mus sp.
PN US955420-A.
XX
PD 21-SEP-1999.
XX
PF 10-MAY-1995; 95US-00438864.
XX
PR 10-MAR-1995; 95US-00402253.
XX
PA (GETH) GENENTECH INC.
XX
PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
XX
XX WPI; 1999-539585/45.
XX
PT Activation of the Rse receptor on a cell, useful for promoting cell
PT proliferation and differentiation.
XX
PS Disclosure; Fig 2; 48pp; English.
XX
CC A method has been developed for activating the Rse receptor on a cell.
CC The method comprises exposing the receptor to the exogenous growth arrest
CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
CC cell proliferation and cell differentiation. The present sequence
CC represents murine gas6 given in the present invention
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 2; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGGCLQICHNKPFGSFCVCHSGFELSDGRTCDIDECADSEACGE 120
DB 87 PRYQCMRKRYGRPEKNPDPFAKCVQNLDPQCTPNPCDRKGTQACODLMGNFFCVCCTDGGW 146

QY 61 GRLCDKDVNECSQENGGCLQICHNKPFGSFCVCHSGFELSDGRTCDIDECADSEACGE 120

Db 147 GRLCDKDVNECSQENGGCLQICHNKPFGSFCVCHSGFELSDGRTCDIDECADSEACGE 206

QY 121 ARCKNLPGSYSCCLDEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 180

DB 207 ARCKNLPGSYSCCLDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266

QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227

DB 267 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 13
AAB33459
ID AAB33459 standard; protein; 673 AA.
XX
AC AAB33459;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO21 protein UNQ21 SEQ ID NO:231.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030995.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX

DR WPI; 2000-572271/53.
 DR N-PSDB; AAC58624.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 33; Fig 92; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridization probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention

XX Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 3; Length 673;
 Best Local Similarity 82.8%; Pred. No. 2.3e-70;
 Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
 QY 1 PRYLDCINKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLGMNFCLCKAGWG 60
 DB 87 PRYQECMRKYGRPEEKNPDPFAKCVQNLPDQCTPNPCDRKGTQACODLGMNFCLCKAGWG 146
 QY 61 GLRLCDKDVNECSQENGGCLQICHNPKGSHFCHSGFELSSDGRTCODIDECADSEACGE 120
 DB 147 GLRLCDKDVNECVKNGGCSQVCHNPKGSHFCHSGFELSSDGRTCODIDECADSEACGE 206
 QY 121 ARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
 DB 207 ARCKNLPGSYCLCDEGYTSSKEKTQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266
 QY 181 LSQMDTCEIDILPCVPFSSVAKSVKSLYLGRMFSGTPIRLFRKLQ 227
 DB 267 LSPDMTCEIDILPCVPFSSVAKSVKSLYLGRMFSGTPIRLFRKLQ 313

RESULT 14

AY57382

ID AAY57382 standard; protein; 673 AA.

XX AC

AY57382;

XX DT 19-JUN-2000 (first entry)

XX DE Amino acid sequence of murine gas6 (m gas6) protein.

XX KW Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
 central nervous system; peripheral nervous system; injury; trauma;
 nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 protein S.

XX OS Mus sp.

XX PN US6033660-A.

XX PD 07-MAR-2000.

XX PF 10-MAY-1995; 95US-00438862.

XX PR 10-MAY-1995; 95US-00438862.

XX PA (GETH) GENENTECH INC.

XX PI Mather JP, Chen J, Li R;

XX DR WPI; 2000-246046/21.

XX PT Repairing nervous system injuries in mammals, by administering human
 PT Schwann cells that have been propagated in medium supplemented with
 PT mitogens.

XX Disclosure; Fig 2; 52pp; English.

XX The invention relates to a method for treating nervous system injuries in
 CC mammals by administering human Schwann cells (SC) that have been cultured
 CC in serum-free medium. The serum-free medium is a nutrient solution
 CC supplemented with two mitogens, one of which, is a Res/Axl receptor
 CC activator, to increase survival and proliferation of SC. The method is
 CC used to treat (or prevent) central or peripheral nervous system injury,
 CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
 CC or lesions associated with nutritional deficiencies, systemic disease,
 CC toxins or demyelination. Culturing cells in the specified medium allows
 CC proliferation of adult SC for use in autologous transplants. The present
 CC sequence represents a murine gas6 (m gas6) protein, having 43% sequence
 CC identity to human protein S. Gas6 is demonstrated to be a potent growth/
 CC survival factor for SCs in defined serum-free culture

XX Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 3; Length 673;
 Best Local Similarity 82.8%; Pred. No. 2.3e-70;
 Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
 QY 1 PRYLDCINKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLGMNFCLCKAGWG 60
 DB 87 PRYQECMRKYGRPEEKNPDPFAKCVQNLPDQCTPNPCDRKGTQACODLGMNFCLCKAGWG 146
 QY 61 GLRLCDKDVNECSQENGGCLQICHNPKGSHFCHSGFELSSDGRTCODIDECADSEACGE 120
 DB 147 GLRLCDKDVNECVKNGGCSQVCHNPKGSHFCHSGFELSSDGRTCODIDECADSEACGE 206
 QY 121 ARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
 DB 207 ARCKNLPGSYCLCDEGYTSSKEKTQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266
 QY 181 LSQMDTCEIDILPCVPFSSVAKSVKSLYLGRMFSGTPIRLFRKLQ 227
 DB 267 LSPDMTCEIDILPCVPFSSVAKSVKSLYLGRMFSGTPIRLFRKLQ 313

RESULT 15

ABB4840

ID ABB84840 standard; protein; 673 AA.
 AC ABB84840;
 XX 16-MAY-2002 (first entry)
 DT Human PRO21 protein sequence SEQ ID NO:48.
 DE Human; angiogenesis; cardiatic; cytosclerotic; antiangiogenic; hypotensive;
 KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX Homo sapiens.
 OS
 PN WO200200690-A2.
 XX 03-JAN-2002.
 PD
 XX 20-JUN-2001; 2001WO-US019692.
 XX 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 24-OCT-2000; 2000US-00665350.
 PR 18-SEP-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001US-00802706.
 PR 09-MAR-2001; 2001US-00808689.
 PR 14-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR N-PSDB; ABL88095.
 DR
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 48; 565pp; English.
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiatic, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 XX Sequence 673 AA;
 SQ
 Query Match 85.8%; Score 1113; DB 5; Length 673;
 Best Local Similarity 82.8%; Pred. No. 2.3e-70;
 Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
 QY 1 PRYLDCKNKYSGPYTKNSGFATCVQNLPDQCTPNPCDKGTQACQDLGMGNFFCLCKAGWG 60
 DB 87 PRYQECMKYGRPEKKNPDKFACVQNLPDQCTPNPCDKGTQACQDLGMGNFFCVCTDGG 146
 QY 61 GRLCDKDVNECSQNGGCLQICHNKPGSFHCSHGPELSDGRTQCDIDECADSEACGE 120
 DB 147 GRLCDKDVNECVQNGGCSQVCHNKPGSFQACHSGFSLASDGTQCDIDECTDSDTCGD 206
 QY 121 ARCKNLPGSYSCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
 DB 207 ARCKNLPGSYSCLDCEGYTYSSKEKTCQDVDECOQDRCEQTCVNSPGSYTCHCDGRGLK 266
 QY 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPIRLRFKELQP 227
 DB 267 LSPDMTDCEDILPCVPFSPMAKSVKSLYLGRMFSGTPIRLRFKELQP 313
 RESULT 16
 ABB95446
 ID ABB95446 standard; protein; 673 AA.
 AC ABB95446;
 XX 19-JUL-2002 (first entry)
 DT Human angiogenesis related protein PRO21 SEQ ID NO: 48.
 DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytosclerotic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 OS Homo sapiens.
 XX WO200208284-A2.
 PN 31-JAN-2002.
 PD
 XX 09-JUL-2001; 2001WO-US021735.
 XX 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000US-00709238.
PR 01-DEC-2000; 2000US-00709238.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-00747259.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00767609.
PR 01-MAR-2001; 2001US-00805620.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001US-00871780.
PR 20-JUN-2001; 2001US-00871780.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95584.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 48; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 673 AA;
Query Match 85.8%; Score 1113; DB 5; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKYSGPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFFCLCKAGWG 60

DB 87 PRYQECMKYGRPEKNPDPFAKCVQNLDPQCTPNPCDKKGTHICQDLMGNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGCLQICHNKPGSFHCSCHSGFELSDDGRTCDIDECADSEACGE 120
DB 147 GRLCDKDVNECVQKNGGCSQVCHNKPGSFQACHGFSGLADGGTCQDIDECTDSDTGD 206
QY 121 ARCKNLPGSYCLCDEGFPAYSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYCLCDEGTYTSKKTQDVDECCQDCRCEQTCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTCTEDILPCVPFVSVAKSLSYLGRMFSCTPVIRLRFKRLQ 227
DB 267 LSPDMTCTEDILPCVPFVSMAKSLSYLGRMFSCTPVIRLRFKRLQ 313
RESULT 17
ADD10337
ID ADD10337 standard; protein; 673 AA.
XX
AC ADD10337;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide #24.
XX
KW human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105011-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223084.
XX
PR 15-SEP-2000; 2000US-0232887P.
PR 20-JUN-2001; 2001US-0019692.
PR 09-JUL-2001; 2001US-0021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2003-810831/76.
DR N-PSDB; ADD10336.
XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS Claim 11; SEQ ID NO 48; 493pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal.
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of Pgf-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis. A PRO
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to

CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;
Query Match 85.8%; Score 1113; DB 7; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKINKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLGMNFFCLCKAGWG 60
Db 87 PRYQECMRKYGRPEEKNPDFAKVCVQNLPDQCTPNPCDKKGGTHICQDLGMNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRTCODIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFGSFQACHSGLASDGTQCDIDECTDSDTCGD 206
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYSLCDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTDCEDILPCVPFVSVAKSGLYLGRMFGTTPVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFVSMAKSGLYLGRMFGTTPVIRLRFKRLQ 313
RESULT 18
ID ADD11297
XX
AC ADD11297;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide #24.
XX
KW human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105013-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223090.
XX
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams FM, Wood WI, Ye W;
XX
DR WPI; 2003-801242/75.
DR N-PSDB; ADD11296.
XX
XX New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, useful for treating a cardiovascular, endothelial, or
PT angiogenic disorder in a mammal, such as cancer or age-related macular
PT degeneration.
XX
XX Claim 11; SEQ ID NO 48; 493pp; English.
PS The invention relates to an isolated nucleic acid encoding a secreted and
XX transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded

CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal.
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of bFGF-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;
Query Match 85.8%; Score 1113; DB 7; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKINKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLGMNFFCLCKAGWG 60
Db 87 PRYQECMRKYGRPEEKNPDFAKVCVQNLPDQCTPNPCDKKGGTHICQDLGMNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRTCODIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFGSFQACHSGLASDGTQCDIDECTDSDTCGD 206
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYSLCDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTDCEDILPCVPFVSVAKSGLYLGRMFGTTPVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFVSMAKSGLYLGRMFGTTPVIRLRFKRLQ 313
RESULT 19
ADD37090
ID ADD37090 standard; protein; 673 AA.
XX
AC ADD37090;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide #24.
XX
KW human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105012-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223088.
XX
PR 15-SEP-2000; 2000US-0232887P.
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams FM, Wood WI, Ye W;

DR WPI; 2003-829354/77.
DR N-PSDB; ADD37089.
XX
PT New isolated nucleic acids encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS Claim 11; SEQ ID NO 48; 492pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGR-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 7; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCKINIKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEEKNPDFAKCVQNLDPDQCTPNPCDKKGTGTHICQDLMGNFVCVCTDGMG 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPFSFHCSCGFSGLSSDGRCTCQDIDECADSEACGE 120
DB 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACCHSGFSLASDGTCTDIDECTSDTCGD 206

QY 121 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYSCLCDEGYTYSKKTCDQVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266

QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 267 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 20
ADE41298
ID ADE41298 standard; protein; 673 AA.
AC ADE41298;
XX
XX 29-JAN-2004 (first entry)
XX Human secreted/transmembrane PRO polypeptide #24.
XX human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
XX US2003100497-A1.
XX
XX 29-MAY-2003.
XX
XX 16-AUG-2002; 2002US-00223085.
XX

PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2004-008957/01.
DR N-PSDB; ADE41297.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or
PT PRO214, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and for treating disorders involving
PT angiogenesis.
XX
PS Claim 11; SEQ ID NO 48; 492pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGR-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 8; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCKINIKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEEKNPDFAKCVQNLDPDQCTPNPCDKKGTGTHICQDLMGNFVCVCTDGMG 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPFSFHCSCGFSGLSSDGRCTCQDIDECADSEACGE 120
DB 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACCHSGFSLASDGTCTDIDECTSDTCGD 206

QY 121 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYSCLCDEGYTYSKKTCDQVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266

QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 267 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 21
ADH43481
ID ADH43481 standard; protein; 673 AA.
XX
XX ADH43481;
XX
XX 25-MAR-2004 (first entry)
XX Human PRO polypeptide #24.
XX Human; PRO; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
KW cell apoptosis; cell tube formation; angiogenesis;
KW

PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.

XX disclosure; seqid 51; 310pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 703 AA;

Query Match 85.8%; Score 1113; DB 8; Length 703;
Best Local Similarity 82.8%; Pred. No. 2.4e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKNGSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLNGNFFCLCKAGWG 60
DB 120 PRYQCEMKYGRPEEKNPDFAKCVQNLDPDQCTPNPCDRKGTQACODLNGNFFCVCTDGMG 179
QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFHCSHGFSLSGDRGTCDIDECADSEACGE 120
DB 180 GRLCDKDVNECVQNGGCSQVCHNKPFSFQACHSFGSLADGGTCCQIDICTSDTDCD 239
QY 121 ARCKNLPGSYCLCDEGFAYSQEAKARDVDECLQRCRCEQVCVNSPGSYTCHCDGRGLK 180
DB 240 ARCKNLPGSYCLCDEGYTSSKERTQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 299
QY 181 LSQDMTDCEDILPCVPFFSVKSLYLGRMFSGTPVIRLRFKLP 227
DB 300 LSPDMTDCEDILPCVPFFSMKSVKSLYLGRMFSGTPVIRLRFKLP 346

RESULT 24
AAR72350
ID AAR72350 standard; protein; 635 AA.

XX AAR72350;

XX AC

XX 29-DEC-1995 (first entry)

XX Mature human protein S.

XX Protein S; PS; vitamin K-dependent protein.

XX Homo sapiens.

XX Key Location/Qualifiers
XX Misc-difference 425..-426
FT /label= I425A/I426A

FT Misc-difference 429
FT /label= K429E

FT Misc-difference 432
FT /label= K432E

XX US5405946-A.

XX 11-APR-1995.

XX 02-DEC-1992; 92US-00985691.

XX 02-DEC-1992; 92US-00985691.

XX (SCRI) SCRIPPS RES INST.

XX Bertina R, Griffin JH, Bouma BN;

XX WPI; 1995-154630/20.

XX New recombinant protein S variants - having reduced C4b binding protein
PT binding activity and anticoagulant activity for treating thrombosis.

XX Claim 1; Col 31-36; 24pp; English.

XX For preparing a protein S (PS) expression vector, partial cDNAs coding
CC for human protein S were first isolated as described by Ploos van Amstel
CC et al., FEBS Lett. 222:186-190 (1987) from a pUC9 human liver cDNA
CC library. The cDNA sequence is given in Q86348. The PS nt sequence is also
CC listed in GenBank having the accession number F00692. The mRNA encodes a
CC preprotein having 676 AAs. After post- translation processing the
CC corresp. translated mature PS consists of 635 AAs as given in R72350. The
CC AA sequence is also listed in GenBank having the accession no. A26157. PS
CC can be modified without significant loss of anticoagulant activity by
CC introducing one or more mutations in the region between residues 425 and
CC 432 to reduce significantly or eliminate the ability of PS to bind C4BP.
CC A variant protein S is claimed having AA residue substitutions selected
CC from the group indicated in R72350 FT

XX Sequence 635 AA;

Query Match 46.5%; Score 602.5; DB 2; Length 635;
Best Local Similarity 43.4%; Pred. No. 2e-34;
Matches 102; Conservative 46; Mismatches 74; Indels 13; Gaps 5;

QY 1 PRYLDCKNKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLNGNFF 52
DB 42 PRYLVCURSFQTGLFTAAKSTNAYPDLRSCVNAIPDQCSFLPCNEDGYNSCKDKGKASFT 101
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSFHCSHGFSLSGDRGTCCDI 109
DB 102 CTCKPGWQGEKCEPDINECKDPNSNINGGCSQICDNTPGSYHCSCKNGFVMLSNKDKCKDV 161
QY 110 DECA-DSEAGEARCKNLPGSYCLCDEGFAYSQEAKARDVDECLQRCRCEQVCVNSPGS 168
DB 162 DECSLKPSICGTAVCKNIPDGFCECEPGRYNLIKSKSCQDIDECSENMAQLCVNYPGG 221
QY 169 YTHCDGRGGIKLSQDMTDCEDILPCVPFFSVKSLYLGRMFSGTPVIRLRFK 223
DB 222 YTCYCDGKGGFKLAQDKQKCEVSVCLPLNLDITKYELLYLAEPAGV-VLYLKF 275

RESULT 25

AAR31875

ID AAR31875 standard; protein; 635 AA.

XX AAR31875;

XX

DT 25-MAR-2003 (revised)
XX 24-MAY-1993 (first entry)
DE Vitamin K-dependent protein S.
XX Diagnosis; immunoassay; PS.
KW Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 32..46
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 187..200
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 188..199
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 347..631
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 347..361
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 408..422
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 413..427
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 413..422
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 413..418
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 417..422
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 418..432
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 420..434
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 421..427
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 423..427
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 427..434
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 427..433
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 603..616
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 621..635
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 621..627
FT /note="inhibits binding of protein S to C4b binding
FT protein"
XX EP524737-A2.
XX

PD 27-JAN-1993.
XX
PF 02-JUL-1992; 92EP-00306116.
XX
PR 02-JUL-1991; 91US-00724746.
PR 01-JUL-1992; 92US-00907190.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Griffin JH, Fernandez JA;
XX WPI; 1993-028796/04.
XX
DR Protein S polypeptide(s) and anti-PS antibodies - capable of inhibiting
FT binding of proteins to C4BP.
XX
PS Disclosure; Page 39; 61pp; English.
XX
CC The sequence is that of vitamin K-dependent protein S (PS), peptides
CC (claimed) derived from the PS sequence (see features) may be used to
CC inhibit the binding of PS to C4b binding protein. These peptides can be
CC used in diagnostic systems and a variety of direct or competitive
CC immunoassay formats for detecting the presence of free protein S in a
CC vascular fluid. The assays are based on the specific binding interaction
CC between a PS peptide or an antibody with free PS. Antibodies
CC immunoreactive with the peptides may be used for purifying free PS from
CC fluid samples. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 635 AA;
Query Match 46.4%; Score 601.5; DB 2; Length 635;
Best Local Similarity 43.4%; Pred. No. 2.3e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCINKY-----GSPTKNS--GPATCVQNLPDCTNPDRKCTQACODLWGHFF 52
DB 42 PRYLCLRSFOTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCDKGASFT 101
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPGSFHCSHGFELSDGRTCDI 109
DB 102 CTCRPGWQGEKCFDINECKDPSNINGSQCSICDTPGSHCSCKNGFVMSLNKKDKDV 161
QY 110 DECA-DSACGEARCNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCBQVCVNSPGS 168
DB 162 DECSLPSICGTAVCKNIPGDFECEPEGYRNLSKSCEDIDECSNCAQLCVNYPGG 221
QY 169 YTCDCRGGLKLSQDMDCEDILPCVPFVSAKSVKSLYLGRMSEGTPIRLRFK 223
DB 222 YTCYDGGKGLAQDQKSCBVSVCPLPLNLDTKYELLYLAEQFAGV-VLYLKR 275
RESULT 26
ADQ17650
ID ADQ17650 standard; protein; 650 AA.
XX
AC ADQ17650;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 467.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX Homo sapiens.
XX WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX

PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Aziz N, Gineburg WM, Zlotnik A;
 XX WPI; 2004-441208/41.
 DR
 XX Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 XX Example 2; SEQ ID NO 467; 210pp; English.
 PS
 XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cyrostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 XX Sequence 650 AA;
 SQ
 Query Match 46.4%; Score 601.5; DB 8; Length 650;
 Best Local Similarity 43.4%; Pred. No. 2.3e-34;
 Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
 QY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDCTNPDCRKGTOACQDLMGNFF 52
 DB 57 PKYLVLRLSFTQGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 116
 QY 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPGSFHSCGHSFELSSDGRTCODI 109
 DB 117 CTCKPGWQGEKCEFDINECKDPSNINGSQSIQDNTFGSYHSCKNGFVMSLNKKDCKDV 176
 QY 110 DECA--DSEACGEARCKNLPGSYCLDGEFAYSGOEKACRDVDECLQRCBQVCVNSPGS 168
 DB 177 DECSLKPSICGTAVCKNIPDGFECCEPGYRNLSKSKCEDIDECSENMCALQCVNPPGG 236
 QY 169 YTHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMPSGTPIRLRFK 223
 DB 237 YTCYCDGKGGKFLAQDQKSCVWSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 290
 RESULT 27
 AA46464
 ID AA46464 standard; protein; 676 AA.
 XX
 AC AA46464;
 XX
 DT 15-MAY-1998 (first entry)
 XX
 DE Human protein S.
 XX
 XX Protein S; mitogenic agent; insulin; growth regulation; treatment;
 KW serum-free culture medium; human; Schwann cell; receptor activator;
 KW erbB receptor; heregulin; cAMP level; proliferation;
 KW nervous system injury.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..52
 FT Domain
 FT /note= "A domain which is rich in gamma-carboxylglutamic
 FT acid residues which mediate the Ca2+ dependent binding of
 FT Protein S to negatively charged phospholipids"
 FT 83..118
 FT Domain

FT /note= "B domain of gas6 comprising a thrombin sensitive
 loop"
 FT
 XX US5714385-A.
 XX 03-FEB-1998.
 XX 10-MAY-1995; 95US-00435434.
 XX 10-MAY-1995; 95US-00435434.
 XX (GETH) GENENTECH INC.
 XX Chen J, Mather JP, Li R;
 XX WPI; 1998-129864/12.
 XX
 XX Medium for culturing human Schwann cells - is serum-free and contains Rse
 XX receptor activator and other mitogens.
 XX Disclosure; Fig 2; 51pp; English.
 XX
 XX The present sequence represents a human protein S, which is a ligand for
 XX tyrosine3. Protein S is a vitamin K dependent plasma protein that
 XX functions as an anticoagulant by acting as a cofactor to stimulate the
 XX proteolytic inactivation of factors Va and VIIIa by activated protein C.
 XX Protein S may also be involved in the complement cascade. Protein S is
 XX used in a serum-free culture medium for culturing human Schwann cells,
 XX which does not support fibroblast growth. It functions as a mitogenic
 XX agent which is a Rse/Axl receptor activator. A second mitogenic agent
 XX e.g. insulin or an erbB receptor activator such as heregulin, is also
 XX required to raise cAMP levels and enhance survival or proliferation of
 XX human Schwann cells. The culture medium additionally comprises a molecule
 XX or composition that provides Fe ions to the Schwann cells, vitamin E, a
 XX protease inhibitor, and progesterone. The Schwann cells can be used to
 XX treat patients with nervous system injuries
 XX
 XX Sequence 676 AA;
 Query Match 46.4%; Score 601.5; DB 2; Length 676;
 Best Local Similarity 43.4%; Pred. No. 2.4e-34;
 Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
 QY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDCTNPDCRKGTOACQDLMGNFF 52
 DB 83 PKYLVLRLSFTQGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
 QY 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPGSFHSCGHSFELSSDGRTCODI 109
 DB 143 CTCKPGWQGEKCEFDINECKDPSNINGSQSIQDNTFGSYHSCKNGFVMSLNKKDCKDV 202
 QY 110 DECA--DSEACGEARCKNLPGSYCLDGEFAYSGOEKACRDVDECLQRCBQVCVNSPGS 168
 DB 203 DECSLKPSICGTAVCKNIPDGFECCEPGYRNLSKSKCEDIDECSENMCALQCVNPPGG 262
 QY 169 YTHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMPSGTPIRLRFK 223
 DB 263 YTCYCDGKGGKFLAQDQKSCVWSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316
 RESULT 28
 AA429795
 ID AA429795 standard; protein; 676 AA.
 XX
 AC AA429795;
 XX
 DT 15-NOV-1999 (first entry)
 XX
 DE Human protein S.
 XX
 XX Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; Gas6;
 KW growth arrest-specific gene 6; proliferation; differentiation;
 KW glial cell; Schwann cell; fusion protein.

XX OS Homo sapiens.
XX PN US5955420-A.
XX XX
XX PD 21-SEP-1999.
XX PF 10-MAY-1995; 95US-00438864.
XX PR 10-MAR-1995; 95US-00402253.
XX PA (GETH) GENENTECH INC.
XX PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
XX DR WPI; 1999-539585/45.
XX PT Activation of the Rse receptor on a cell, useful for promoting cell
XX PT proliferation and differentiation.
XX PS Disclosure; Fig 2; 48pp; English.
XX CC A method has been developed for activating the Rse receptor on a cell.
XX CC The method comprises exposing the receptor to the exogenous growth arrest
XX CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
XX CC cell proliferation and cell differentiation. The present sequence
XX CC represents human protein S given in the present invention
XX SQ Sequence 676 AA;
Query Match 46.4%; Score 601.5; DB 2; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKYK-----GSPYTKNS--GFATCVONLPDQCTNPDRKGTQACODLMGNFF 52
DB 83 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGMYMCKDGKASFT 142
QY 53 CLCKAGWGGRCLCDKDVNEC---SOENGGLQICHNKPGRSFGHSCSGFELSDDGRTCDI 109
DB 143 CTCRPGWQGEKCEFDINECKDPFNGGCSQICDNTPGSYHSCSKNGFVWLSNKKDKDV 202
QY 110 DECA-DSEACGEARCKNLPGRSYSCLDDEGFAYSSQEKACRDVDECLQRCQGVCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDFECCEPGRYNLKSKCEDIDECSENWCAQLCVNYPGG 262
QY 169 YTCRCDGRGGLKLSQDMDTCEILPCVPFVSAKSVKSLYLGRMFSCTPVIRLRFK 223
DB 263 YTCYCDGKKGKFLAQDQKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKER 316
RESULT 29
AAV57384
ID AAV57384 standard; protein; 676 AA.
XX AC AAV57384;
XX DT 19-JUN-2000 (first entry)
XX DE Amino acid sequence of human protein S.
XX KW Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
XX KW central nervous system; peripheral nervous system; injury; trauma;
XX KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
XX KW protein S.
XX OS Homo sapiens.
XX PN US6033660-A.
XX PD 07-MAR-2000.
XX PF 10-MAY-1995; 95US-00438862.

XX PR 10-MAY-1995; 95US-00438862.
XX PA (GETH) GENENTECH INC.
XX PI Mather JP, Chen J, Li R;
XX DR WPI; 2000-246046/21.
XX PR Repairing nervous system injuries in mammals, by administering human
XX PT Schwann cells that have been propagated in medium supplemented with
XX PT mitogens.
XX PS Disclosure; Fig 2; 52pp; English.
XX CC The invention relates to a method for treating nervous system injuries in
XX CC mammals by administering human Schwann cells (SC) that have been cultured
XX CC in serum-free medium. The serum-free medium is a nutrient solution
XX CC supplemented with two mitogens, one of which, is a Res/Axl receptor
XX CC activator, to increase survival and proliferation of SC. The method is
XX CC used to treat (or prevent) central or peripheral nervous system injury,
XX CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
XX CC or lesions associated with nutritional deficiencies, systemic disease,
XX CC toxins or demyelination. Culturing cells in the specified medium allows
XX CC proliferation of adult SC for use in autologous transplants. The present
XX CC sequence represents a human protein S, having 43% and 44% sequence
XX CC identity to murine and human gas6. Gas6 is demonstrated to be a potent
XX CC growth/survival factor for SCs in defined serum-free culture
XX SQ Sequence 676 AA;
Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKYK-----GSPYTKNS--GFATCVONLPDQCTNPDRKGTQACODLMGNFF 52
DB 83 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGMYMCKDGKASFT 142
QY 53 CLCKAGWGGRCLCDKDVNEC---SOENGGLQICHNKPGRSFGHSCSGFELSDDGRTCDI 109
DB 143 CTCRPGWQGEKCEFDINECKDPFNGGCSQICDNTPGSYHSCSKNGFVWLSNKKDKDV 202
QY 110 DECA-DSEACGEARCKNLPGRSYSCLDDEGFAYSSQEKACRDVDECLQRCQGVCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDFECCEPGRYNLKSKCEDIDECSENWCAQLCVNYPGG 262
QY 169 YTCRCDGRGGLKLSQDMDTCEILPCVPFVSAKSVKSLYLGRMFSCTPVIRLRFK 223
DB 263 YTCYCDGKKGKFLAQDQKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKER 316
RESULT 30
ADD46140
ID ADD46140 standard; protein; 676 AA.
XX AC ADD46140;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein P07225, SEQ ID NO 11815.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.

```
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
FR 26-NOV-2001; 2001US-0333347P.  
XX (GHEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
XX GENBANK; P07225.  
DR New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
PS Claim 1; Page; 1017pp; English.  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published_pct_sequences.  
XX Sequence 676 AA;  
SQ  
Query Match 46.4%; Score 601.5; DB 7; Length 676;  
Best Local Similarity 43.4%; Pred. No. 2.4e-34;  
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;  
QY 1 PRYLDCKIN-----GSPYTKNS--GFATCVQNLPDQCTPNPCDRKGTQACQDLMGNFF 52  
Db 83 KYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKGKASFT 142  
QY 53 CLCAGWGRCLDKDNEC---SQNGGCLCICHNKGSHCSHSGFELSSDGRCTODI 109  
Db 143 CTCFPGWQGEKCFDINPKDPSNNGGCSQICDNTPGSHCSKNGFVMLSNKDKCKDV 202  
QY 110 DECA-DSRACGEARCKNLPFGSVSLCDLDEGFAYSSQEKACRVDVDECLQGRCEQVCVNSPGS 168  
Db 203 DECSLKPSICGTAVCNIPGDFECHECPGGRYNLKSCKSCEDIDECSENWCAQLCVNYPGG 262  
QY 169 YTHCDGRRGLKLSQDMOTCEDILPCVPFVSVAKSYSILGRMFSGTPIRLRFK 223  
Db 263 YTCYCDGKKGFKLAQDKSCSEVSVCLPLNLDTKVELLYLAEQFAGV-VLYLKER 316  
RESULT 31  
ADE62065  
ID ADE62065 standard; protein; 676 AA.  
XX
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AC ADE62065;  
XX 29-JAN-2004 (first entry)  
DT  
XX Human Protein P07225, SEQ ID NO 7994.  
DE  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX Homo sapiens.  
OS  
XX WO2003016475-A2.  
PN  
XX 27-FEB-2003.  
PD  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX (GHEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
XX GENBANK; P07225.  
DR New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
PS Claim 1; Page; 1017pp; English.  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published_pct_sequences.  
XX Sequence 676 AA;  
SQ  
Query Match 46.4%; Score 601.5; DB 7; Length 676;  
Best Local Similarity 43.4%; Pred. No. 2.4e-34;  
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;  
QY 1 PRYLDCKIN-----GSPYTKNS--GFATCVQNLPDQCTPNPCDRKGTQACQDLMGNFF 52  
Db 83 KYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKGKASFT 142
```

QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPGSFHSCSGFELSDGRTCCDI 109
DB 143 CTCKPGWQGEKECFDINECKDPNSNGGCSQICDNTPGSYHCCKNGFVNLNKKDKCDV 202
QY 110 DECA-DSEACGEARCKNLPGSYSCLDGCFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDFECEPEGYRYNLKSKCEDIDECSENCAQLCVNYPGG 262
QY 169 YTHCHDGRGGLKLSQDMTCEDILPCVPFSAKSVKSLYLGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKGFKLADQKSCVSVCLPLNLDTKVELLYLAQFAGV-VLYLKF 316

RESULT 32
ADP24054
ID ADP24054 standard; protein; 676 AA.
XX
AC ADP24054;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:1232.
XX
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX Unidentified.
XX WO2004041170-A2.
XX
XX 21-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX
XX (GETH) GENENTECH INC.
XX
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI: 2004-419628/39.
DR N-PSDB; ADP24053.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 7; SEQ ID NO 1232; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 676 AA;
Query Match 46.4%; Score 601.5; DB 8; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLIPDOCTNPDRKGTQACQDLMGNPF 52
DB 83 PKYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCDKGASPT 142
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPGSFHSCSGFELSDGRTCCDI 109
DB 143 CTCKPGWQGEKECFDINECKDPNSNGGCSQICDNTPGSYHCCKNGFVNLNKKDKCDV 202
QY 110 DECA-DSEACGEARCKNLPGSYSCLDGCFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDFECEPEGYRYNLKSKCEDIDECSENCAQLCVNYPGG 262
QY 169 YTHCHDGRGGLKLSQDMTCEDILPCVPFSAKSVKSLYLGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKGFKLADQKSCVSVCLPLNLDTKVELLYLAQFAGV-VLYLKF 316

RESULT 33
AAP81136
ID AAP81136 standard; protein; 675 AA.
XX
AC AAP81136;
XX
DT 25-MAR-2003 (revised)
DT 17-OCT-1990 (first entry)
XX
DE Bovine Protein S.
XX
KW Protein S; anti-thrombolytic agent; antibodies.
XX
OS Bos taurus.
XX
XX EP255771-A.
XX
XX 10-FEB-1988.
XX
XX 24-JUL-1987; 87EP-00306564.
XX
XX 25-JUL-1986; 86US-00890401.
XX
XX (INUA) INTEGRATED GENETICS INC.
XX
XX Wydro R, Cohen E, Dackowski W, Stenflo J, Lundwall A, Dahlback B;
PI WPI: 1988-037719/06.
XX
XX N-PSDB; AAP81441.
XX
XX Recombinant DNA encoding mature human Protein S - used therapeutically as
XX anti-thrombolytic agent and for producing antibodies for diagnostic use.
XX Disclosure; Page 7; 22pp; English.
XX
XX See also AAP81442. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 675 AA;
Query Match 46.0%; Score 596.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 5.5e-34;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

Qy 1 PRYLDCKNGSPYTKNSGFAT-----CVQLPDQCTNPDRKGTQACQDLGNFF 52
 Db 83 PKYLGLCSFRAGLFTAARLSNAYPDLRSVNAISDQCNPDPNEDGFMTCCKGQATFT 142
 Qy 53 CLCKAGWGRLCDKDVNECSQE---NGGCLQICHNKPGSFHCSHGSELSGDSGRTQODI 109
 Db 143 CTCKSGWQGEKCESDINECKDPVNINGGCSQICENTPGSYHCSCKNGFVMSLNKKDKDV 202
 Qy 110 DECA-DSEACGEARKCNLPGSYSCLDEGFAYSQEKACRDVDECLQRCCEQVCVNSPGS 168
 Db 203 DECVLKPISCTGAVCKNIPGDFECBCEAGYKYNPVSKSCDDVDECAENLCAQLCVNYPGG 262
 Qy 169 YTHCDGRGGLKLSQDMTCDIEDILPCVPFVSVAKSVKSLYLGRMFSGTPIRLRFK 223
 Db 263 YSCYCDGKKFKLAQDKSCAEVPCLPDLDDKXVELLYLAEQFGV-VLYLKER 316
 RESULT 34
 AAR70730
 ID AAR70730 standard; protein; 390 AA.
 XX
 AC AAR70730;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX
 DE Human protein S deletion mutant 401-C-terminus.
 XX
 XX Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
 KW deletion mutant 401-C-terminus.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..41
 FT /note= "pre-pro leader sequence"
 FT Disulfide-bond 56..61
 FT Domain 59..70
 FT /note= "GLA domain"
 FT Domain 86..280
 FT /note= "growth factor domains"
 FT Disulfide-bond 86..111
 FT Disulfide-bond 119..132
 FT Disulfide-bond 124..141
 FT Disulfide-bond 143..152
 FT Disulfide-bond 159..173
 FT Disulfide-bond 169..182
 FT Disulfide-bond 184..197
 FT Disulfide-bond 203..215
 FT Disulfide-bond 210..224
 FT Disulfide-bond 226..239
 FT Disulfide-bond 245..254
 FT Disulfide-bond 250..263
 FT Disulfide-bond 265..280
 XX WO9501433-A1.
 PN
 XX
 PD 12-JAN-1995.
 XX
 XX 28-JUN-1994; 94WO-NL000149.
 PP
 PR 30-JUN-1993; 93EP-00201906.
 XX
 XX (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Bouma BN, Bertina RM;
 XX
 XX WPI; 1995-060997/08.
 DR
 XX
 XX New deletion mutants of protein S retaining anticoagulant activity - are
 PT not neutralised by C4b binding protein, useful in treating thrombosis,
 PT sepsis etc.
 XX

PS Claim 3; Fig 5; 3lpp; English.
 XX
 CC AAR70728 is the human protein S, from which the new deletion mutants
 CC described in AAR70729-R70733 were derived. The mutants retain the
 CC anticoagulant activity of the wild type protein, useful for the treatment
 CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
 CC lack the 2 putative C4b binding protein domains of the sex hormone
 CC binding globulin domain of the wild type protein. As the mutants are
 CC resistant to neutralisation by C4b binding protein they can provide
 CC increased plasma levels of free protein S, and higher potency per unit
 CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 SQ Sequence 390 AA;
 Query Match 45.3%; Score 587.5; DB 2; Length 390;
 Best Local Similarity 43.0%; Pred. No. 1.4e-33;
 Matches 101; Conservative 45; Mismatches 76; Indels 13; Gaps 5;
 Qy 1 PRYLDCKNGSPYTKNS--GFATCVQNLPDQCTNPDRKGTQACQDLGNFF 52
 Db 81 PKYLGLCSFRAGLFTAAARQSTNAYPDLRSVNAIPDQCSPLPCNEDGYMSCKDGKASFT 140
 Qy 53 CLCKAGWGRLCDKDVNEC---SOENGGLQICHNKPGSFHCSHGSELSGDSGRTQODI 109
 Db 141 CTCKSGWQGEKCFDINECKDPVNINGGCSQICDNTPGSYHCSCKNGFVMSLNKKDKDV 200
 Qy 110 DECA-DSEACGEARKCNLPGSYSCLDEGFAYSQEKACRDVDECLQRCCEQVCVNSPGS 168
 Db 201 DECVLKPISCTGAVCKNIPGDFECBCEAGYKYNPVSKSCDDIDECSENMAQLCVNYPGG 260
 Qy 169 YTHCDGRGGLKLSQDMTCDIEDILPCVPFVSVAKSVKSLYLGRMFSGTPIRLRFK 223
 Db 261 YTCYCDGKKFKLAQDKSCAEVPCLPDLDDKXVELLYLAEQFGV-VLYLKER 314
 RESULT 35
 AAR70729
 ID AAR70729 standard; protein; 565 AA.
 XX
 AC AAR70729;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE Human protein S deletion mutant 401-457, 583-635.
 XX
 XX Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
 KW deletion mutant 401-457, 583-635.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..41
 FT /note= "pre-pro leader sequence"
 FT Disulfide-bond 56..61
 FT Domain 59..70
 FT /note= "GLA domain"
 FT Domain 86..280
 FT /note= "growth factor domains"
 FT Disulfide-bond 86..111
 FT Disulfide-bond 119..132
 FT Disulfide-bond 124..141
 FT Disulfide-bond 143..152
 FT Disulfide-bond 159..173
 FT Disulfide-bond 169..182
 FT Disulfide-bond 184..197
 FT Disulfide-bond 203..215
 FT Disulfide-bond 210..224
 FT Disulfide-bond 226..239
 FT Disulfide-bond 245..254
 FT Disulfide-bond 250..263
 FT Disulfide-bond 265..280

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FT Disulfide-bond 286..509
FT Disulfide-bond 527..555
XX WO9501433-A1.
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-NL000149.
XX
XX 30-JUN-1993; 93EP-00201906.
XX (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Bouma BN, Bertina RM;
XX WPI; 1995-060997/08.
XX
XX New deletion mutants of protein S, from which the new deletion mutants
XX described in AAR70728-R70733 were derived. The mutants retain the
XX anticoagulant activity of the wild type protein, useful for the treatment
XX of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
XX lack the 2 putative C4b binding protein domains of the sex hormone
XX binding globulin domain of the wild type protein. As the mutants are
XX resistant to neutralisation by C4b binding protein they can provide
XX increased plasma levels of free protein S, and higher potency per unit
XX wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
XX to correct PN field.)
XX
XX Sequence 565 AA;
XX
XX Query Match 45.3%; Score 587.5; DB 2; Length 565;
XX Best Local Similarity 43.0%; Pred. No. 28-33;
XX Matches 101; Conservative 45; Mismatches 76; Indels 13; Gaps 5;
XX
XX 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFF 52
XX 81 PKYLVCLRSFQTGLFTAAARQSTNAVPLDLRSCVNAIPDQCSPLPCNEDGYMCKDGKASFT 140
XX
XX 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSFHCSCHSFELSDDGRTCDI 109
XX 141 CTCKDGWQGEKCEFDINECKDPSNNGGCSQICDNTPGSYHCCKNGFVWLSNKKDKDV 200
XX
XX 110 DECA-DSEACGEARCNLPKGSYCLDDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
XX 201 DECSLKPSICGTAVCKNIPGDFECPCEGYRYNLKSKSCEDIDECSENMAQLCVNYPGG 260
XX
XX 169 YTCCHDGRGLXSQDMDFCEBILPCVPFSVAKSVKSLYLGRMFGSTPVIRLREK 223
XX 261 YTCYCDGKKGPKLAQDKSCVSVCLPLNLTDTKELLYLAQPAQGV-VLYLKR 314
XX
XX RESULT 36
XX AAR70728
XX ID AAR70728 standard; protein; 675 AA.
XX
XX AAR70728;
XX
XX 25-MAR-2003 (revised)
XX 20-SEP-1995 (first entry)
XX
XX Human protein S.
XX
XX Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key
```

```
FT Peptide
FT Disulfide-bond 1..41
FT Disulfide-bond /note= "pre-pro leader sequence"
FT Domain 56..61
FT Domain 59..70
FT /note= "UGLA domain"
FT Domain 86..280
FT /note= "growth factor domains"
FT Disulfide-bond 86..111
FT Disulfide-bond 119..132
FT Disulfide-bond 124..141
FT Disulfide-bond 143..152
FT Disulfide-bond 159..173
FT Disulfide-bond 169..182
FT Disulfide-bond 184..197
FT Disulfide-bond 203..215
FT Disulfide-bond 210..224
FT Disulfide-bond 226..239
FT Disulfide-bond 245..254
FT Disulfide-bond 250..263
FT Disulfide-bond 265..280
FT Disulfide-bond 286..566
FT Disulfide-bond 447..473
FT Disulfide-bond 638..666
XX WO9501433-A1.
XX
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-NL000149.
XX
XX 30-JUN-1993; 93EP-00201906.
XX (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Bouma BN, Bertina RM;
XX WPI; 1995-060997/08.
XX
XX New deletion mutants of protein S retaining anticoagulant activity - are
XX not neutralised by C4b binding protein, useful in treating thrombosis,
XX sepsis etc.
XX
XX Disclosure; Fig 5; 3lpp; English.
XX
XX AAR70728 is the human protein S, from which the new deletion mutants
XX described in AAR70729-R70733 were derived. The mutants retain the
XX anticoagulant activity of the wild type protein, useful for the treatment
XX of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
XX lack the 2 putative C4b binding protein domains of the sex hormone
XX binding globulin domain of the wild type protein. As the mutants are
XX resistant to neutralisation by C4b binding protein they can provide
XX increased plasma levels of free protein S, and higher potency per unit
XX wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
XX to correct PN field.)
XX
XX Sequence 675 AA;
XX
XX Query Match 45.3%; Score 587.5; DB 2; Length 675;
XX Best Local Similarity 43.0%; Pred. No. 2.3e-33;
XX Matches 101; Conservative 45; Mismatches 76; Indels 13; Gaps 5;
XX
XX 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFF 52
XX 81 PKYLVCLRSFQTGLFTAAARQSTNAVPLDLRSCVNAIPDQCSPLPCNEDGYMCKDGKASFT 140
XX
XX 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSFHCSCHSFELSDDGRTCDI 109
XX 141 CTCKDGWQGEKCEFDINECKDPSNNGGCSQICDNTPGSYHCCKNGFVWLSNKKDKDV 200
XX
XX 110 DECA-DSEACGEARCNLPKGSYCLDDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
XX 201 DECSLKPSICGTAVCKNIPGDFECPCEGYRYNLKSKSCEDIDECSENMAQLCVNYPGG 260
XX
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QY 169 YTHCDGRGGLKLSQDMTCEDILPCVFPFSAKSVKSLYLGRMFSGTPVIRLRFK 223
AAP81137
DB 261 YTCYCDGKKPKLAQDKSCVWSVCLPLNLDTKYELLYLAEQAGV-VLYLKER 314

RESULT 37
ID AAP81137 standard; protein; 650 AA.
XX AAP81137;
AC AAP81137;
DT 25-MAR-2003 (revised)
DT 17-OCT-1990 (first entry)
XX Human protein S.
XX Protein S; anti-thrombolytic agent; antibodies.
XX Homo sapiens.
XX EP255771-A.
XX 10-FEB-1988.
XX 24-JUL-1987; 87EP-00306564.
XX 25-JUL-1986; 86US-00890401.
XX (INUA) INTEGRATED GENETICS INC.
XX Wydro R, Cohen E, Dackowski W, Stenflo J, Lundwall A, Dahlback B;
XX WPI: 1988-037719/06.
DR N-PSDB; AAN81442.
XX Recombinant DNA encoding mature human Protein S - used therapeutically as
PT anti-thrombolytic agent and for producing antibodies for diagnostic use.
XX Disclosure; Page ?; 22pp; English.
XX The mature human Protein S is used therapeutically as an antithrombolytic
CC agent and for producing antibodies for diagnostic use. See also AAN81441.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 650 AA;
SQ Query Match 45.2%; Score 586.5; DB 1; Length 650;
Best Local Similarity 42.6%; Pred. No. 2.7e-33;
Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

QY 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQNLDPDOCTPNPCDKGTQACQDLMGNFF 52
DB 57 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 116

QY 53 CLCKAGWGRLLCKDQVNEC---SQBNQGGCLQICHNKGPSFHCSCHSGFELSSDGRCTCQDI 109
DB 117 CTCKPQWQGEKEFDINECKDPSNNGCSQICDNTPGSYHCSCXNGFVMSLNKKDKDV 176

QY 110 DECA-DSBAQCGARCNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCRQVCVNSPGS 168
DB 177 DECSLKPSICGTAVCKNIIIGDFECPCPGYRYNLKSKSCEDIDECSENNCAQLCVNYPGG 236

QY 169 YTHCDGRGGLKLSQDMTCEDILPCVFPFSAKSVKSLYLGRMFSGTPVIRLRFK 223
DB 237 HTCYCDGKKFKLAQDKSCVWSVCLPLNLDTKYELLYLAEQAGV-VLYLKER 290

RESULT 38
ADD48900
ID ADD48900 standard; protein; 650 AA.
XX ADD48900;
AC ADD48900;
XX

DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
DE Human Protein AAA60181, SEQ ID NO 14611.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS Unidentified.
PN WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
FA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI: 2003-268312/26.
DR GENBANK; AAA60181.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Example 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 650 AA;
SQ

Query Match 45.2%; Score 586.5; DB 7; Length 650;
Best Local Similarity 42.6%; Pred. No. 2.7e-33;
Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

QY 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQNLDPDOCTPNPCDKGTQACQDLMGNFF 52
DB 57 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 116

QY 53 CLKAGWGRLCDKDVNEC---SQENGGLQICHNKPQSFHCSHGSGFELSSDGRTCQDI 109
Db 117 CTCKPGWQGEKCEFDINECKDPSNNGSGSQICDNTPGSYHCSKNGFVMLSNNKDKDV 176
QY 110 DECA-DSEACGEARCKNLPGSYSCLDGEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 177 DCSLKPSTCGTAVCKNIIGDFECEPEGYRNLKSKSCDIDECSENNCAQLCVNYPGG 236
QY 169 YTCHCDGRGLKLSQDMTCEIDILPCVPFVSVAKSVKSLYLGRMFSGTPIRLRFK 223
Db 237 HTCYCDGKKGKFLAQDQKSEVSVCLPLNLTQVLYLAQFAGV-VLYLKFR 290
RESULT 39
ADD48898
ID ADD48898 standard; protein; 675 AA.
XX
AC ADD48898;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAC60704, SEQ ID NO 14609.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI: 2003-268312/26.
DR GENBANK; AAC60704.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 675 AA;
Query Match 45.1%; Score 585.5; DB 7; Length 675;
Best Local Similarity 43.0%; Pred. No. 3.2e-33;
Matches 101; Conservative 41; Mismatches 80; Indels 13; Gaps 5;
QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLPDQCTPNPCDRKGTQACQDLGNHFF 52
Db 83 PKYLGLGAFRVGAFSAARQSANAYPDLRSVCNAIPDQCDMPNCNEDGVLSCKDQGAFT 142
QY 53 CLKAGWGRLCDKDVNEC---SQENGGLQICHNKPQSFHCSHGSGFELSSDGRTCQDI 109
Db 143 CTCKPGWQGEKCEFDINECKDPSNNGSGSQICDNTPGSYHCSKNGFVMLSNNKDKDV 202
QY 110 DECA-DSEACGEARCKNLPGSYSCLDGEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSTCGTAVCKNIIGDFECEPEGYRNLKSKSCDIDECSENNCAQLCVNYPGG 262
QY 169 YTCHCDGRGLKLSQDMTCEIDILPCVPFVSVAKSVKSLYLGRMFSGTPIRLRFK 223
Db 263 YSCYCDGKKGKFLAQDQKSEVSVCLPLNLTQVLYLAQFAGV-VLYLKFR 316
RESULT 40
AAP70083
ID AAP70083 standard; protein; 676 AA.
XX
AC AAP70083;
XX
DT 25-MAR-2003 (revised)
DT 20-JAN-1991 (first entry)
XX
DE Human recombinant protein-S.
XX
KW Protein-S; plasma; anticoagulant; blood; ss.
XX
OS Homo sapiens.
XX
PN EP247843-A.
XX
PD 02-DEC-1987.
XX
PF 27-MAY-1987; 87EP-00304676.
XX
PR 27-MAY-1986; 86US-00866662.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Hoskins JA, Long GL;
XX
DR WPI: 1987-336481/48.
DR N-PSDB; AAN70080.
XX
PT Recombinant human protein S - a plasmin protein regulator of hemostasis
PT obtd. from a cDNA clone prepd. from human liver mRNA.
XX
PS Disclosure; Page 8; 100pp; English.
XX
CC The protein may be used in antithrombolytic therapy. It may be given as
CC i.v. infusions to patients with recurrent deep-vein thrombosis-pulmonary
CC embolism. It may also be used to treat: i. acquired protein-S deficiency
CC during pregnancy; ii. lupus erythematosus; iii. nephrotic syndrome; and
CC iv. other autoimmune and infectious diseases. (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX

```
SQ Sequence 676 AA;
Query Match 44.5%; Score 577.5; DB 1; Length 676;
Best Local Similarity 42.1%; Pred. No. 1.2e-32;
Matches 99; Conservative 45; Mismatches 78; Indels 13; Gaps 5;

QY 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACQDLMGNF 52
DB 83 PKYLVLRLSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDRYMSCKDGKASFT 142
QY 53 CLCKAGWGRLCDKDVNRC---SQENGGLQICHNKPSCFHCSCHSFELSSDGRTCQDI 109
DB 143 CTCKPGWQGEKCFDINECKDPSNINEGCSQICDNTPGSYHCSCXNGFVMSLNKKDKDV 202
QY 110 DECA--DSEACGEARCKNLPGSYCLCDRGFAYSSOEKACRDVDECLQRCQVQVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDFECEPEGYRYNLKSKSCEDIDECSENMCQALCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMOTCEDILPCVPFVSVAKSVKSLYLGKMFSGTGVIRLRFK 223
DB 263 YTCYCDGKKEPKLAQDQKSCVSVCLPLNLDTKVELLYLAEQFAGV-VLYLKFR 316

RESULT 41
AAR70731
ID AAR70731 standard; protein; 244 AA.
XX
AC AAR70731;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Human protein S deletion mutant 243-C-terminus.
XX
KW Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
KW deletion mutant 243-C-terminus.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..41
FT Disulfide-bond 56..61 /note= "pre-pro leader sequence"
FT Domain 59..70 /note= "GLA domain"
FT Domain 86..243
FT Disulfide-bond 86..111
FT Disulfide-bond 119..132
FT Disulfide-bond 124..141
FT Disulfide-bond 143..152
FT Disulfide-bond 159..173
FT Disulfide-bond 169..182
FT Disulfide-bond 184..197
FT Disulfide-bond 203..215
FT Disulfide-bond 210..224
FT Disulfide-bond 226..239
XX
FN WO9501433-A1.
XX
PD 12-JAN-1995.
XX
PF 28-JUN-1994; 94WO-NL000149.
XX
PR 30-JUN-1993; 93EP-00201906.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Bouma BN, Bertina RM;
XX
DR WPI; 1995-060997/08.
XX
PT New deletion mutants of protein S retaining anticoagulant activity - are
```

```
PT not neutralised by C4b binding protein, useful in treating thrombosis,
PT sepsis etc.
XX
PS Claim 5; Fig 5; 31pp; English.
XX
CC AAR70728 is the human protein S, from which the new deletion mutants
CC described in AAR70729-R70733 were derived. The mutants retain the
CC anticoagulant activity of the wild type protein, useful for the treatment
CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
CC lack the 2 putative C4b binding protein domains of the sex hormone
CC binding globulin domain of the wild type protein. As the mutants are
CC resistant to neutralisation by C4b binding protein they can provide
CC increased plasma levels of free protein S, and higher potency per unit
CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 244 AA;
Query Match 32.2%; Score 418; DB 2; Length 244;
Best Local Similarity 43.3%; Pred. No. 8.1e-22;
Matches 71; Conservative 30; Mismatches 51; Indels 12; Gaps 4;

QY 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACQDLMGNF 52
DB 81 PKYLVLRLSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDRYMSCKDGKASFT 140
QY 53 CLCKAGWGRLCDKDVNRC---SQENGGLQICHNKPSCFHCSCHSFELSSDGRTCQDI 109
DB 141 CTCKPGWQGEKCFDINECKDPSNINEGCSQICDNTPGSYHCSCXNGFVMSLNKKDKDV 200
QY 110 DECA--DSEACGEARCKNLPGSYCLCDRGFAYSSOEKACRDVDE 152
DB 201 DECSLKPSICGTAVCKNIPGDFECEPEGYRYNLKSKSCEDIDE 244

RESULT 42
AAR70733
ID AAR70733 standard; protein; 244 AA.
XX
AC AAR70733;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Human protein S deletion mutant 243-C-terminus, 49, 60, 70.
XX
KW Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
KW deletion mutant 243-C-terminus; 49, 60, 70 substitution.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..41
FT Misc-difference 49 /note= "pre-pro leader sequence"
FT Disulfide-bond 56..61 /note= "may be substituted"
FT Domain 59..70 /note= "GLA domain"
FT Misc-difference 60 /note= "may be substituted"
FT Misc-difference 70 /note= "may be substituted"
FT /note= "may be substituted; at least one of the three
FT possible substitutions must occur"
FT Domain 86..243
FT Disulfide-bond 86..111
FT Disulfide-bond 119..132
FT Disulfide-bond 124..141
FT Disulfide-bond 143..152
FT Disulfide-bond 159..173
FT Disulfide-bond 169..182
FT Disulfide-bond 184..197
```

FT Disulfide-bond 203. .215
 FT Disulfide-bond 210. .224
 XX Disulfide-bond 226. .239
 PN WO9501433-A1.
 PD 12-JAN-1995.
 XX 28-JUN-1994; 94WO-NL000149.
 XX 30-JUN-1993; 93EP-00201906.
 XX (UYLE-) RIJKSUNIV LEIDEN.
 XX Bouma BN, Bertina RM;
 PI WPI; 1995-060997/08.
 DR New deletion mutants of protein S retaining anticoagulant activity - are
 XX not neutralised by C4b binding protein, useful in treating thrombosis,
 PT sepsis etc.
 XX Claim 8; Fig 5; 31pp; English.
 XX AAR70728 is the human protein S, from which the new deletion mutants
 CC described in AAR70729-R70733 were derived. The mutants retain the
 CC anticoagulant activity of the wild type protein, useful for the treatment
 CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
 CC lack the 2 putative C4b binding protein domains of the sex hormone
 CC binding globulin domain of the wild type protein. As the mutants are
 CC resistant to neutralisation by C4b binding protein they can provide
 CC increased plasma levels of free protein S, and higher potency per unit
 CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX Sequence 244 AA;
 SQ
 Query Match 32.2%; Score 418; DB 2; Length 244;
 Best Local Similarity 43.3%; Pred. No. 8.1e-22;
 Matches 71; Conservative 30; Mismatches 51; Indels 12; Gaps 4;
 QY 1 PRYLCLINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
 DB 81 PKYLVCLRSFQTGLFTFAARQSTNAYPDLRSQVNAIPDQCSPLPCNEDGYMCKDGKASFT 140
 QY 53 CLCKAGWGRCLCDKDVNEC---SQENGGLQICHNKPQSGHSCSHGSPFELSDDGRTCDI 109
 DB 141 CTCKDGMQGEKCEFDINECKDPSNNGGCSQICDNTPGSYHCCKNGFVMLSNKKDKDV 200
 QY 110 DECA-DSEACGEARCKNLPQSYSCLCDEGFAYSSQEKACRDVDE 152
 DB 201 DECSLKPSICGTAVCKNIPGDFECPCEGPGYRNLSKSCEDIDE 244
 RESULT 43
 ID AAR70732 standard; protein; 244 AA.
 AC AAR70732;
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX Human protein S deletion mutant 243-C-terminus, 45-72 mutation.
 DE Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
 KW deletion mutant 243-C-terminus; 45-72 mutation.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..41
 FT /note= "pre-pro leader sequence"
 FT

FT Misc-difference 45. .72
 FT /note= "thrombin sensitive loop region where at least one
 FT mutation has occurred"
 FT Disulfide-bond 56. .61
 FT Domain 59. .70
 FT /note= "GLA domain"
 FT Domain 86. .243
 FT /note= "growth factor domains"
 FT Disulfide-bond 86. .111
 FT Disulfide-bond 119. .132
 FT Disulfide-bond 124. .141
 FT Disulfide-bond 143. .152
 FT Disulfide-bond 159. .173
 FT Disulfide-bond 169. .182
 FT Disulfide-bond 184. .197
 FT Disulfide-bond 203. .215
 FT Disulfide-bond 210. .224
 FT Disulfide-bond 226. .239
 XX WO9501433-A1.
 PN 12-JAN-1995.
 XX 28-JUN-1994; 94WO-NL000149.
 XX 30-JUN-1993; 93EP-00201906.
 XX (UYLE-) RIJKSUNIV LEIDEN.
 XX Bouma BN, Bertina RM;
 PI WPI; 1995-060997/08.
 DR New deletion mutants of protein S retaining anticoagulant activity - are
 XX not neutralised by C4b binding protein, useful in treating thrombosis,
 PT sepsis etc.
 XX Claim 7; Fig 5; 31pp; English.
 PS AAR70728 is the human protein S, from which the new deletion mutants
 CC described in AAR70729-R70733 were derived. The mutants retain the
 CC anticoagulant activity of the wild type protein, useful for the treatment
 CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
 CC lack the 2 putative C4b binding protein domains of the sex hormone
 CC binding globulin domain of the wild type protein. As the mutants are
 CC resistant to neutralisation by C4b binding protein they can provide
 CC increased plasma levels of free protein S, and higher potency per unit
 CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX Sequence 244 AA;
 SQ
 Query Match 32.2%; Score 418; DB 2; Length 244;
 Best Local Similarity 43.3%; Pred. No. 8.1e-22;
 Matches 71; Conservative 30; Mismatches 51; Indels 12; Gaps 4;
 QY 1 PRYLCLINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
 DB 81 PKYLVCLRSFQTGLFTFAARQSTNAYPDLRSQVNAIPDQCSPLPCNEDGYMCKDGKASFT 140
 QY 53 CLCKAGWGRCLCDKDVNEC---SQENGGLQICHNKPQSGHSCSHGSPFELSDDGRTCDI 109
 DB 141 CTCKDGMQGEKCEFDINECKDPSNNGGCSQICDNTPGSYHCCKNGFVMLSNKKDKDV 200
 QY 110 DECA-DSEACGEARCKNLPQSYSCLCDEGFAYSSQEKACRDVDE 152
 DB 201 DECSLKPSICGTAVCKNIPGDFECPCEGPGYRNLSKSCEDIDE 244
 RESULT 44
 ADT49855
 ID ADT49855 standard; protein; 397 AA.
 XX

ADT49855;
16-DEC-2004 (first entry)
Murine FBLN1 partial sequence/betacellulin antibody SEQ ID NO:62.
FBLN1; BTC; betacellulin; antidiabetic; antilipemic;
antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
cytostatic; antiinflammatory; immunosuppressive; osteopathic;
antiarthritic; neuroprotective; antitropic; gene therapy;
diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
retinopathy; cardiovascular disease; cancer; fibrosis;
autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
Alzheimer's disease; neurodegenerative disorder;
cell proliferative disorder.
Mus musculus.
WO2004083241-A2.
30-SEP-2004.
18-MAR-2004; 2004WO-JP003699.
19-MAR-2003; 2003US-0456007P.
02-APR-2003; 2003US-0459944P.
(TAKE) TAKEDA CHEM IND LTD.
Sakamoto T, Takeda S;
WPI; 2004-691021/67.
New protein complexes comprising BTC and a second protein (e.g.
mLOC243548, mDLK1 or mPACE4) useful for diagnosing, preventing or
treating disorders such as diabetes mellitus, nephropathy, cardiovascular
disease or cancer.
Disclosure; SEQ ID NO 62; 493pp; English.
The invention relates to an isolated protein complex having a first
protein which is betacellulin (BTC) or its homologue, derivative or
fragment, interacting with a second protein selected from mLOC243548,
mDLK1, mPACE4, mBC032073 (1598), mTHB52, mFBLN5, mAK009011, mHRMT112,
mMATN3, mNID1, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
CAMLG, or homologue, derivative or fragment. A complex of the invention
has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,
ophthalmological, cardiovascular-gen., cytostatic, antiinflammatory,
immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
neotropic activity, and may have a use in gene therapy. The composition
and methods are useful for treating physiological disorders associated
with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
disease, neurodegenerative disorder or cell proliferative disorder. These
may also be used for diagnosing or preventing the disorders cited above,
or for screening for agents that may be used to prevent or treat those
disorders. The present sequence is used in the exemplification of the
invention.
Sequence 397 AA;
Query Match 28.2%; Score 365.5; DB 8; Length 397;
Best Local Similarity 35.9%; Pred. No. 6.2e-18;
Matches 88; Conservative 28; Mismatches 74; Indels 55; Gaps 13;
6 CINKYSPYTKNSGPATCVQNLPT-----DQCTP--NPDRKGTQACQ 45
122 CINTEGS-----YTCQKNVPCRGYHLNBEGRTRCVDVDECSPPAEPG-KG-HHCL 171
46 DLMGNFFCLCKAGWG-----GRLCDKDVNCSQENGK-CLQICHNKPQSFHCSHGSELS 100
172 NSPGSFRCEKAGFYFDGISRTC-VDINECQYFGRGHCRCENTPGSFHCSAGFRLS 230

QY 101 SDGRTCODIDECADSEACGEARCKNLPGSYSCLEGFAYSSOE-KACRDVDECLQGR-- 157
DB 231 VDGRSCEDVNECLNSPCSQE--CANVYGSQCYCRGYQLSDVDGVTCEDIDECALPTGG 288
QY 158 --CSQVCNVPSPGTYTCHDGRGGLKLSQDMDTCEIDLPCVP-----FSVAKSVK 204
DB 289 HICSYRCINIPGSPQCSCPS-SGYRLAPNGRNCQIDECVTGIHNCINETCFNIQGSFR 347
QY 205 SLYLG 209
DB 348 CLSFG 352
RESULT 45
ABO84707
ID ABO84707 standard; protein; 705 AA.
XX
AC ABO84707;
XX
DT 18-NOV-2004 (first entry)
XX
DE Mouse cancer-associated protein MP21-032.1.
XX
KW Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;
KW Lymphoma; CAP.
XX
OS Mus musculus.
XX
FN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
DR N-PSDB; ABD33008.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS disclosure; seqid 781; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an

PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
XX PA
XX PI Morris DW, Morris DW, Malandro MS;
XX DR N-PSDB; ABD32567.
XX PT New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.
XX claim 18; seqid 54; 310pp; English.
XX PS
XX CC The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising
XX the isolated nucleic acid cited above, a host cell comprising the above
XX recombinant nucleic acid or expression vector, a microarray for detecting
XX a cancer-associated (CA) nucleic acid comprising at least one probe
XX comprising at least 10 contiguous nucleotides of any of the above-
XX mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX an open reading frame of a CA sequence selected from any of the 95
XX polynucleotide sequences as mentioned in the specification, or its
XX complement), an isolated antibody, (or its antigen binding fragment) that
XX binds to the above polypeptide, a hybridoma that produces the above
XX monoclonal antibody, a pharmaceutical composition comprising the above
XX antibody and a pharmaceutical excipient, a kit for detecting cancer
XX cells (comprising the antibody cited above, methods for diagnosing cancer
XX or for detecting the presence or absence of cancer cells in an
XX individual, a method for inhibiting growth of cancer cells in an
XX individual, a method for delivering a therapeutic agent to cancer cells
XX in an individual, an electronic library comprising the above
XX polynucleotide or polypeptide (or their fragments), methods of screening
XX for anticancer activity or for a bioactive agent capable of modulating
XX the activity of a CA protein (CAP), methods for detecting cancer
XX associated with expression of a polypeptide in a test cell sample, a
XX method for treating cancers and a method for inhibiting the expression of
XX CA gene in a cell. The composition and methods are useful for detecting,
XX diagnosing, preventing and treating cancers, especially lymphoma and
XX leukaemia. These may also be used in screening for agents that modulate
XX cancer. The present sequence is a human CAP protein sequence. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 518 AA;
Query Match 27.8%; Score 361; DB 8; Length 518;
Best Local Similarity 35.7%; Pred. No. 1.6e-17;
Matches 81; Conservative 0; Mismatches 0; Indels 146; Gaps 1;
Qy 1 PRYLDICINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
76 PRYLDICINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFFCLCKAGWG 118
Qy 61 GRLCDKDVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRCTQDIDECADSEACGE 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
119 ----- 118
Qy 121 ARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQRCQECVNVSPGSYTCHCDGRGLK 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
119 ----- 118
Qy 181 LSQMDMTCEDILPCVPFVSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQP 227
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 119 -----DILPCVPFVSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQP 156
RESULT 48
ADT49854
ID ADT49854 standard; protein; 258 AA.
XX AC
XX ADT49854;
XX DT 16-DEC-2004 (first entry)
XX Murine FBLN1 partial sequence/betacellulin antibody SEQ ID NO:61.
XX FBLN1; BTC; betacellulin; antidiabetic; antilipemic;
XX antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
XX cytosstatic; antiinflammatory; immunosuppressive; osteopathic;
XX antiarthritic; neuroprotective; nootropic; gene therapy;
XX diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
XX retinopathy; cardiovascular disease; cancer; fibrosis;
XX autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
XX Alzheimer's disease; neurodegenerative disorder;
XX cell proliferative disorder.
XX Mus musculus.
XX WO2004083241-A2.
XX 30-SEP-2004.
XX 18-MAR-2004; 2004WO-JP003699.
XX 19-MAR-2003; 2003US-0456007P.
XX 02-APR-2003; 2003US-0459944P.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Sakamoto T, Takeda S;
XX WPI; 2004-691021/67.
XX New protein complexes comprising BTC and a second protein (e.g.
XX mLOC243548, MDLKI or mPACE4) useful for diagnosing, preventing or
XX treating disorders such as diabetes mellitus, nephropathy, cardiovascular
XX disease or cancer.
XX Disclosure; SEQ ID NO 61; 493pp; English.
XX The invention relates to an isolated protein complex having a first
XX protein which is betacellulin (BTC) or its homologue, derivative or
XX fragment, interacting with a second protein selected from mLOC243548,
XX MDLKI, mPACE4, mBC032073(1598), mTHBS2, mPBLN5, mAK009011, mHRMT1L2,
XX mMATN3, mNIDI, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
XX CAMLG, or homologue, derivative or fragment. A complex of the invention
XX has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,
XX ophthalmological, cardiovascular-gen., cytosstatic, antiinflammatory,
XX immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
XX nootropic activity, and may have a use in gene therapy. The composition
XX and methods are useful for treating physiological disorders associated
XX with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
XX retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
XX disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
XX disease, neurodegenerative disorder or cell proliferative disorder. These
XX may also be used for diagnosing or preventing the disorders cited above,
XX or for screening for agents that may be used to prevent or treat those
XX disorders. The present sequence is used in the exemplification of the
XX invention.
XX SQ Sequence 258 AA;
Query Match 27.7%; Score 359; DB 8; Length 258;
Best Local Similarity 37.7%; Pred. No. 1.2e-17;
Matches 83; Conservative 25; Mismatches 68; Indels 44; Gaps 12;

```
QY 6 CINKYSPYTKNSGFATCVQNL-----DQCTP--NPCDRKGTQACQ 45
Db 17 CINTGSG-----YTCQKNFVNCGRGYHLNBEGRTRCVDVDECSPAPPCQ-KG-HHCL 66
QY 46 DIMGNFFCLCKAGW---GRLCDKDVNCSOENG-CLQICHNKPGSFHCSHSGFELS 100
Db 67 NSFGSFRCEKAGFFDGIISRT-CVDINECQYPRGLCGHKCENTPGSFHCSAGFRLS 125
QY 101 SGRTCCQIDECADSEACGEARCKNLPGSYCLDDEGFAYSQE-KACRDVDECLQGR-- 157
Db 126 VDRGSCEDVNECLNSPCSQE--CANVGSYQCYCRRGYQLSDVDGVTCEIDIDECALPTGG 183
QY 158 --CEQVCNPSGSYCHCDGRGGLKLSQDMDCEDILPCV 195
Db 184 HICSYRCINIPGNFQCSPS-SGRLAPSGRNCQIDECV 222

RESULT 49
ID ABP56756 standard; protein; 911 AA.
AC ABP56756;
XX
DT 31-MAR-2003 (first entry)
XX
DE Mouse EGF-like 1 protein SEQ ID NO:4.
XX
KW Human; secreted protein; epidermal growth factor protein subfamily;
KW epidermal growth factor; EGF; gene therapy; therapeutic; drug screening;
KW biological activity; immune response.
XX
OS Mus musculus.
XX
PN WO2002101080-A2.
XX
PD 19-DEC-2002.
XX
PF 07-MAY-2002; 2002WO-US022278.
XX
PR 16-MAY-2001; 2001US-00855824.
XX
PA (PEKE ) PE CORP NY.
PA (GONG/) GONG F.
PA (DFRA/) DI FRANCESCO V.
XX
PI Gong F, Di Francesco V, Yan C, Beasley EM;
XX
WPI; 2003-167407/16.
XX
PT New isolated human secreted peptides, useful for diagnosing or treating a
PT disease characterized by an absence of, inappropriate or unwanted
PT expression of the secreted protein, and in drug screening assays.
XX
PS Disclosure; Fig 2D-E; 185pp; English.
XX
CC The present sequence encodes a human secreted peptide (I) related to the
CC epidermal growth factor (EGF) protein subfamily. (I) can be used in gene
CC therapy. (I) and the nucleic acid molecules encoding (I) can be used as
CC models for the development of human therapeutic targets, to aid in the
CC identification of therapeutic proteins, and to serve as targets for the
CC development of human therapeutic agents. (I) may be used in drug
CC screening assays, in assays to determine the biological activity of the
CC protein, to raise antibodies or to elicit another immune response, as a
CC reagent in assays designed to quantitatively determine levels of the
CC protein in biological fluids, or as markers for tissues in which the
CC corresponding protein is preferentially expressed. (I) can also be used
CC for diagnosing or treating a disease or disorder characterised by an
CC absence of, inappropriate or unwanted expression of the protein. (I) is
CC located to human chromosome 22. The present sequence represents mouse EGF
CC -like 1 protein which is given in comparison with (I) in the
CC exemplification of the present invention
XX
SQ Sequence 911 AA;
```

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Query Match 27.6%; Score 357.5; DB 6; Length 911;
Best Local Similarity 38.6%; Pred. No. 4.8e-17;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY 14 YTKNSGFATCVQNLPDQCTPN--PCDRKGTQACQDLMGNFFCLCKAGW---GRLCDK 67
Db 232 YALHADGRGTCTET-----CAVNNGGCDR-----TCKDXTATGVRCSVPVGTLPDQKTC-KD 282
QY 68 VNECSQENGGCLQICHNKPGSFHCSHSGFELSSDGRTCQIDECADSEACGEARCKNL 127
Db 283 INECLMNNGGCDHFCRNTVGSFEGCGCKGKHLLDERTCQIDIDECSPERTCDHI-CINSP 341
QY 128 GSYSLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCNPSGYSYTHCDGRGGLKLSQD 184
Db 342 GSFQCLCRRGYTLGTTH--CGDVDECSMNNGSCBQGCVNTRGSEYCVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFVSVAKSLSLYLGRM 211
Db 398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

RESULT 50
ID ADI27635 standard; protein; 961 AA.
XX
AC ADI27635;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse SCUBE1 protein.
XX
KW human; SCUBE; secretory signal region; EGF-like domain chain; CUB domain;
KW endothelial cell; chromosome 22q13; antiarteriosclerotic; vasotropic;
KW thrombolytic; atherosclerosis; ischaemia; coagulation disorder;
KW thrombosis; mouse; murine; SCUBE1.
XX
OS Mus musculus.
XX
PN US2003219813-A1.
XX
PD 27-NOV-2003.
XX
PF 03-APR-2003; 2003US-00406073.
XX
PR 05-APR-2002; 2002US-0369876P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Yang R, Ng CKD, Tomlinson JE, Komuves LG, Topper JN, Robison KB;
XX
WPI; 2004-097334/10.
XX
PT New isolated polypeptide such as SCUBE1, SCUBE2 and SCUBE3, useful for
PT identifying an agent which modulates an activity of the new polypeptide.
XX
PS Example 1; SEQ ID NO 13; 86pp; English.
XX
CC The invention relates to a novel isolated human SCUBE polypeptide having
CC a sequence of 784, 386, 919, 914 or 993 amino acids and their encoding
CC nucleic acids. The invention specifically relates to SCUBE1, SCUBE2, and
CC SCUBE3. The SCUBE family has genes containing a secretory signal region,
CC a chain of EGF-like domains, and a CUB domain, that can be differentially
CC expressed in human endothelial cells compared to other human cell types.
CC The SCUBE1 gene has been found on human chromosome 22q13. The novel SCUBE
CC polypeptides have antiarteriosclerotic, vasotropic, and thrombolytic
CC activities. The isolated human SCUBE polypeptide is useful for
CC identifying an agent which modulates the expression of a nucleic acid
CC encoding the human SCUBE polypeptide. The human SCUBE polynucleotides are
CC useful for diagnosing a disease state in a subject which involves
CC determining the level of expression of the human SCUBE polynucleotides.
CC The human SCUBE polynucleotides and polypeptides are useful in a method
CC for treating a disorder such as atherosclerosis, ischaemia, coagulation
```

CC disorder or thrombosis, in a subject. This sequence represents a mouse
CC SCUBE1 protein of the invention.

XX
SQ Sequence 961 AA;
Query Match 27.6%; Score 357.5; DB 8; Length 961;
Best Local Similarity 38.6%; Pred. No. 5e-17;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
Qy 14 YTKNSGFATCVQNLDPDQTPN--PCDRKGTQACQDLMGNFFCLCKAGW----GGRLCDKD 67
Db 232 YALHADGRTCIET-----CAVNNGGCDR----TCKDTATGVRCSFCVGFLLQPDGKTC-KD 282
Qy 68 VNECSQENGGLQICHNKPGSFHCSHGFELSDGRTCDIDECADSEACGEARCKNLP 127
Db 283 INECLMNNGGCDHFCRNTVGSFECCQKGKLLTDERTCQDIDECSPERTCDHI-CINSP 341
Qy 128 GSYSCLCDGFA-YSSQKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGGGLKLSQD 184
Db 342 GSFQCLCRRGVTLGTTH--CGDVDECSMNGSCQGGCVNTRGSEYCVCP--PGRRLHWN 397
Qy 185 MDTCEDILPCVPFFSVAKSVKSLYLGRM 211
Db 398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

Search completed: July 7, 2005, 09:31:35
Job time : 416.39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:51:19 ; Search time 303.706 Seconds
(without alignments)
382.745 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PRLDCINKYSPYTKNSGF.....LGRMSPGTPVIRLPRKRLQP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_spport.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Description
1	1265.5	97.6	721	1 GAS6 HUMAN
2	1117	86.1	674	1 GAS6_RAT
3	1117	86.1	674	1 GAS6_RAT
4	1113	85.8	674	1 GAS6_MOUSE
5	810	62.5	668	2 O6PAE0
6	810	62.5	668	2 O6PAE0
7	647	49.9	648	2 Q73H4
8	609.5	47.0	649	1 PRTS_MACMU
9	601.5	46.4	497	2 Q72715
10	601.5	46.4	676	1 PRTS_HUMAN
11	596.5	46.0	675	1 PRTS_BOVIN
12	591.5	45.6	675	1 PRTS_MOUSE
13	586.5	45.2	646	1 PRTS_RABIT
14	586.5	45.2	650	2 Q16519
15	586.5	45.2	650	2 Q29SD0
16	585.5	45.1	648	2 Q29094
17	585.5	45.1	675	1 PRTS_RAT
18	376	29.0	907	2 Q68EF9
19	363	28.0	705	1 FBUL_MOUSE
20	358.5	27.6	992	2 Q8C9Q4
21	358	27.6	1018	2 Q6NZL8
22	357.5	27.6	961	2 Q9BQC6
23	356	27.4	1666	1 LTB4_MOUSE
24	355	27.4	708	2 P87363
25	354.5	27.3	1577	2 Q9V589
26	354.5	27.3	1587	2 Q00508
27	353.5	27.3	997	2 Q9JJ50
28	353.5	27.3	1222	2 Q7PFC0
29	353.5	27.3	1511	2 Q75412
30	351.5	27.1	3857	2 Q88840
31	350.5	27.0	2872	2 Q9WUH8

32	349.5	26.9	2871	1 FBNI_BOVIN
33	349	26.9	988	2 Q81WY4
34	348.5	26.9	1365	2 Q75N88
35	348.5	26.9	2871	1 FBNI_HUMAN
36	348.5	26.9	2871	2 Q75N87
37	345	26.6	971	2 Q6ZW11
38	345	26.6	999	2 Q9NQ36
39	345	26.6	2871	1 FBNI_MOUSE
40	344.5	26.6	798	1 FBLL_CABEL
41	342.5	26.4	2809	1 FBN3_HUMAN
42	342	26.4	704	1 FBLL_CHICK
43	339	26.1	638	2 Q8NEH6
44	339	26.1	703	1 FBUL_HUMAN
45	339	26.1	1174	2 Q99K58
46	339	26.1	1221	1 FBLL_MOUSE
47	338	26.1	576	2 Q9Y3V7
48	337	26.0	1184	1 FBLL2_HUMAN
49	337	26.0	1184	2 Q86V58
50	337	26.0	1231	2 Q81UI0
51	337	26.0	1231	2 Q81UI1
52	336.5	25.9	517	2 Q9NP01
53	334.5	25.8	1302	1 LTB3_HUMAN
54	334.5	25.8	1664	2 Q8TVQ2
55	333	25.7	880	2 Q8NAU9
56	333	25.7	1289	2 Q75JU6
57	331.5	25.6	893	2 Q8MJK0
58	331.5	25.6	1167	2 Q6KAT1
59	331.5	25.6	2911	1 FBNI2_HUMAN
60	331	25.5	1398	2 Q8AXM6
61	331	25.5	1399	2 Q8JFZ4
62	331	25.5	2871	1 FBNI_PIG
63	330.5	25.5	1394	1 LTB5_HUMAN
64	330.5	25.5	1595	1 LTBEL_HUMAN
65	328.5	25.3	2906	2 Q9WUH9
66	327	25.2	598	1 FBLL_CERAE
67	327	25.2	993	2 Q8IX30
68	326.5	25.2	1095	2 Q60784
69	326.5	25.2	2907	1 FBNI2_MOUSE
70	325	25.1	827	2 Q68FG9
71	325	25.1	992	2 Q86UZ9
72	325	25.1	993	2 Q66PV1
73	324.5	25.0	1062	2 Q60789
74	323.5	24.9	443	2 Q9H3D5
75	323.5	24.9	682	2 Q6ZMN9
76	323	24.9	448	1 FBLL5_HUMAN
77	323	24.9	448	1 FBLL5_RAT
78	323	24.9	545	2 Q86TV4
79	322	24.8	937	2 Q86FT5
80	322	24.8	1016	2 Q8NDE6
81	321	24.7	448	1 FBLL5_MOUSE
82	321	24.7	493	1 FBLL3_HUMAN
83	321	24.7	493	2 Q7YQD7
84	320.5	24.7	1260	2 Q72YV5
85	320	24.7	493	1 FBLL3_RAT
86	320	24.7	493	2 Q6AXN2
87	319.5	24.6	1712	1 LTB1_RAT
88	319.5	24.6	1821	1 LTB2_HUMAN
89	319.5	24.6	1821	2 Q6AZ94
90	319	24.6	387	2 Q8K0J4
91	319	24.6	448	2 Q8UWA3
92	319	24.6	477	2 Q8Y3N6
93	319	24.6	493	2 Q8BPB5
94	318	24.5	451	2 Q8N2G3
95	318	24.5	589	2 Q7ZX63
96	318	24.5	915	2 Q6UWA5
97	318	24.5	956	1 MTN2_HUMAN
98	318	24.5	3775	2 Q7PMEF9
99	317.5	24.5	741	2 Q96K89
100	317.5	24.5	1244	2 Q69YJ3
101	317	24.4	1268	1 LTB3_MOUSE
102	316.5	24.4	443	1 FBLL4_CRICR
103	316.5	24.4	937	2 Q8BLJ1
104	316.5	24.4	1246	1 EFL3_HUMAN

P98133	bos taurus
Q81wy4	homo sapien
Q75n88	homo sapien
P35555	homo sapien
Q75n87	homo sapien
Q62wil	homo sapien
Q9nq36	homo sapien
Q15554	mus musculus
Q77469	caenorhabdi
Q75n90	homo sapien
Q73775	gallus gall
Q8bhb6	homo sapien
P23142	homo sapien
Q9K58	mus musculus
P37889	mus musculus
Q9Y3V7	homo sapien
P98095	homo sapien
Q86v58	homo sapien
Q81ui0	homo sapien
Q81ui1	homo sapien
Q9np01	homo sapien
Q9na15	homo sapien
Q8tvq2	caenorhabdi
Q8na9	homo sapien
Q75j6	dictyosteli
Q6kat1	mus musculus
Q8mjko	cercopithe
P35556	homo sapien
Q8axm6	homo sapien
Q8jz4	homo sapien
Q9tv36	mus musculus
P22064	homo sapien
Q14766	homo sapien
Q9wuh9	rattus norv
Q8mj9	cercopithe
Q8ax30	homo sapien
Q60784	mus musculus
Q61555	mus musculus
Q68fg9	mus musculus
Q86uz9	homo sapien
Q66pv1	mus musculus
Q60789	mus musculus
Q9h3d5	homo sapien
Q6zmn9	homo sapien
Q9ubx5	homo sapien
Q9wvh8	rattus norv
Q86tv4	homo sapien
Q86ft5	homo sapien
Q8nd6	homo sapien
Q9wvh9	mus musculus
Q12805	homo sapien
Q7ygd7	macaca fasc
Q72yv5	oncorhynch
Q35568	rattus norv
Q6axn2	rattus norv
Q00918	rattus norv
Q14767	homo sapien
Q6az94	homo sapien
Q8k0j4	mus musculus
Q6uwa3	homo sapien
Q6y3n6	mus musculus
Q8bpb5	mus musculus
Q8n2g3	homo sapien
Q7zx63	homo sapien
Q6uwa5	homo sapien
Q00339	homo sapien
Q7pmf9	anopheles g
Q96k89	homo sapien
Q69y33	homo sapien
Q61810	mus musculus
O55058	cricetulus
Q9blj1	ciona inces
Q75095	homo sapien

105	316.5	24.4	1389	1	LTBS_MOUSE	Q8cg18 mus musculus	178	270.5	20.9	2470	1	NTC2_MOUSE	O35516 mus musculus
106	316.5	24.4	1713	1	LTBL_MOUSE	Q8cg19 mus musculus	179	270	20.8	2037	2	O7QF52	O7qfs2 anopheles g
107	316	24.4	486	2	O8SYF5	Q8syf5 drosophila	180	270	20.8	2437	1	NTC1_BRARE	P46530 brachydanio
108	315.5	24.3	715	2	O7Z5X1	Q7z5x1 homo sapien	181	270	20.8	2656	2	O9GNO3	Q9gm3 paracentrot
109	314.5	24.2	443	1	FBLA_HUMAN	Q95967 homo sapien	182	269	20.7	652	1	CD93_HUMAN	Q9np11 oikopleura
110	314.5	24.2	443	2	O96TF5	Q96tf5 homo sapien	183	268.5	20.7	1972	2	O8WPL1	Q8wpl1 oikopleura
111	314.5	24.2	443	2	O6PH22	Q6ph22 homo sapien	184	268.5	20.7	2653	2	O7PSV8	Q7psv8 anopheles g
112	314.5	24.2	2428	2	O816X6	Q816x6 boophilus m	185	268.5	20.7	2653	2	O25253	O25253 lucilia cup
113	313	24.1	886	1	EMRI_HUMAN	Q14246 homo sapien	186	268	20.7	161	2	O75440	O75440 homo sapien
114	312.5	24.1	528	2	O6CXD8	Q6cxd8 mus musculus	187	268	20.7	452	1	MTN3_CHICK	O42401 gallus gall
115	312	24.1	839	2	O6FPN7	Q6fpn7 xenopus tro	188	268	20.7	652	2	O81XK1	O81xk1 homo sapien
116	312	24.1	872	2	O6ZNB8	Q6znb8 homo sapien	189	268	20.7	1961	1	O6MG89	Q6mg89 rattus norv
117	311.5	24.0	1842	1	LTB2_BOVIN	Q28019 bos taurus	190	266	20.5	1961	1	NTC4_MOUSE	P31695 mus musculus
118	310.5	23.9	443	1	FBLA_MOUSE	Q9wvj9 mus musculus	191	265.5	20.5	1218	1	JAG1_HUMAN	P78504 homo sapien
119	310.5	23.9	443	2	O9JM06	Q9jmo6 mus musculus	192	265.5	20.5	1242	1	JAG1_BRARE	Q90y57 brachydanio
120	310.5	23.9	1574	1	EFLJ3_RAT	Q8j281 rattus norv	193	265.5	20.5	2471	1	NTC2_RAT	Q9gw30 rattus norv
121	309.5	23.8	2189	2	O9BI05	Q9bi05 eimeria ten	194	264.5	20.4	1213	1	JAG3_BRARE	Q90y54 brachydanio
122	308.5	23.8	1813	1	LTB2_MOUSE	O89999 mus musculus	195	264	20.4	1214	2	O90YD2	Q90yd2 xenopus lae
123	307.5	23.7	1764	1	LTB2_RAT	O35806 rattus norv	196	264	20.4	2139	1	CRB_DROME	P10040 drosophila
124	304	23.4	2360	2	O7YZP0	Q7yzp0 eimeria max	197	264	20.4	2146	2	O9VC97	O9vc97 drosophila
125	302.5	23.3	681	1	FBLI_BRARE	O42182 brachydanio	198	264	20.4	2531	2	O16004	O16004 lytechinus
126	302.5	23.3	23015	2	O8IQ18	Q8iq18 drosophila	199	263.5	20.3	1247	1	JAG2_MOUSE	Q9gyes mus musculus
127	302	23.3	917	2	O9V4B8	Q9v4b8 drosophila	200	263.5	20.3	2524	1	NOTC_XENLA	P21783 xenopus lae
128	301	23.2	823	2	O7PSQ4	Q7psq4 anopheles g	201	263.5	20.3	2556	1	NTC1_HUMAN	P46531 homo sapien
129	300	23.1	65	2	O77692	Q77692 oryctolagus	202	263.5	20.3	3623	2	O70244	O70244 rattus norv
130	300	23.1	2673	2	O6S8C3	Q6s8c3 homo sapien	203	262.5	20.2	1081	2	O76809	O76809 hydra atten
131	299.5	23.1	733	2	O25678	Q25678 podocoryne	204	262.5	20.2	2531	1	NTC1_MOUSE	Q01705 mus musculus
132	299.5	23.1	2321	1	NTC3_HUMAN	Q9um47 homo sapien	205	261.5	20.2	2471	1	NTC2_HUMAN	Q04721 homo sapien
133	299	23.1	5636	2	O96RW7	Q96rw7 homo sapien	206	261.5	20.2	2516	2	O7TQ52	Q7tc52 mus musculus
134	298.5	23.0	2319	1	NTC3_RAT	Q9r172 rattus norv	207	261.5	20.2	2526	2	O7TQ51	Q7tc51 mus musculus
135	297.5	22.9	643	1	CD93_RAT	Q9et61 rattus norv	208	261.5	20.2	2531	2	O8K428	O8k428 mus musculus
136	297	22.9	2524	2	O9GPAS	Q9gas5 branchiosto	209	261.5	20.2	2531	2	O7TQ50	O7tc50 mus musculus
137	294	22.7	396	2	O6LCD7	Q6lcd7 mus musculus	210	261	20.1	486	1	MTN3_HUMAN	O15232 homo sapien
138	294	22.7	931	1	EMRI_MOUSE	Q61549 mus musculus	211	260.5	20.1	537	2	O96AA0	Q96aa0 homo sapien
139	292	22.5	867	2	O6ZMN0	Q6zmn0 homo sapien	212	260.5	20.1	1317	2	O6IQ50	Q6iq50 homo sapien
140	291.5	22.5	787	2	O8K061	Q8k061 mus musculus	213	259.5	20.0	1064	1	FBP1_STRPU	P10079 strongyloce
141	291.5	22.5	1519	2	O8WPN0	Q8wpn0 oikopleura	214	259.5	20.0	2531	1	NTC1_RAT	Q7008 rattus norv
142	291.5	22.5	2318	1	NTC3_MOUSE	Q61982 mus musculus	215	258.5	19.9	713	2	O962W9	O962w9 podocoryne
143	291	22.4	810	2	O8C435	Q8c435 mus musculus	216	257.5	19.9	420	2	O8I499	O8i499 cupienius
144	291	22.4	956	2	O8R542	Q8r542 mus musculus	217	257	19.8	297	2	O08743	O08743 mus musculus
145	291	22.4	956	2	O99K64	Q99k64 mus musculus	218	257	19.8	491	2	O8BJB5	Q8bjb5 mus musculus
146	291	22.4	1115	2	O7QB67	Q7qb67 anopheles g	219	257	19.8	577	1	TRBM_MOUSE	P15306 mus musculus
147	289.5	22.3	729	2	O8BNH3	Q8bnh3 mus musculus	220	256.5	19.8	487	2	O8MSX5	Q8msx5 drosophila
148	289	22.3	956	1	MTN2_MOUSE	O88746 mus musculus	221	256	19.7	463	2	O68QF3	Q68qf3 lithobius f
149	287	22.1	347	2	O86TI6	Q86ti6 homo sapien	222	255	19.7	509	2	O6UXI9	Q6uxi9 homo sapien
150	284.5	21.9	2528	2	O8AXP0	Q8axp0 cynops pyrr	223	255	19.7	561	2	O91V88	Q91v88 mus musculus
151	283	21.8	590	2	O8C088	Q8c088 mus musculus	224	255	19.7	561	2	O6NV58	Q6nv58 mus musculus
152	282.5	21.8	304	2	O80744	O80744 mus musculus	225	255	19.7	608	2	O8OV54	Q8ov54 mus musculus
153	279.5	21.5	2468	2	O800E4	O800e4 brachydanio	226	255	19.7	619	1	MTN4_HUMAN	O95460 homo sapien
154	279	21.5	821	2	O6PYX2	Q6pyx2 brachydanio	227	254.5	19.6	1208	2	O80YA8	Q80ya8 mus musculus
155	278	21.4	2585	2	O23587	Q23587 caenorhabdi	228	253	19.5	580	2	O8HZ48	O8hz48 oryctolagus
156	277.5	21.4	191	2	O9DEDO	Q9ded0 gallus gall	229	253	19.5	1403	2	O8R5G0	Q8r5g0 mus musculus
157	277.5	21.4	832	2	O8MQJ4	Q8mqj4 drosophila	230	253	19.5	1403	2	O8CFA3	Q8cf3 mus musculus
158	277.5	21.4	870	2	O8ITQ6	Q8iqg6 drosophila	231	253	19.5	3567	2	O9ES77	Q9es77 mus musculus
159	277	21.4	669	2	O75441	Q75441 homo sapien	232	252.5	19.5	904	2	O6P424	O6p424 xenopus tro
160	275.5	21.2	647	2	O8P3V5	Q8p3v5 homo sapien	233	252.5	19.5	955	2	O96DN2	Q96dn2 homo sapien
161	275.5	21.2	950	2	O8MQN5	Q8mqn5 drosophila	234	252.5	19.5	1316	2	O96JU7	Q96ju7 homo sapien
162	275.5	21.2	1114	2	O75WG2	Q75wg2 penaeus jap	235	252	19.4	1294	2	O8C622	Q8c622 mus musculus
163	275.5	21.2	1407	2	O9VB65	Q9vb65 drosophila	236	252	19.4	1376	1	CRBH_HUMAN	P82279 homo sapien
164	275.5	21.2	1408	1	SERR_DROME	P18168 drosophila	237	252	19.4	1403	2	O7TQF0	Q7tcq0 mus musculus
165	275.5	21.2	2003	1	NTC4_HUMAN	Q99466 homo sapien	238	252	19.4	1406	2	O8WY70	O8wyy0 homo sapien
166	275	21.2	644	1	CD93_MOUSE	O89103 mus musculus	239	252	19.4	3646	2	O7Q737	Q7q737 anopheles g
167	274.5	21.2	481	1	MTN3_MOUSE	Q3701 mus musculus	240	251.5	19.4	1106	2	O17494	O17494 caenorhabdi
168	274.5	21.2	481	2	O61R12	Q61r12 mus musculus	241	251	19.4	376	2	O95LNO	Q95lno macaca fasc
169	274.5	21.2	2447	2	O13149	O13149 figu rubrip	242	251	19.4	578	2	O912D3	Q912d3 mus musculus
170	273.5	21.1	255	2	O80745	O80745 mus musculus	243	251	19.4	1375	1	NID2_HUMAN	Q1412 homo sapien
171	273	21.0	1193	2	O90819	Q90819 gallus gall	244	251	19.4	1403	1	NID2_MOUSE	O88322 mus musculus
172	272	21.0	2703	1	NOTC_DROME	P07207 drosophila	245	250.5	19.3	439	2	O9DAW5	O9daws m mus muscu
173	271.5	20.9	1218	1	JAG1_MOUSE	Q9qxx0 mus musculus	246	250	19.3	135	2	O9PUC8	Q9puc8 gallus gall
174	271.5	20.9	1219	1	JAG1_RAT	Q63722 rattus norv	247	250	19.3	339	2	O80WW7	O80ww7 mus musculus
175	271	20.9	176	2	O9PUC7	Q9puc7 gallus gall	248	250	19.3	1247	1	NIDO_HUMAN	P14543 homo sapien
176	271	20.9	827	2	O702I4	Q702i4 bos taurus	249	249.5	19.2	439	2	O8N9G0	O8n9g0 homo sapien
177	270.5	20.9	2352	2	O61240	O61240 halocynthia	250	249.5	19.2	961	2	O8C9P6	O8c9p6 mus musculus

251	249.5	19.2	978	2	Q8BQI3	Q8bqi3 mus musculus	324	228	17.6	816	1	NEL2_HUMAN	Q99435 homo sapien
252	249.5	19.2	1176	2	Q6ZW16	Q6zw16 homo sapien	325	228	17.6	1202	1	JAG2_RAT	P97607 rattus norv
253	249.5	19.2	1245	1	NIDO_MOUSE	P10493 mus musculus	326	228	17.6	1905	2	Q76LJ2	Q76LJ2 rattus norv
254	249.5	19.2	1245	2	Q8C3U8	Q8c3u8 mus musculus	327	227.5	17.5	347	1	Q9DDR4	Q9ddr4 gallus gall
255	249.5	19.2	529	2	Q25058	Q25058 heliocidari	328	227.5	17.5	811	1	LDLR_PIG	Q28832 sus scrofa
256	249.5	19.2	575	1	TRBM_HUMAN	P07204 homo sapien	329	227.5	17.5	837	2	Q9UH51	Q9uh51 homo sapien
257	249.5	19.2	575	1	TREB_SALSC	Q71u07 salmiri sci	330	227.5	17.5	860	1	LDLR_HUMAN	P01130 homo sapien
258	249.5	19.2	577	2	Q8IV29	Q8iv29 homo sapien	331	227.5	17.5	1687	2	Q61204	Q61204 mus musculus
259	249.5	19.2	1032	2	Q35370	Q35370 rattus norv	332	227	17.5	721	2	Q91902	Q91902 xenopus lae
260	249.5	19.2	1032	2	Q75WG1	Q75wg1 penaeus jap	333	226.5	17.5	1455	2	Q86FJ9	Q86fj9 caenorhabdi
261	248.5	19.2	356	2	Q7Q6R6	Q7q6r6 anopheles g	334	226	17.4	739	1	ELT1_MOUSE	Q923x1 mus musculus
262	248	19.1	461	2	P97883	P97883 rattus norv	335	225.5	17.4	236	2	Q7Z3S9	Q7z3s9 homo sapien
263	248	19.1	624	1	MTM4_MOUSE	Q89029 mus musculus	336	225.5	17.4	853	2	Q6S4M2	Q6s4m2 macaca mula
264	246	19.0	891	2	Q7T2X3	Q7t2x3 gallus gall	337	225.5	17.4	1531	1	SLT1_RAT	Q88279 rattus norv
265	246	19.0	1315	2	Q71JF2	Q71jf2 mus musculus	338	224.5	17.3	297	2	Q7YUE5	Q7yue5 herdtmania c
266	246	19.0	3871	2	Q2Q911	Q2q911 caenorhabdi	339	224.5	17.3	1531	1	SLT1_MOUSE	Q80tr4 mus musculus
267	245.5	18.9	752	2	Q42374	Q42374 brachydanio	340	224.5	17.3	1537	2	Q8WY29	Q8wy29 homo sapien
268	245	18.9	969	2	Q8IV28	Q8iv28 homo sapien	341	224	17.3	726	2	Q8AM87	Q8aw87 cynops pyrr
269	245	18.9	1216	2	Q90Y55	Q90y55 brachydanio	342	224	17.3	869	2	Q6ND126	Q6nd126 xenopus lae
270	245	18.9	1254	2	Q90Y56	Q90y56 brachydanio	343	224	17.3	869	2	Q6NS01	Q6ns01 xenopus lae
271	245	18.9	1254	2	Q9YHU2	Q9yhu2 brachydanio	344	224	17.3	1295	1	GLP1_CAEEL	P13508 caenorhabdi
272	244.5	18.9	722	1	DL11_MOUSE	Q61483 mus musculus	345	224	17.3	1847	2	Q76952	Q76952 aedes aegypt
273	244.5	18.9	722	2	Q6PFV7	Q6pfv7 mus musculus	346	223.5	17.2	261	2	Q7PRJ2	Q7prj2 anopheles g
274	244	18.8	508	2	Q6DHG1	Q6dhg1 brachydanio	347	223.5	17.2	911	2	Q7ZZT0	Q7zzt0 brachydanio
275	242.5	18.7	714	1	DL11_RAT	P97677 rattus norv	348	223	17.2	642	2	P79941	P79941 xenopus lae
276	242.5	18.7	3687	2	Q9W332	Q9w332 drosophila	349	223	17.2	772	2	Q6DI48	Q6di48 brachydanio
277	242	18.7	468	2	Q9UC32	Q9uc32 homo sapien	350	223	17.2	802	2	O57462	O57462 brachydanio
278	242	18.7	1238	1	JAG2_HUMAN	Q9Y219 homo sapien	351	222.5	17.2	338	2	Q6UXJ1	Q6uxj1 homo sapien
279	241.5	18.6	1534	1	SLT1_HUMAN	Q75093 homo sapien	352	222.5	17.2	553	2	Q8IUX8	Q8lux8 homo sapien
280	241.5	18.6	1551	2	Q9NGV4	Q9ngv4 drosophila	353	222.5	17.2	553	2	Q8NBV0	Q8nbv0 homo sapien
281	241.5	18.6	3396	2	Q9VM55	Q9vm55 drosophila	354	222.5	17.2	554	2	Q9NZL7	Q9nzt7 homo sapien
282	241	18.6	1403	2	Q70E20	Q70e20 mus musculus	355	222.5	17.2	1216	2	Q9BEA0	Q9bea0 canis famil
283	240.5	18.5	1212	2	O42347	O42347 gallus gall	356	222.5	17.2	4599	1	LR1B_HUMAN	Q9nzt2 homo sapien
284	240.5	18.5	1569	2	Q7Q3I9	Q7q3i9 anopheles g	357	222.5	17.2	339	2	Q9BIJ2	Q9bij2 toxoplasma
285	240	18.5	1065	2	Q810H2	Q810h2 mus musculus	358	222	17.1	473	1	FP2_MITGA	Q22464 mytilus gal
286	239	18.4	389	2	Q9DDR5	Q9ddr5 gallus gall	359	222	17.1	728	2	Q90656	Q90656 gallus gall
287	239	18.4	544	2	Q8AVH7	Q8avh7 xenopus lae	360	222	17.1	558	2	Q7UFG6	Q7ufk6 homo sapien
288	239	18.4	1530	2	Q90WZ3	Q90wz3 xenopus lae	361	221.5	17.1	219	2	Q7Z7L6	Q7z7l6 homo sapien
289	239	18.4	3620	2	Q9TU53	Q9tu53 canis famil	362	221	17.0	237	2	Q8IVT0	Q8ivt0 homo sapien
290	238.5	18.4	636	2	Q8N2S1	Q8n2s1 homo sapien	363	221	17.0	642	2	Q8IXT4	Q8ixt4 xenopus lae
291	238.5	18.4	835	1	CD97_HUMAN	P48960 homo sapien	364	221	17.0	287	2	Q8WVJ7	Q8wvj7 boletia vi
292	238	18.4	816	1	NEL_CHICK	Q90827 gallus gall	365	220.5	17.0	356	1	TRBM_BOVIN	P06579 bos taurus
293	238	18.4	1405	2	Q8VHS2	Q8vhs2 mus musculus	366	220.5	17.0	542	2	Q7Q0Z8	Q7q0z8 anopheles g
294	237.5	18.3	761	2	Q6ST50	Q6st50 mus musculus	367	220.5	17.0	1210	2	Q95ND4	Q95nd4 felis silve
295	237	18.3	1515	2	Q9DE37	Q9de37 brachydanio	368	220.5	17.0	824	2	Q6GS04	Q6gs04 oikopleura
296	237	18.3	3494	2	Q7LCS3	Q7lcs3 homo sapien	369	220	17.0	1200	2	Q8VD07	Q8vd07 mus musculus
297	237	18.3	3623	2	Q6O494	Q6o494 homo sapien	370	220	17.0	1217	2	EGF_MOUSE	P01132 mus musculus
298	235.5	18.2	450	2	Q869J7	Q869j7 glomeris ma	371	220	17.0	996	1	LRP8_MOUSE	Q924x6 mus musculus
299	235.5	18.2	592	2	Q9IXL5	Q9ixl5 mus musculus	372	220	17.0	1476	2	Q30285	Q30285 catassius a
300	235.5	18.2	609	2	Q923T5	Q923t5 mus musculus	373	219.5	16.9	239	2	Q7Z618	Q7z618 homo sapien
301	234	18.0	570	1	FBP3_STRPU	P49013 strongyloce	374	219.5	16.9	816	1	NEL2_RAT	Q62220 mus musculus
302	233.5	18.0	406	2	Q25059	Q25059 heliocidari	375	219	16.9	816	1	Q8R417	Q8r417 rattus norv
303	233	18.0	342	2	Q6PL92	Q6pl92 homo sapien	376	219	16.9	819	2	Q80UM5	Q80um5 mus musculus
304	233	18.0	366	2	Q9DDR6	Q9ddr6 gallus gall	377	219	16.9	858	2	Q8BM06	Q8bm06 mus musculus
305	233	18.0	778	2	Q91BG4	Q91bg4 xenopus lae	378	219	16.9	784	2	Q8BM43	Q8bm43 m mus muscu
306	233	18.0	2019	2	Q68FE0	Q68fe0 mus musculus	379	219	16.9	816	1	NEL2_MOUSE	Q61220 mus musculus
307	232.5	17.9	585	2	Q90UE2	Q90ue2 tribolium c	380	219	16.9	816	1	Q8R417	Q8r417 rattus norv
308	232	17.9	1372	2	P91526	P91526 caenorhabdi	381	219	16.9	819	2	Q80UM5	Q80um5 mus musculus
309	232	17.9	1905	1	LRP4_MOUSE	Q8vi56 mus musculus	382	218.5	16.8	1207	1	EGF_HUMAN	P01133 homo sapien
310	231.5	17.8	823	1	EMR2_HUMAN	Q9ubx3 homo sapien	383	217.5	16.8	783	2	Q90XG2	Q90xg2 gallus gall
311	231	17.8	269	2	Q8NC23	Q8nc23 homo sapien	384	217.5	16.8	950	2	Q90Z44	Q90z44 gallus gall
312	231	17.8	1282	2	Q8TER0	Q8ter0 homo sapien	385	217.5	16.8	1132	2	Q6P6T8	Q6p6t8 rattus norv
313	231	17.8	1905	1	LRP4_RAT	Q9gyp1 rattus norv	386	217	16.7	757	2	Q9HCU0	Q9hcu0 homo sapien
314	231	17.8	3523	2	Q7QCP4	Q7qcp4 anopheles g	387	217	16.7	1114	2	Q6VQAZ	Q6vqaz brachydanio
315	230.5	17.8	814	2	Q7ZXL5	Q7zxl5 xenopus lae	388	216.5	16.7	546	2	Q8R4V5	Q8r4v5 mus musculus
316	230	17.7	356	2	Q96FY1	Q96fy1 homo sapien	389	216.5	16.7	717	2	P87357	P87357 brachydanio
317	229.5	17.7	723	1	DL11_HUMAN	Q00548 homo sapien	390	216.5	16.7	720	2	Q8UWJ4	Q8uwj4 brachydanio
318	229	17.7	1950	1	LRP4_HUMAN	Q75096 homo sapien	391	216.5	16.7	1429	1	Li12_CAEEL	P14585 caenorhabdi
319	228.5	17.6	236	2	Q8WUQ9	Q8wuq9 homo sapien	392	216	16.7	684	2	Q8I498	Q8i498 cupienius
320	228.5	17.6	271	2	Q8CJG6	Q8cjpg6 rattus norv	393	215.5	16.6	664	2	Q9IAT6	Q9iat6 brachydanio
321	228.5	17.6	327	2	Q8BPM8	Q8bpm8 mus musculus	394	215.5	16.6	917	1	LRP8_CHICK	Q98931 gallus gall
322	228.5	17.6	550	2	Q9JUZ5	Q9jjz5 mus musculus	395	215.5	16.6	1521	1	SLT1_MOUSE	Q9rib9 mus musculus
323	228	17.6	815	2	Q96J52	Q96j52 homo sapien	396	215	16.6	738	1	ELT1_RAT	Q9esc1 rattus norv

397	214.5	16.5	546	2	Q6V0K7	Q6v0k7 rattus norv	470	201	15.5	1529	2	Q7ZXI2	Q7zxi2 xenopus lae
398	214.5	16.5	546	2	Q811T0	Q811t0 mus musculus	471	201	15.5	4544	1	LRP1_HUMAN	Q07954 homo sapien
399	214.5	16.5	546	2	Q8C9U1	Q8c9u1 mus musculus	472	200	15.4	689	2	Q80VA2	Q80va2 mus musculus
400	214.5	16.5	991	2	Q7SWG0	Q7swg0 penaeus jap	473	200	15.4	1209	2	Q80Z45	Q80z45 gallus gall
401	214	16.5	318	2	Q8CJG7	Q8cjg7 rattus norv	474	200	15.4	1209	2	Q80XT9	Q80xt9 mus musculus
402	214	16.5	604	2	Q6T3J7	Q6t3j7 drosophila	475	199.5	15.4	644	2	Q64ZD6	Q64zd6 rattus norv
403	214	16.5	833	1	DL_DROME	P10041 drosophila	476	199.5	15.4	3183	1	Q65ZC2	Q65zc2 caenorhabdi
404	214	16.5	1245	2	Q6PPB4	Q6ppb4 gallus gall	477	199.5	15.4	3767	1	MUA3_CAEEL	P34576 caenorhabdi
405	214	16.5	2571	1	SN1_MOUSE	Q8r4y4 mus musculus	478	199	15.3	650	2	Q7Q0M5	Q7q0m5 anopheles g
406	212.5	16.4	500	2	Q864U4	Q864u4 bos taurus	479	199	15.3	881	2	Q8WY31	Q8wy31 homo sapien
407	212.5	16.4	765	2	Q91V98	Q91v98 mus musculus	480	199	15.3	1060	2	Q968S4	Q968s4 drosophila
408	212.5	16.4	765	2	Q91ZV1	Q91zv1 mus musculus	481	199	15.3	1060	2	Q9VM97	Q9vm97 drosophila
409	212	16.3	340	2	Q7Q0KC9	Q7qkc9 anopheles g	482	199	15.3	1286	2	Q7QCT2	Q7qct2 anopheles g
410	212	16.3	678	2	Q68EY0	Q68ey0 xenopus lae	483	199	15.3	1523	1	SLT3_HUMAN	Q75094 homo sapien
411	212	16.3	1441	2	Q867Q2	Q867q2 caenorhabdi	484	199	15.3	4753	1	LRP_CAEEL	Q04833 caenorhabdi
412	211.5	16.3	674	2	Q6N0Z7	Q6n0z7 homo sapien	485	198.5	15.3	454	2	Q8TB42	Q8tb42 homo sapien
413	211.5	16.3	810	1	NEL1_HUMAN	Q92832 homo sapien	486	198.5	15.3	545	2	Q8WMZ8	Q8wmz8 homo sapien
414	211.5	16.3	810	1	Q6NSY8	Q6nsy8 homo sapien	487	198.5	15.3	674	2	Q8T4N9	Q8t4n9 strongyloce
415	211.5	16.3	1059	2	Q9VQ47	Q9vq47 drosophila	488	198.5	15.3	737	2	Q8NFT8	Q8nft8 homo sapien
416	211.5	16.3	1101	2	Q7KU08	Q7ku08 drosophila	489	197.5	15.2	382	1	EFL9_MOUSE	Q8k1e3 mus musculus
417	211.5	16.3	1529	1	SLT2_HUMAN	Q94813 homo sapien	490	197.5	15.2	644	1	UROM_RAT	P27590 rattus norv
418	211.5	16.3	3222	2	Q6V0I7	Q6v0i7 homo sapien	491	197.5	15.2	4543	1	LRP1_CHICK	P98157 gallus gall
419	211	16.3	2025	2	Q8CJA0	Q8cja0 mus musculus	492	197	15.2	474	2	Q8WYG3	Q8wyg3 homo sapien
420	211	16.3	642	2	Q91X17	Q91x17 mus musculus	493	197	15.2	863	1	LDVR_CHICK	P98165 gallus gall
421	211	16.3	1133	1	EGF_RAT	P07522 rattus norv	494	196.5	15.2	383	1	EFL9_HUMAN	Q6uy11 homo sapien
422	210.5	16.2	97	2	Q91WZ4	Q91wz4 mus ep. fib	495	196.5	15.2	737	2	Q81VT0	Q81vt0 homo sapien
423	210.5	16.2	492	2	P37806	P37806 mus musculus	496	196.5	15.2	739	2	Q8IGR9	Q8igr9 drosophila
424	210.5	16.2	4599	1	LR1B_MOUSE	Q9j1l8 mus musculus	497	196.5	15.2	818	1	CD97_MOUSE	Q9z0m6 mus musculus
425	210	16.2	615	2	O57409	O57409 brachydanio	498	196.5	15.2	883	2	Q6VBN1	Q6vbn1 drosophila
426	209.5	16.2	879	1	LDLR_RAT	P35952 rattus norv	499	196.5	15.2	996	2	Q6NP71	Q6np71 drosophila
427	209.5	16.2	1214	2	Q9BDQ0	Q9bdq0 sus scrofa	500	196.5	15.2	1031	2	Q9VBN0	Q9vbn0 drosophila
428	209	16.1	854	1	LDLR_CRIGR	P35950 cricetus	501	196.5	15.2	1037	2	Q6NP66	Q6np66 drosophila
429	209	16.1	1270	2	Q9GPN0	Q9gpn0 caenorhabdi	502	196.5	15.2	1952	2	Q95SN5	Q95sn5 drosophila
430	209	16.1	4569	2	Q7PFS35	Q7pfs35 anopheles g	503	196.5	15.2	4547	2	Q9W343	Q9w343 drosophila
431	208.5	16.1	810	1	NEL1_RAT	Q62919 rattus norv	504	196	15.1	4545	2	Q91ZX7	Q91zx7 mus musculus
432	208	16.0	792	2	Q9OZ43	Q9oz43 gallus gall	505	196	15.1	4545	2	Q920Y4	Q920y4 mus musculus
433	208	16.0	838	2	Q9VQA9	Q9vqa9 drosophila	506	196	15.1	4545	2	Q61291	Q61291 mus musculus
434	208	16.0	1095	2	Q90XG4	Q90xg4 gallus gall	507	195.5	15.1	192	2	Q9UDM2	Q9udm2 homo sapien
435	208	16.0	1984	1	YL_DROME	P98163 drosophila	508	195.5	15.1	737	2	Q8VD97	Q8vd97 mus musculus
436	208	16.0	2570	1	SN1_HUMAN	Q9ny15 homo sapien	509	195	15.0	738	2	Q7QK75	Q7qk75 anopheles g
437	207.5	16.0	732	2	Q95L62	Q95l62 sus scrofa	510	195	15.0	749	2	Q7QK77	Q7qk77 anopheles g
438	207.5	16.0	1308	2	Q9GPM8	Q9gpm8 caenorhabdi	511	195	15.0	845	2	Q91YY0	Q91yy0 mus musculus
439	207.5	16.0	4610	2	Q9AXB7	Q9axb7 brachydanio	512	195	15.0	873	1	LDVR_MOUSE	P98156 mus musculus
440	207	16.0	1809	2	Q8AMP02	Q8amp02 periplaneta	513	195	15.0	887	2	Q9U1T9	Q9u1t9 caenorhabdi
441	206	15.9	1523	1	SLT3_MOUSE	Q9rvb4 mus musculus	514	195	15.0	909	1	LDL1_XENLA	Q99087 xenopus lae
442	205	15.8	237	2	Q804J3	Q804j3 gallus gall	515	195	15.0	4655	1	LRP2_HUMAN	P98164 homo sapien
443	205	15.8	862	2	Q90UF98	Q9uf98 homo sapien	516	195	15.0	4655	2	Q7Z5C0	Q7z5c1 homo sapien
444	205	15.8	1410	2	Q20204	Q20204 caenorhabdi	517	195	15.0	4655	2	Q7Z5C1	Q7z5c1 homo sapien
445	205	15.8	1523	2	SLT3_RAT	Q88280 rattus norv	518	194.5	15.0	762	2	O42373	O42373 brachydanio
446	205	15.8	2551	1	SN2_HUMAN	Q8wqg8 h stabilin	519	194.5	15.0	837	1	LDLR_RABIT	P20063 cryctolagus
447	204.5	15.8	642	2	Q822E5	Q822e5 mus musculus	520	194.5	15.0	891	2	Q7YM57	Q7ym57 aedes aegyp
448	204.5	15.8	643	1	UROM_BOVIN	P48733 bos taurus	521	194	15.0	471	2	Q804X6	Q804x6 gallus gall
449	204	15.7	1512	2	Q9DE36	Q9de36 brachydanio	522	194	15.0	857	2	P79708	P79708 chiloscyll
450	204	15.7	1722	2	Q19350	Q19350 caenorhabdi	523	193.5	14.9	308	2	O46370	O46370 bos taurus
451	204	15.7	4589	2	Q9WU10	Q9wu10 rattus norv	524	193.5	14.9	425	2	Q7SY86	Q7sy86 xenopus lae
452	203.5	15.7	611	2	Q91YG0	Q91yg0 homo sapien	525	193	14.9	225	2	Q7PFQ7	Q7pfq7 anopheles g
453	203.5	15.7	640	1	UROM_HUMAN	P07911 homo sapien	526	193	14.9	873	1	LDVR_RABIT	P35953 cryctolagus
454	203.5	15.7	826	2	Q86B77	Q86b77 drosophila	527	193	14.9	873	1	LDVR_RAT	P98166 rattus norv
455	203.5	15.7	861	2	Q7YTZ6	Q7ytz6 drosophila	528	193	14.9	4590	1	FATH_HUMAN	Q14517 homo sapien
456	203.5	15.7	1064	2	Q7YU01	Q7yu01 drosophila	529	192	14.8	261	2	Q9GM41	Q9gm41 macaca fasc
457	203.5	15.7	1069	2	Q9VBN2	Q9vbn2 drosophila	530	192	14.8	813	2	Q6ZK10	Q6zkl0 oryza sativ
458	203	15.7	306	2	Q8C6U7	Q8c6u7 mus musculus	531	192	14.8	883	2	O46131	O46131 locusta mig
459	203	15.7	796	2	Q8MY77	Q8my77 branchiosto	532	191.5	14.8	433	2	Q804X5	Q804x5 gallus gall
460	203	15.7	1782	2	Q6X0I2	Q6x0i2 solenopsis	533	191.5	14.8	722	2	Q9DC42	Q9dc42 mus musculus
461	202.5	15.6	734	1	CD97_BOVIN	Q8esqa bos taurus	534	191	14.7	798	2	Q75WV8	Q75wv8 branchiosto
462	202	15.6	1859	2	Q7PFS28	Q7pfs28 anopheles g	535	190.5	14.7	353	2	Q86UC0	Q86uc0 homo sapien
463	201.5	15.5	389	2	Q8R226	Q8r226 mus musculus	536	190	14.6	122	2	Q869J5	Q869j5 archispiros
464	201.5	15.5	737	2	Q8JZM4	Q8jzm4 mus musculus	537	190	14.6	199	2	Q6SPF9	Q6spf9 tribolium c
465	201.5	15.5	737	2	Q8R4T6	Q8r4t6 mus musculus	538	190	14.6	752	2	Q8NAN7	Q8nan7 homo sapien
466	201.5	15.5	862	2	Q9VCT0	Q9vct0 mus musculus	539	190	14.6	873	1	LDVR_HUMAN	P98155 homo sapien
467	201.5	15.5	862	2	Q91ZJ1	Q91zj1 mus musculus	540	190	14.6	873	2	Q6S4M1	Q6s4m1 macaca mula
468	201.5	15.5	864	1	LDLR_MOUSE	P35951 mus musculus	541	190	14.6	892	1	LDL2_XENLA	Q99088 xenopus lae
469	201.5	15.5	2559	1	SN2_MOUSE	Q8r4u0 mus musculus	542	189.5	14.6	353	2	Q6UXH1	Q6uxh1 homo sapien

543	189.5	14.6	794	2	Q8T4P0	Q8T4P0 lytechinus	616	177.5	13.7	456	1	PRTC_CANFA	Q28278 canis faml
544	189.5	14.6	963	1	LRP6_HUMAN	Q14114 homo sapien	617	177	13.6	241	2	Q8C101	Q8C101 mus musculus
545	189.5	14.6	1156	2	Q963T3	Q963T3 aedes aegypt	618	177	13.6	344	2	Q9CVK2	Q9CVK2 mus musculus
546	189	14.6	663	2	Q44247	Q44247 hemiceitrot	619	176.5	13.6	350	2	Q9CYA0	Q9CYA0 mus musculus
547	189	14.6	747	2	Q6UWL2	Q6UWL2 homo sapien	620	176	13.6	459	1	PRTC_PIG	Q9G1P2 sus scrofa
548	189	14.6	780	2	Q6DJD9	Q6DJD9 xenopus lae	621	175.5	13.5	273	1	ESL7_HUMAN	Q9UHF1 homo sapien
549	188.5	14.5	227	2	Q7KPY6	Q7KPY6 lucilia cup	622	175.5	13.5	321	2	Q9BU47	Q9BU47 homo sapien
550	188.5	14.5	341	2	Q7SXF6	Q7SXF6 brachydanio	623	175.5	13.5	383	2	Q7O534	Q7O534 rattus norv
551	188.5	14.5	806	1	DLMP01	Q9J171 mus musculus	624	175.5	13.5	383	2	Q7O534	Q62779 rattus norv
552	188.5	14.5	807	2	Q8MP01	Q8MP01 halocynthia	625	175.5	13.5	482	1	FA10_RAT	Q63207 rattus norv
553	188	14.5	845	2	Q77505	Q77505 bos taurus	626	175.5	13.5	770	2	Q9U2D5	Q9U2D5 caenorhabdi
554	187.5	14.5	498	2	Q66NE4	Q66NE4 bombyx mori	627	175.5	13.5	1170	1	TSP1_BOVIN	Q8U2H7 bos taurus
555	187.5	14.5	587	2	Q8NBS4	Q8NBS4 homo sapien	628	175	13.5	438	2	Q8I497	Q8I497 cupiemius
556	187.5	14.5	758	2	Q66NE3	Q66NE3 bombyx mori	629	175	13.5	991	1	BMP1_MOUSE	Q9P063 mus musculus
557	187	14.4	721	2	Q95YGO	Q95YGO ciona savig	630	174.5	13.5	584	2	Q73920	Q73920 oncorhynch
558	186.5	14.4	383	2	Q969Y6	Q969Y6 homo sapien	631	174.5	13.5	589	1	DL13_RAT	Q88671 rattus norv
559	186.5	14.4	574	2	Q62759	Q62759 sus scrofa	632	174.5	13.5	619	2	Q73921	Q73921 oncorhynch
560	186.5	14.4	4660	1	LRP2_RAT	Q98158 rattus norv	633	174.5	13.5	775	2	Q6P550	Q6P550 mus musculus
561	186	14.3	553	2	Q8HXE2	Q8HXE2 macaca fasc	634	174.5	13.5	986	1	BMP1_MOUSE	Q8I497 homo sapien
562	185.5	14.3	376	1	FA10_TROCA	Q8428 tropidechis	635	174.5	13.5	991	2	Q6NZM2	Q6NZM2 mus musculus
563	185.5	14.3	383	1	DLK_HUMAN	Q80370 homo sapien	636	174.5	13.5	1012	2	Q9WVM6	Q9WVM6 mus musculus
564	185.5	14.3	585	2	Q8OW06	Q8OW06 mus musculus	637	174.5	13.5	1504	1	SLIT_DROME	Q24014 drosophila
565	185.5	14.3	592	1	DL13_MOUSE	Q88516 mus musculus	638	174	13.4	737	2	Q6IR63	Q6IR63 xenopus lae
566	185.5	14.3	686	2	Q9DBU9	Q9DBU9 mus musculus	639	173	13.3	684	2	Q8BIN7	Q8BIN7 toxoplasma
567	185.5	14.3	2104	2	Q21281	Q21281 caenorhabdi	640	172.5	13.3	559	2	Q9VZ44	Q9VZ44 drosophila
568	185.5	14.3	2104	2	Q964N4	Q964N4 caenorhabdi	641	172.5	13.3	947	2	Q8BKX7	Q8BKX7 mus musculus
569	185	14.3	138	2	Q6UTY0	Q6UTY0 bos taurus	642	172.5	13.3	1140	2	Q8OT91	Q8OT91 mus musculus
570	185	14.3	1431	1	SNB2_RAT	Q8CFM6 rattus norv	643	172	13.3	952	2	Q6ZTA9	Q6ZTA9 homo sapien
571	185	14.3	5175	2	Q8TOL3	Q8TOL3 caenorhabdi	644	171.5	13.2	463	2	Q6IT10	Q6IT10 pseudonaja
572	185	14.3	5198	2	Q76518	Q76518 caenorhabdi	645	171.5	13.2	475	2	Q8O4W9	Q8O4W9 fugu rubrip
573	184.5	14.2	348	2	Q6O438	Q6O438 cricetus	646	171.5	13.2	504	2	Q6DJF5	Q6DJF5 xenopus lae
574	184	14.2	475	1	FA10_CHICK	Q25155 gallus gall	647	171	13.2	156	2	Q26661	Q26661 strongyloe
575	183.5	14.1	490	1	FA10_RABIT	Q19045 oryctolagus	648	171	13.2	422	2	Q96HDI	Q96HDI homo sapien
576	183	14.1	340	2	Q8OY26	Q8OY26 mus musculus	649	171	13.2	422	2	Q619X5	Q619X5 mus musculus
577	183	14.1	481	1	FA10_MOUSE	Q88947 mus musculus	650	171	13.2	974	2	Q8UAGO	Q8UAGO ephydatia f
578	182.5	14.1	443	2	Q8JHC9	Q8JHC9 brachydanio	651	170.5	13.1	261	2	Q8IY13	Q8IY13 homo sapien
579	182.5	14.1	450	2	Q8KOH9	Q8KOH9 mus musculus	652	170.5	13.1	598	2	Q6P6N1	Q6P6N1 mus musculus
580	182.5	14.1	685	1	DL14_HUMAN	Q9NR61 homo sapien	653	170.5	13.1	4705	1	FAT2_DROME	Q9VW71 drosophila
581	182.5	14.1	844	2	Q7TSG9	Q7TSG9 mus musculus	654	170	13.1	432	2	Q6GNA2	Q6GNA2 xenopus lae
582	182.5	14.1	844	2	Q6Y857	Q6Y857 morone amer	655	169.5	13.1	219	2	Q9OWZ2	Q9OWZ2 gallus gall
583	182	14.0	292	2	Q86SMO	Q86SMO homo sapien	656	169.5	13.1	403	2	Q18375	Q18375 drosophila
584	182	14.0	296	2	Q727K9	Q727K9 homo sapien	657	169.5	13.1	417	2	Q9Y409	Q9Y409 homo sapien
585	182	14.0	439	2	Q6P7J2	Q6P7J2 homo sapien	658	169.5	13.1	420	2	Q8NFT4	Q8NFT4 homo sapien
586	182	14.0	733	2	Q6P7G8	Q6P7G8 xenopus lae	659	169.5	13.1	808	2	Q7YU36	Q7YU36 drosophila
587	181.5	14.0	444	1	FA7_RABIT	Q98139 oryctolagus	660	169.5	13.1	1067	1	TLD_DROME	Q25723 drosophila
588	181	14.0	138	2	Q7Q6T4	Q7Q6T4 anopheles g	661	169	13.0	936	2	Q81FX2	Q81FX2 crassostrea
589	181	14.0	263	2	Q8MYU6	Q8MYU6 homo sapien	662	169	13.0	977	2	Q91925	Q91925 xenopus lae
590	181	14.0	623	2	Q93484	Q93484 pisum sativ	663	169	13.0	1070	2	Q91972	Q91972 aplysia cal
591	180.5	13.9	618	1	DL13_HUMAN	Q9NYJ7 homo sapien	664	169	13.0	1075	2	Q9NC90	Q9NC90 strongyloe
592	180	13.9	238	2	Q8QGG9	Q8QGG9 gallus gall	665	168.5	13.0	467	2	Q6IT09	Q6IT09 pseudonaja
593	180	13.9	263	2	Q99740	Q99740 mus musculus	666	168.5	13.0	492	1	FA10_BOVIN	P00743 bos taurus
594	180	13.9	399	1	PROZ_MOUSE	Q9CQW3 mus musculus	667	168.5	13.0	1013	2	Q623B1	Q623B1 mus musculus
595	180	13.9	907	2	Q9XTS9	Q9XTS9 caenorhabdi	668	168.5	13.0	3616	2	Q7PPE9	Q7PPE9 anopheles g
596	179.5	13.8	272	2	Q99119	Q99119 mus musculus	669	168	13.0	452	1	FA9_CANFA	P15540 canis faml
597	179.5	13.8	290	2	Q9DAU5	Q9DAU5 mus musculus	670	168	13.0	1666	2	Q8MXG2	Q8MXG2 oryctolagus
598	179.5	13.8	385	1	DLK_MOUSE	Q99163 mus musculus	671	168	13.0	1666	2	Q8MXG2	Q8MXG2 caenorhabdi
599	179.5	13.8	385	2	Q925U3	Q925U3 mus musculus	672	168	13.0	1949	2	Q8MXG3	Q8MXG3 caenorhabdi
600	179.5	13.8	488	1	FA10_HUMAN	P00742 homo sapien	673	167.5	12.9	616	2	Q20852	Q20852 caenorhabdi
601	179	13.8	360	2	Q9AWB4	Q9AWB4 physcomitre	674	167	12.9	433	2	Q90YK1	Q90YK1 brachydanio
602	179	13.8	407	1	FA7_BOVIN	P22457 bos taurus	675	167	12.9	459	1	FA9_MOUSE	P18294 mus musculus
603	179	13.8	456	1	PRTC_BOVIN	P00745 bos taurus	676	167	12.9	460	1	PRTC_MOUSE	P33587 mus musculus
604	179	13.8	642	2	Q8GZ23	Q8GZ23 canis faml	677	167	12.9	623	2	P93026	P93026 arabidopsis
605	178.5	13.8	513	2	Q90YA5	Q90YA5 anguilla ja	678	167	12.9	623	2	P94037	P94037 arabidopsis
606	178.5	13.8	847	2	Q9OW12	Q9OW12 oncorhynch	679	167	12.9	623	2	Q94ACO	Q94ACO arabidopsis
607	178	13.7	420	2	Q91XD7	Q91XD7 mus musculus	680	166.5	12.8	267	2	Q8BXV5	Q8BXV5 mus musculus
608	178	13.7	446	1	FA7_RAT	Q8K3U6 rattus norv	681	166.5	12.8	476	2	Q661L7	Q661L7 xenopus tro
609	178	13.7	844	2	Q7ZTG7	Q7ZTG7 oreochromis	682	166.5	12.8	1007	2	Q8U128	Q8U128 xenopus lae
610	178	13.7	1081	2	Q8T4N8	Q8T4N8 penaeus sem	683	166.5	12.8	1019	2	Q57382	Q57382 xenopus lae
611	178	13.7	1650	2	Q9QVTE	Q9QVTE rattus sp.	684	166.5	12.8	4587	2	Q9QX23	Q9QX23 mus musculus
612	178	13.7	4569	2	Q7PV66	Q7PV66 anopheles g	685	166	12.8	305	2	Q9N028	Q9N028 macaca fasc
613	177.5	13.7	373	2	Q90YA4	Q90YA4 conger myri	686	166	12.8	356	2	Q19267	Q19267 caenorhabdi
614	177.5	13.7	376	1	FA10_HOPST	P83370 hoplocephal	687	166	12.8	470	2	Q8T3A1	Q8T3A1 clona intes
615	177.5	13.7	446	1	FA7_MOUSE	P70375 mus musculus	688	166	12.8	626	2	Q7XHX6	Q7XHX6 oryza sativ

689	166	12.8	1278	2	Q7Q440	Q7q440 anopheles g	762	158.5	12.2	838	2	Q27422	Q27422 caenorhabdi
690	165.5	12.8	462	2	Q6PAG2	Q6pag2 xenopus lae	763	158.5	12.2	890	2	Q7Q41	Q7qj41 anopheles g
691	165.5	12.8	504	2	Q6PGW7	Q6pgw7 brachydanio	764	158.5	12.2	925	2	Q9UB95	Q9ub95 caenorhabdi
692	165	12.7	434	2	Q7T3B6	Q7t3b6 brachydanio	765	158.5	12.2	942	2	Q7QYW9	Q7qyw9 giardia lam
693	165	12.7	466	1	FA7_HUMAN	P08709 homo sapien	766	158.5	12.2	951	2	Q20176	Q20176 caenorhabdi
694	165	12.7	624	2	O48662	O48662 cucurbita c	767	158.5	12.2	961	2	Q86TG2	Q86tg2 homo sapien
695	165	12.7	679	2	Q86PQ8	Q86pq8 homo sapien	768	158.5	12.2	1147	2	O6DIB5	O6dib5 mus musculus
696	165	12.7	1051	2	Q8TA75	Q8ta75 caenorhabdi	769	158.5	12.2	3712	1	LMA_DROME	Q00174 drosophila
697	165	12.7	1090	2	Q95QP6	Q95qp6 caenorhabdi	770	158.5	12.2	3712	2	Q9VFW0	Q9vrw0 drosophila
698	164.5	12.7	537	2	Q804W8	Q804w8 fugu rubrip	771	158	12.2	138	2	Q28S94	Q28s94 sus scrofa
699	164.5	12.7	591	2	Q6LBN5	Q6lbn5 homo sapien	772	158	12.2	252	2	Q9NTF1	Q9ntf1 homo sapien
700	164.5	12.7	949	1	TSP4_BRARE	Q81gw0 brachydanio	773	158	12.2	692	2	O6PDN4	O6pdn4 mus musculus
701	164.5	12.7	1022	1	TLD_BRARE	O57460 brachydanio	774	158	12.2	1045	2	Q8T3A6	Q8t3a6 caenorhabdi
702	164	12.6	338	2	Q7QGV2	Q7qgv2 anopheles g	775	158	12.2	1070	2	Q8T3A7	Q8t3a7 caenorhabdi
703	164	12.6	433	2	Q8JHDO	Q8jhd0 brachydanio	776	158	12.2	1111	2	Q9XWD6	Q9xwd6 caenorhabdi
704	164	12.6	461	1	PRTC_HUMAN	P04070 homo sapien	777	158	12.2	1235	2	Q65YF9	Q65yf9 ciona intes
705	164	12.6	582	2	Q7QPM3	Q7qpm3 giardia lam	778	158	12.2	1501	2	Q75JAS	Q75jas dictyostell
706	163.5	12.6	626	2	Q8ND91	Q8nd91 homo sapien	779	158	12.2	1615	2	Q7QZU9	Q7qzu9 giardia lam
707	163.5	12.6	726	2	Q7SY09	Q7sy09 brachydanio	780	157.5	12.1	406	2	O6UXH8	Q6uxh8 homo sapien
708	163.5	12.6	969	2	Q96KG6	Q96kg6 homo sapien	781	157.5	12.1	418	2	Q8TF19	Q8tf19 homo sapien
709	163.5	12.6	1827	2	Q20535	Q20535 caenorhabdi	782	157.5	12.1	1104	2	Q8CGA7	Q8cga7 mus musculus
710	163	12.6	461	2	Q68FY8	Q68fy8 rattus norv	783	157	12.1	1810	2	Q90824	Q90824 gallus gall
711	163	12.6	574	2	Q68R18	Q68r18 rattus norv	784	157	12.1	768	1	LEM3_MOUSE	Q01102 mus musculus
712	163	12.6	628	2	O80979	O80979 arabidopsis	785	157	12.1	841	2	O6R8J3	Q6r8j4 brachydanio
713	163	12.6	630	2	P93027	P93027 arabidopsis	786	157	12.1	935	2	Q6R8J2	Q6r8j3 brachydanio
714	163	12.6	820	2	Q96NT6	Q96nt6 homo sapien	787	157	12.1	977	2	Q6R8J2	Q6r8j2 brachydanio
715	163	12.6	1170	1	TSP1_MOUSE	P35441 mus musculus	788	157	12.1	1004	2	Q8CGA7	Q8cga7 mus musculus
716	163	12.6	1171	2	Q80YQ1	Q80yq1 mus musculus	789	157	12.1	1170	1	TSP1_HUMAN	P07996 homo sapien
717	163	12.6	1171	2	Q8CGB2	Q8cgb2 mus musculus	790	156.5	12.1	1584	2	Q93791	Q93791 caenorhabdi
718	163	12.6	1731	2	Q8WY30	Q8wy30 homo sapien	791	156.5	12.1	155	2	O6YIL9	Q6yil9 drosophila
719	162.5	12.5	424	2	Q7Q3P0	Q7q3p0 anopheles g	792	156.5	12.1	155	2	Q7YSR5	Q7ysr5 drosophila
720	162.5	12.5	1013	2	O43897	O43897 mus musculus	793	156.5	12.1	155	2	Q7ZIJ0	Q7zlj0 drosophila
721	162.5	12.5	1013	2	Q9NQS4	Q9nqs4 homo sapien	794	156.5	12.1	567	2	Q8WUL3	Q8wul3 homo sapien
722	162	12.5	628	2	O80977	O80977 arabidopsis	795	156.5	12.1	909	2	Q7JP81	Q7jpb1 caenorhabdi
723	162	12.5	832	2	Q80YX0	Q80yx0 mus musculus	796	156.5	12.1	911	2	Q7JP80	Q7jpb0 caenorhabdi
724	162	12.5	1008	2	Q3DER7	Q3der7 gallus gall	797	156.5	12.1	1140	2	Q96KG7	Q96kg7 homo sapien
725	162	12.5	1170	2	Q71SA3	Q71sa3 rattus norv	798	156.5	12.1	1140	2	Q68DE5	Q68de5 homo sapien
726	162	12.5	1532	2	Q90994	Q90994 gallus gall	799	156	12.0	1768	2	Q7QEK9	Q7qek9 anopheles g
727	162	12.5	1714	2	Q90995	Q90995 gallus gall	800	155.5	12.0	512	2	Q95RQ1	Q95rq1 drosophila
728	162	12.5	1808	1	TENA_CHICK	P10039 gallus gall	801	155.5	12.0	374	2	Q9VPJ0	Q9vpj0 drosophila
729	162	12.5	2019	2	Q64706	Q64706 mus musculus	802	155.5	12.0	685	2	Q7QWD9	Q7qwd9 giardia lam
730	162	12.5	2019	2	Q80YX2	Q80yx2 mus musculus	803	155.5	12.0	915	2	O02364	O02364 caenorhabdi
731	162	12.5	2110	2	Q80YX1	Q80yx1 mus musculus	804	155.5	12.0	927	2	Q7JKS6	Q7jks6 caenorhabdi
732	161.5	12.5	469	2	Q9GMD9	Q9gmd9 ornithorhyn	805	155.5	12.0	980	1	TSP4_RAT	P49744 rattus norv
733	161.5	12.5	752	2	Q93473	Q93473 caenorhabdi	806	155.5	12.0	1015	2	Q9Y6L7	Q9y6l7 homo sapien
734	161.5	12.5	1097	2	Q8TDW7	Q8tdw7 homo sapien	807	155.5	12.0	1078	2	Q9UQ00	Q9uq00 homo sapien
735	161.5	12.5	2811	2	Q7Q434	Q7q434 anopheles g	808	155.5	12.0	3672	1	LML2_CAEEL	Q21313 caenorhabdi
736	161.5	12.5	4555	2	Q8R508	Q8r508 rattus norv	809	155.5	12.0	3704	2	F91904	P91904 caenorhabdi
737	161	12.4	441	2	Q804X2	Q804x2 fugu rubrip	810	155	12.0	5147	1	FAT_DROME	P33450 drosophila
738	161	12.4	461	1	PRTC_RAT	P31394 rattus norv	811	155	12.0	337	2	Q8NHD3	Q8nhd3 homo sapien
739	161	12.4	1027	2	Q7QK54	Q7qk54 anopheles g	812	155	12.0	342	2	Q8NHD5	Q8nhd5 homo sapien
740	161	12.4	4699	2	Q9V383	Q9v383 drosophila	813	155	12.0	466	2	O6SA95	O6sa95 felis silve
741	160.5	12.4	211	2	Q6H8Q4	Q6h8q4 canis fami	814	155	12.0	515	2	O7QYS0	Q7qys0 giardia lam
742	160.5	12.4	280	2	Q7ZXTO	Q7zxt0 xenopus lae	815	155	12.0	528	2	Q8NHD4	Q8nhd4 caenorhabdi
743	160.5	12.4	362	2	Q9U483	Q9u483 neospora ca	816	155	12.0	569	2	Q8NHD2	Q8nhd2 homo sapien
744	160.5	12.4	474	2	O8THC8	O8thc8 brachydanio	817	155	12.0	744	2	Q8NHD2	Q8nhd2 homo sapien
745	160.5	12.4	625	2	Q8L7E3	Q8l7e3 arabidopsis	818	155	12.0	830	1	SREC_HUMAN	Q6e0k3 didelphis m
746	160.5	12.4	1464	2	Q23995	Q23995 drosophila	819	155	12.0	1117	2	O6E0K3	Q00546 gallus gall
747	160.5	12.4	1464	2	Q24132	Q24132 drosophila	820	155	12.0	1353	2	Q00546	Q00546 gallus gall
748	160.5	12.4	1464	2	Q9VC47	Q9vc47 drosophila	821	155	12.0	2517	2	Q7QLI9	Q7qli9 anopheles g
749	160	12.3	378	2	Q21756	Q21756 caenorhabdi	822	155	12.0	3695	1	LMAS_HUMAN	O15230 homo sapien
750	160	12.3	2201	1	TENA_HUMAN	P24821 homo sapien	823	154.5	11.9	3695	1	Q8TDF8	Q8tdf8 homo sapien
751	159.5	12.3	220	2	Q8TCT8	Q8tct8 homo sapien	824	154.5	11.9	277	2	Q63404	Q63404 rattus norv
752	159.5	12.3	400	1	PRTZ_HUMAN	P22891 homo sapien	825	154.5	11.9	220	2	Q6QH77	Q6qh77 brachydanio
753	159.5	12.3	628	2	Q7Q0C4	Q7q0c4 anopheles g	826	154.5	11.9	747	2	Q8VHF4	Q8vhf4 mus musculus
754	159.5	12.3	961	1	TSP4_HUMAN	P35443 homo sapien	827	154.5	11.9	963	1	TSPA_MOUSE	Q9z1c2 mus musculus
755	159.5	12.3	1581	2	Q73809	Q73809 fugu rubrip	828	154.5	11.9	1034	2	O8VHL7	Q8vhl7 mus musculus
756	159	12.3	442	2	Q804X1	Q804x1 fugu rubrip	829	154.5	11.9	1034	2	O8VIK5	Q8vik5 mus musculus
757	159	12.3	1746	1	TENA_PIG	Q29116 sus scrofa	830	154	11.9	144	2	O12973	O12973 gallus gall
758	158.5	12.2	408	2	Q8BFW1	Q8bfw1 m mus muscu	831	153.5	11.8	488	2	Q8N2M7	Q8n2m7 homo sapien
759	158.5	12.2	408	2	Q8BMT1	Q8bmt1 mus musculus	832	153.5	11.8	540	2	Q8N2M5	Q8n2m5 homo sapien
760	158.5	12.2	600	2	Q8N369	Q8n369 homo sapien	833	153.5	11.8	1089	2	Q8T3A0	Q8t3a0 ciona intes
761	158.5	12.2	838	2	Q18761	Q18761 caenorhabdi	834	153	11.8	416	1	FA9_BOVIN	P00741 bos taurus

835	153	11.8	502	2	017692	017692 caenorhabdi	908	145.5	11.2	360	2	Q7Q114	Q7q114 anopheles g
836	153	11.8	576	2	Q6YID6	Q6yid6 penaeus mon	909	145.5	11.2	2515	2	Q24551	Q24551 drosophila
837	153	11.8	619	2	Q93X09	Q93x09 vigna mungo	910	145.5	11.2	2731	2	018366	018366 drosophila
838	153	11.8	647	2	Q71Z69	Q71z69 notophthalm	911	145.5	11.2	2731	2	061307	061307 drosophila
839	153	11.8	925	2	044191	044191 caenorhabdi	912	145.5	11.2	2731	2	Q9VNU6	Q9vnu6 drosophila
840	153	11.8	925	2	Q9U4E4	Q9u4e4 caenorhabdi	913	145.5	11.2	2972	2	P90891	P90891 caenorhabdi
841	153	11.8	925	2	Q9UB94	Q9ub94 caenorhabdi	914	145	11.2	1036	2	Q97378	Q97378 strongyloce
842	152.5	11.8	624	2	Q9LLR3	Q9llr3 triticum ae	915	145	11.2	1136	1	TIE1_BOVIN	TIE1_BOVIN
843	152.5	11.8	647	2	Q8MLX3	Q8mlx3 caenorhabdi	916	144.5	11.1	124	2	Q659B4	Q659b4 homo sapien
844	152.5	11.8	647	2	Q8NM25	Q8nm25 caenorhabdi	917	144.5	11.1	474	2	Q919K4	Q919k4 gallus gall
845	152.5	11.8	647	2	Q8MV49	Q8mv49 caenorhabdi	918	144.5	11.1	637	2	Q655Y8	Q655y8 oryza sativ
846	152.5	11.8	647	2	Q8MV50	Q8mv50 caenorhabdi	919	144.5	11.1	664	2	Q6WS87	Q6ws87 hyalomma an
847	152.5	11.8	647	2	Q8MV51	Q8mv51 caenorhabdi	920	144.5	11.1	1935	2	Q6QHS3	Q6qhs3 lytechinus
848	152.5	11.8	647	2	Q8MV52	Q8mv52 caenorhabdi	921	144.5	11.1	2643	2	001552	001552 caenorhabdi
849	152.5	11.8	647	2	Q8MV53	Q8mv53 caenorhabdi	922	143.5	11.1	631	2	Q94HD5	Q94hd5 oryza sativ
850	152.5	11.8	661	2	Q9TVY6	Q9tvy6 caenorhabdi	923	143.5	11.1	643	2	Q8H8K1	Q8h8k1 oryza sativ
851	152.5	11.8	954	2	Q75UQ6	Q75uq6 achaearanaea	924	143.5	11.1	650	1	BM86_BOOMI	BM86_BOOMI
852	152.5	11.8	2009	2	Q9VXM0	Q9vxm0 drosophila	925	143.5	11.1	754	2	Q6DFX1	Q6dfx1 mus musculu
853	152	11.7	594	2	Q6U705	Q6uy05 homo sapien	926	143.5	11.1	3170	2	Q7PN80	Q7pn80 anopheles g
854	152	11.7	765	2	Q9NL50	Q9nl50 sarcophaga	927	143	11.0	300	2	Q9BIM6	Q9bim6 toxoplasma
855	152	11.7	803	2	Q7QSK8	Q7qsk8 giardia lam	928	143	11.0	474	2	Q68EF1	Q68ef1 mus musculu
856	152	11.7	3718	1	LMA5_MOUSE	L61001 mus musculu	929	143	11.0	681	2	Q7ZT70	Q7zt70 lampetra ja
857	151.5	11.7	155	2	Q7Z1J1	Q7z1j1 drosophila	930	143	11.0	748	1	AD10_HUMAN	AD10_HUMAN
858	151.5	11.7	638	2	Q7PM27	Q7pm27 anopheles g	931	142.5	11.0	278	1	EFL7_MOUSE	EFL7_MOUSE
859	151.5	11.7	849	2	Q96SQ3	Q96sq3 homo sapien	932	142.5	11.0	317	2	Q9NGD3	Q9ngd3 drosophila
860	151	11.6	656	1	EFL3_MOUSE	Q8ov70 mus musculu	933	142.5	11.0	317	2	Q9NGD4	Q9ngd4 drosophila
861	151	11.6	835	2	Q69ZY6	Q69zy6 mus musculu	934	142.5	11.0	317	2	Q9NGD5	Q9ngd5 drosophila
862	151	11.6	860	2	Q7QAH1	Q7qah1 anopheles g	935	142.5	11.0	317	2	Q9NGD7	Q9ngd7 drosophila
863	150.5	11.6	866	1	SRC2_HUMAN	Q96gp6 homo sapien	936	142.5	11.0	317	2	Q9NGD9	Q9ngd9 drosophila
864	150	11.6	279	1	EFL7_RAT	Q6az60 rattus norv	937	142.5	11.0	806	1	ITB7_MOUSE	ITB7_MOUSE
865	150	11.6	299	2	Q8BX64	Q8bx64 mus musculu	938	142.5	11.0	833	1	SRC2_MOUSE	SRC2_MOUSE
866	150	11.6	461	1	FA9_HUMAN	P00740 homo sapien	939	142.5	11.0	979	2	Q9VB78	Q9vb78 drosophila
867	150	11.6	461	1	FA9_PANTR	Q95nd7 pan troglod	940	142	10.9	403	2	014549	014549 homo sapien
868	150	11.6	461	2	Q95ND6	Q95nd6 pan troglod	941	142	10.9	430	2	Q804X0	Q804x0 fugu rubrip
869	150	11.6	574	2	Q7R5J3	Q7r5j3 giardia lam	942	142	10.9	648	2	Q9NKD7	Q9nkd7 drosophila
870	150	11.6	851	2	Q7Q1J5	Q7q1j5 anopheles g	943	142	10.9	648	2	Q9VJU4	Q9vju4 drosophila
871	150	11.6	881	2	Q9W0A0	Q9w0a0 drosophila	944	142	10.9	701	2	Q86BL2	Q86bl2 drosophila
872	150	11.6	1107	1	YLK2_CAEEL	P41950 caenorhabdi	945	142	10.9	2765	1	TSF3_BRARE	TSF3_BRARE
873	150	11.6	1350	2	Q9V5J7	Q9v5j7 drosophila	946	142	10.9	962	1	Q9R1K2	Q9r1k2 rattus norv
874	150	11.6	1370	2	Q7KQX6	Q7kqx6 drosophila	947	142	10.9	5141	2	Q700K0	Q700k0 rattus norv
875	150	11.6	1451	2	Q7R2Y9	Q7r2y9 giardia lam	948	141.5	10.9	384	2	Q9W630	Q9w630 cyprinus ca
876	149.5	11.5	112	2	Q9H557	Q9h557 homo sapien	949	141.5	10.9	1823	2	Q7PRP5	Q7prp5 anopheles g
877	149.5	11.5	293	1	EFL8_MOUSE	Q6guq1 mus musculu	950	141	10.9	494	2	Q8VDV0	Q8vdv0 mus musculu
878	149	11.5	396	1	PRTZ_BOVIN	P00744 bos taurus	951	141	10.9	494	2	Q8BMS0	Q8bms0 mus musculu
879	149	11.5	592	2	Q7QT99	Q7qt99 giardia lam	952	141	10.9	808	2	Q9XXU1	Q9xxul caenorhabdi
880	149	11.5	663	2	Q7X6L7	Q7x6l7 oryza sativ	953	141	10.9	810	2	Q9NL29	Q9nl29 caenorhabdi
881	149	11.5	892	2	Q25243	Q25243 lucilia cup	954	141	10.9	1358	2	Q15568	Q15568 homo sapien
882	149	11.5	956	1	TSF3_HUMAN	P49746 homo sapien	955	141	10.9	1358	2	Q92752	Q92752 homo sapien
883	148.5	11.4	673	2	Q7PPD2	Q7ppd2 anopheles g	956	141	10.9	4998	2	Q8CG65	Q8cg65 mus musculu
884	148.5	11.4	4135	2	018977	018977 bos taurus	957	141	10.9	5086	2	Q7Q3K5	Q7q3k5 anopheles g
885	148	11.4	320	2	Q8N780	Q8n780 homo sapien	958	140.5	10.8	569	2	Q9Y0V1	Q9y0v1 boophilus m
886	148	11.4	626	2	Q49438	Q49438 arabidopsis	959	140.5	10.8	640	2	Q09182	Q09182 rattus norv
887	148	11.4	1751	2	Q7PXP5	Q7pxf5 anopheles g	960	140	10.8	40	2	Q8IXC8	Q8ixc8 homo sapien
888	148	11.4	1827	2	Q8UHV6	Q8jnv6 brachydanio	961	140	10.8	40	2	Q86Z10	Q86z10 homo sapien
889	147.5	11.4	159	2	Q9SDR8	Q9sdr8 prunus dulc	962	140	10.8	494	2	Q9S965	Q9s965 homo sapien
890	147.5	11.4	219	2	Q8BMS15	Q8bms15 mus musculu	963	140	10.8	625	2	Q22925	Q22925 arabidopsis
891	147.5	11.4	1521	2	Q7QYW5	Q7qyw5 giardia lam	964	140	10.8	784	2	Q97702	Q97702 canis famil
892	147	11.3	109	2	Q15972	Q15972 homo sapien	965	140	10.8	784	2	Q9TUN7	Q9tun7 canis famil
893	147	11.3	291	1	EFL8_RAT	Q6mg84 rattus norv	966	139.5	10.8	317	2	Q9NGD6	Q9ngd6 drosophila
894	147	11.3	425	2	Q804X7	Q804x7 gallus gall	967	139.5	10.8	317	2	Q9NGD8	Q9ngd8 drosophila
895	147	11.3	884	2	Q7QT01	Q7qt01 giardia lam	968	139.5	10.8	799	1	ITEN_DROME	ITEN_DROME
896	147	11.3	956	1	TSF3_MOUSE	Q05895 mus musculu	969	139.5	10.8	1162	2	Q7WTP0	Q7wtp0 halocynthia
897	147	11.3	956	1	Q7TN15	Q7tn15 mus musculu	970	139.5	10.8	2633	2	Q7OK12	Q7ok12 anopheles g
898	147	11.3	13133	2	Q71A42	Q71a42 caenorhabdi	971	139.5	10.8	2923	1	CLR2_HUMAN	CLR2_HUMAN
899	146.5	11.3	448	2	Q9VJU8	Q9vju8 drosophila	972	139	10.7	266	2	Q9R1K1	Q9r1k1 rattus norv
900	146.5	11.3	647	2	Q8MV54	Q8mv54 caenorhabdi	973	139	10.7	544	1	AD10_RAT	AD10_RAT
901	146.5	11.3	220	1	LMG3_MOUSE	Q9r0b6 mus musculu	974	139	10.7	852	2	Q75S85	Q75s85 halocynthia
902	146	11.3	1581	2	Q8MVP0	Q8mvp0 boltenia vi	975	139	10.7	1125	1	TIE2_BOVIN	TIE2_BOVIN
903	146	11.3	421	2	Q9NKE1	Q9nke1 drosophila	976	138.5	10.7	744	2	Q7Q7D9	Q7q7d9 anopheles g
904	146	11.3	766	2	Q7XVH9	Q7xvh9 oryza sativ	977	138.5	10.7	837	2	Q75S84	Q75s84 halocynthia
905	146	11.3	1356	2	Q05546	Q05546 rattus norv	978	138.5	10.7	1639	1	LMG1_DROME	LMG1_DROME
906	146	11.3	1358	2	Q8BY19	Q8by19 mus musculu	979	138.5	10.7	2212	2	Q7Q112	Q7q112 anopheles g
907	145.5	11.2	293	1	EFL8_HUMAN	Q99944 homo sapien	980	138.5	10.7	2764	2	Q9WTS5	Q9wts5 mus musculu

981 138.5 10.7 3005 2 Q6BFG4 paramecium
 982 138 10.6 211 2 Q6TPK5 O6tpk5 gallus gall
 983 138 10.6 400 2 Q5QP8 Q5qpr8 caenorhabdi
 984 138 10.6 504 2 Q7QWR4 Q7qwr4 giardia lam
 985 138 10.6 721 2 Q818V6 Q81rv6 giardia lam
 986 138 10.6 1299 2 Q7R4A6 Q7r4a6 giardia lam
 987 138 10.6 2427 2 Q8MQ36 Q8mq36 caenorhabdi
 988 138 10.6 2705 2 Q9W6V6 Q9w6v6 gallus gall
 989 138 10.6 4006 2 Q35452 Q35452 mus musculu
 990 138 10.6 4114 2 Q34796 Q34796 mus musculu
 991 138 10.6 4288 2 Q3NPX9 Q3npk9 homo sapien
 992 138 10.6 4289 1 TENX_HUMAN P22105 homo sapien
 993 137.5 10.6 639 1 BNPX_STRPU P98069 strongyloce
 994 137.5 10.6 891 1 Q6NNG1 Q6nng1 drosophila
 995 137.5 10.6 955 1 Q6Q441 Q6q441 xenopus lae
 996 137.5 10.6 1039 2 Q9VQB1 Q9vqb1 drosophila
 997 137.5 10.6 1050 2 Q71G60 Q71g60 red sea bre
 998 137.5 10.6 2330 1 EFL4_MOUSE P60882 mus musculu
 999 137 10.6 337 2 Q9RLK0 Q9rlk0 rattus norv
 1000 137 10.6 798 1 ITB5_MOUSE O70309 mus musculu

ALIGNMENTS

RESULT 1

AS6_HUMAN STANDARD; PRT; 721 AA.
 AC Q14393; Q7Z7N3;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth-arrest-specific protein 6 precursor (GAS-6).
 GN Name=GAS6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=93330291; PubMed=8336730;
 RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
 RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
 RT member of the vitamin K-dependent proteins related to protein S, a
 RT negative regulator in the blood coagulation cascade.";
 RL Mol. Cell. Biol. 13:4976-4985(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Munoz X., Sunoy L., de Frutos P., Sala N.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Uterus;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiroaka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togawa S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
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 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 Nat. Genet. 36:40-45(2004).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=fetal lung, and fetal spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler N.K.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-85 FROM N.A.
 RA Maree A.O., Hillmann A., McRedmond J.P., Fitzgerald D.J.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP RECEPTOR INTERACTION.
 RX PubMed=7854420; DOI=10.1038/373623a0;
 RA Varnum B.C., Young C., Elliott G., Garcia A., Bartley T.D.,
 Fridell Y.W., Hunt R.W., Trail G., Clogston C., Toso R.J.,
 RA Yanagihara D., Bennett L., Sylber M., Merewether L.A., Tseng A.,
 Escobar E., Liu E.T., Yamane H.K.;
 RT "Axl receptor tyrosine kinase stimulated by the vitamin K-dependent
 RT protein encoded by growth-arrest-specific gene 6.";
 RL Nature 373:623-626(1995).
 RN [7]
 RP RECEPTOR INTERACTION.
 RX PubMed=7867073; DOI=10.1016/0092-8674(95)90520-0;
 RA Matt T.N., Conn G., Gore M., Lai C., Bruno J., Radziejewski C.,
 Sattison K., Fisher J., Gies D.R., Jones P.F., Masiakowski P.,
 Ryan T.E., Tobkes N.J., Chen D.H., DiStefano P.S., Long G.L.,
 RA Basilico C., Goldfarb M.P., Lemke G., Glass D.J., Yancopoulos G.D.;
 RT "The anticosagulation factor protein S and its relative, Gas6, are
 RT ligands for the Tyro 3/Axl family of receptor tyrosine kinases.";
 RL Cell 80:661-670(1995).
 RN [8]
 RP ALTERNATIVE SPLICING (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX PubMed=9326368; DOI=10.1016/S0014-5793(97)01094-6;
 RA Marcandalli P., Gostissa M., Varnum B., Goruppi S., Schneider C.;
 RT "Identification and tissue expression of a splice variant for the
 RT growth arrest-specific gene gas6.";
 RL FEBS Lett. 415:56-58(1997).
 RN [9]
 RP RECEPTOR INTERACTION.
 RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;
 RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
 Mizuno K.;

RT Identification of the product of growth arrest-specific gene 6 as a
common ligand for Axl, Sky, and Mer receptor tyrosine kinases.,"
J. Biol. Chem. 271:30022-30027(1996).
[10]
RN RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND PROCESSING.
RX PubMed=9326369; DOI=10.1016/S0014-5793(97)01093-4; Clogston C.,
Goruppi S., Yamane H., Marchandalli P., Garcia A., Clogston C.,
Gostissa M., Varnum B., Schneider C.;
RA "The product of a gas6 splice variant allows the release of the domain
responsible for Axl tyrosine kinase receptor activation.,"
RT PEBB Lett. 415:59-63(1997).
RL [11]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 261-721 (ISOFORM 2), AND
RP MUTAGENESIS OF PHE-530; LEU-663 AND TYR-703.
RX PubMed=8621659; DOI=10.1074/jbc.271.16.9785;
RA Mark M.R., Chen J., Hammonds R.G., Sadick M., Godowsk P.J.;
RT "Characterization of Gas6, a member of the superfamily of G domain-
containing proteins, as a ligand for Rse and Axl.,"
RL J. Biol. Chem. 271:9785-9789(1996).
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
and MER whose signaling is implicated in cell growth and survival,
cell adhesion and cell migration. Plays a role in thrombosis by
amplifying platelet aggregation and secretion in response to known
agonists (by similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=gas6SV;
CC IsoId=Q14393-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q14393-2; Sequence=VSP_010494;
CC Name=3;
CC IsoId=Q14393-3; Sequence=VSP_010492, VSP_010493, VSP_010494;
CC Note-No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Plasma. Isoform 1 and isoform 2 are widely
expressed. Isoform 1 is the predominant form in spleen.
CC -!- PTM: Isoform 1 is proteolytically processed after secretion to
yield a N-terminal 36 kDa protein and a C-terminal 50 kDa protein
including the laminin G-like domains which activates AXL.
CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
dependent carboxylation. These residues are essential for the
binding of calcium (by similarity).
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC
DR EMBL; L13720; AAA58494.1; -.
DR EMBL; AY256843; AAO84057.1; -.
DR EMBL; AY256830; AAO84057.1; JOINED.
DR EMBL; AY256831; AAO84057.1; JOINED.
DR EMBL; AY256832; AAO84057.1; JOINED.
DR EMBL; AY256833; AAO84057.1; JOINED.
DR EMBL; AY256834; AAO84057.1; JOINED.
DR EMBL; AY256835; AAO84057.1; JOINED.
DR EMBL; AY256836; AAO84057.1; JOINED.
DR EMBL; AY256837; AAO84057.1; JOINED.
DR EMBL; AY256838; AAO84057.1; JOINED.
DR EMBL; AY256839; AAO84057.1; JOINED.
DR EMBL; AY256840; AAO84057.1; JOINED.
DR EMBL; AY256841; AAO84057.1; JOINED.
DR EMBL; AY256842; AAO84057.1; JOINED.
DR EMBL; AK126533; BAC6580.1; -.
DR EMBL; BC038984; AAH38984.1; -.

DR EMBL; AY170372; AAO41859.1; -.
DR PIR; B48089; B48089.
DR PDB; 1H30; X-ray; A=257-678.
DR Genew; HGNC:4168; GAS6.
DR MIM; 600441; -.
DR GO; GO:0005102; P:receptor binding; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
Query Match 97.6%; Score 1265.5; DB 1; Length 721;
Best Local Similarity 84.1%; Pred. No. 2.6e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
QY 1 PRYLDCINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 60
DB 90 PRYLDCINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 149
QY 61 GLRLCDKDVNECSQENGGCLQICHNKPFSFHCSSGFLSSDGRTCQDIDECADSEACGE 120
DB 150 GLRLCDKDVNECSQENGGCLQICHNKPFSFHCSSGFLSSDGRTCQDIDECADSEACGE 209
QY 121 ARCKNLPGSYCLCDEGFPAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGLK 180
DB 210 ARCKNLPGSYCLCDEGFPAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGLK 269
QY 181 LSQMDMTCE-----DILPCVPFF 197
DB 270 LSQMDMTCELEAGWPCPRRRDGSPPAARPGAGQSRSEGHIPDRRGRPRWQDILPCVPFF 329
QY 198 SVAKSVKSLYLGRMFSGTPTVIRLRFKRLQ 227
DB 330 SVAKSVKSLYLGRMFSGTPTVIRLRFKRLQ 359
RESULT 2
GAS6 RAT STANDARD; PRT; 674 AA.
ID GAS6 RAT STANDARD; PRT; 674 AA.
AC Q63772;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-arrest-specific protein 6 precursor (GAS-6) (Growth-
potentiating factor) (GPF).
GN Name=Gas6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95197586; PubMed=7890695; DOI=10.1074/jbc.270.11.5702;
RA Nakano T., Higashino K., Kikuchi N., Kishino J., Nomura K., Fujita H.,
Ohara O., Arita H.;
RT "Vascular smooth muscle cell-derived, Gla-containing growth-
potentiating factor for Ca(2+)-mobilizing growth factors.,"
RL J. Biol. Chem. 270:5702-5705(1995).
RN [2]
RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=7559388; DOI=10.1074/jbc.270.39.22681;
RA Ohashi K., Nagata K., Toshima J., Nakano T., Arita H., Teuda H.,
Suzuki K., Mizuno K.;
RT "Stimulation of sky receptor tyrosine kinase by the product of growth
arrest-specific gene 6.,"
RL J. Biol. Chem. 270:22681-22684(1995).
RN [3]
RP RECEPTOR INTERACTION.
RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;
RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
Mizuno K.;
RT "Identification of the product of growth arrest-specific gene 6 as a
common ligand for Axl, Sky, and Mer receptor tyrosine kinases.,"
RL J. Biol. Chem. 271:30022-30027(1996).
RN [4]

GAMMA-CARBOXYGLUTAMIC ACIDS.

RP PubMed-9163328;
 RA Nakano T., Kawamoto K., Kishino J., Nomura K., Higashino K., Arita H.;
 RT "Requirement of gamma-carboxyglutamic acid residues for the biological
 RT activity of Gas6; contribution of endogenous Gas6 to the proliferation
 RT of vascular smooth muscle cells.";
 RL Biochem. J. 323:387-392(1997).
 CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
 CC and MER whose signaling is implicated in cell growth and survival,
 CC cell adhesion and cell migration. Plays a role in thrombosis by
 CC amplifying platelet aggregation and secretion in response to known
 CC agonists (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
 CC dependent carboxylation. These residues are essential for the
 CC binding of calcium (Probable).
 CC -!- SIMILARITY: Contains 4 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC -!- SIMILARITY: Contains 2 laminin G-like domains.

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 CC or send an email to license@isb-sib.ch).

 DR EMBL; D42148; BAA0719.1; -;
 DR PIR; I55476; I55476.
 DR HSP; P00740; ICFH.
 DR GSD; 61913; Gas6.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR008985; ConA like_lec_gl.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR003129; TSP N.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00054; Laminin_G; 2.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF 1; 1.
 DR PROSITE; PS01186; EGF 2; 3.
 DR PROSITE; PS50026; EGF 3; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS50998; GLA_2; 1.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
 KW Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid;
 KW Growth regulation; Repeat; Signal; Vitamin K.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 674 Growth-arrest-specific protein 6.
 FT DOMAIN 50 91 Gla.
 FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).
 FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).
 FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 295 467 Laminin G-like 1.
 FT DOMAIN 474 666 Laminin G-like 2.
 FT METAL 326 326 Calcium (By similarity).
 FT METAL 328 328 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 437 437 Calcium (via carbonyl oxygen) (By similarity).
 FT METAL 652 652 Calcium (By similarity).
 FT DISULFID 117 130 By similarity.
 FT DISULFID 122 139 By similarity.
 FT DISULFID 141 150 By similarity.
 FT DISULFID 157 168 By similarity.
 FT DISULFID 164 177 By similarity.
 FT DISULFID 179 192 By similarity.
 FT DISULFID 198 209 By similarity.
 FT DISULFID 204 218 By similarity.
 FT DISULFID 220 233 By similarity.
 FT DISULFID 239 248 By similarity.
 FT DISULFID 244 257 By similarity.
 FT DISULFID 259 274 By similarity.
 FT DISULFID 280 286 By similarity.
 FT DISULFID 441 467 By similarity.
 FT DISULFID 639 666 By similarity.
 FT CARBOHYD 189 189 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 674 AA; 74637 MW; FBF8F6B8664D6F2E CRC64;
 Query Match 86.1%; Score 1117; DB 1; Length 674;
 Best Local Similarity 82.8%; Pred. No. 4.5e-84;
 Matches 188; Conservative 17; Mismatches 22; Indels 0; Gaps 0;
 Qy 1 PRLDCINKYGPSYTKNSGFATCVQNLPDQCTNPCKDRKGTQACQDLMGNFCLCKAGWG 60
 Db 87 PRYQCKMRYGRPEDKNPNFATCVKNLPDQCTNPCKDKGTQLCQDLMGNFCLCKDGGW 146
 Qy 61 GRLCDKDVNECSQBNNGCLQI CHNPGSFHCSHGFEISSLSDGRTQCIDDECADSEACGE 120
 Db 147 GRLCDKDVNECSQKNGGCSQVCHNPGSFQCAHSGFSLOSDNKSQCIDDECTDSTCGD 206
 Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
 Db 207 ARCKNLPGSYSLCDEKGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCNGRGLK 266
 Qy 181 LSQDMDCEDILPCVPSPVAKSVKSLYLGMFSGTVPVIRLFKRLQ 227
 Db 267 LSPDMDCEDILPCVPSPVAKSVKSLYLGMFSGTVPVIRLFKRLQ 313
 RESULT 3
 Q6IRL1 ID Q6IRL1 PRELIMINARY; PRT; 674 AA.
 AC Q6IRL1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Gas6 protein.
 GN Name=Gas6;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC070881; AAH70881.1; -;
DR HSSP; P00736; IAPQ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; ASx hydroxyl S.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR003129; TSP N.
DR InterPro; IPR000234; Vit_k_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF CA; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF02210; Laminin G 2; 2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF CA; 4.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF CA; 3.
DR PROSITE; PS00011; GLA 1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 674 AA; 74671 MW; CC9A5EBD04480AE7 CRC64;

Query Match 86.1%; Score 1117; DB 2; Length 674;
Best Local Similarity 82.8%; Pred. No. 4.5e-84;
Matches 188; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 1 PRLDCLINKGSPYKNSGFATCVQLPQCTPNFCDRKGTQACQDLGNFPLCKAGWG 60
DB 87 PRYQCMRYGKRPEDKNFNFATCVRLPQCTPNFCDRKGTQACQDLGNFPLCKAGWG 146
QY 61 GLRLCDKDVNECSQNGGCLQIHNKPGSFCHSGFELSDGRCTDIDECADSEACGE 120
DB 147 GLRLCDKDVNECSQNGGCSQVHNKPGSQACGFSLSQDNKSCQDIDECSDTCDG 206
QY 121 ARCKNLPGSYSLCDGEGFAYSSQEKACRDVDECLQRCGEQVCVNSPGSYTCHDGRGGLK 180
DB 207 ARCKNLPGSYSLCDKGYTSSKEKTCQDVDECCQDRCEQTVCNPSGYSYTCNCRGGGLK 266
QY 181 LSQDMTCDIDILPCVPFVSVAKSVKSLYLGRMFGTPTVIRLKRLOP 227
DB 267 LSPDMTCDIDILPCVPFVSNAKSVKSLYLGRMFGTPTVIRLKRLOP 313

RESULT 4
GAS6_MOUSE
ID GAS6_MOUSE STANDARD; PRT; 674 AA.

AC Q61592; Q99K57;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-arrest-specific protein 6 precursor (GAS-6).
GN Name=GAS6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330291; PubMed=8336730;
RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
member of the vitamin K-dependent proteins related to protein S, a
negative regulator in the blood coagulation cascade.";
RL Mol. Cell. Biol. 13:4976-4985(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX PubMed=11175853; DOI=10.1038/94667;
RA Angelillo-Scherer A., de Frutos P., Aparicio C., Melis E., Savi P.,
RA Lupu F., Arnout J., Deverchin M., Hoylaerts M., Herbert J., Collen D.,
RA Dahlback B., Carmeliet P.;
RT "Deficiency or inhibition of Gas6 causes platelet dysfunction and
protects mice against thrombosis.";
RL Nat. Med. 7:215-221(2001).
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
and MER whose signaling is implicated in cell growth and survival,
cell adhesion and cell migration (By similarity). Plays a role in
thrombosis by amplifying platelet aggregation and secretion in
response to known agonists.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
dependent carboxylation. These residues are essential for the
binding of calcium (By similarity).
CC -!- MISCELLANEOUS: GAS6 deficient mice show protection against
thrombosis, but no spontaneous bleeding.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>)

or send an email to license@iab-sib.ch).

CC EMBL; X59846; CAA42507.1; -.
 DR EMBL; BC005444; AAH05444.1; -.
 DR PIR; A48089; A48089.
 DR HSSP; P00740; 1CFH.
 DR MGD; MGI:95660; Gas6.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR008985; ConA_like_1ec_gl.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR003129; TSP_N.
 DR InterPro; IPR000294; Vtck_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00054; Laminin_G; 2.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00025; Lam_G_DOMAIN; 2.
 KW Calcium-binding; EGF-Like domain; Gamma-carboxyglutamic acid;
 KW Growth regulation; Repeat; Signal; Vitamin K.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 674 Growth-arrest-specific protein 6.
 FT DOMAIN 50 91 Gla.
 FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).
 FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).
 FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 295 467 Laminin G-like 1.
 FT DOMAIN 474 666 Laminin G-like 2.
 FT METAL 326 326 Calcium (via carbonyl oxygen) (By
 FT METAL 328 328 similarity).
 FT METAL 437 437 Calcium (via carbonyl oxygen) (By
 FT METAL 437 437 similarity).
 FT METAL 652 652 Calcium (By similarity).
 FT DISULFID 117 130 By similarity.
 FT DISULFID 122 139 By similarity.
 FT DISULFID 141 150 By similarity.
 FT DISULFID 157 168 By similarity.
 FT DISULFID 164 177 By similarity.
 FT DISULFID 179 192 By similarity.
 FT DISULFID 198 209 By similarity.
 FT DISULFID 204 218 By similarity.
 FT DISULFID 220 233 By similarity.
 FT DISULFID 239 248 By similarity.
 FT DISULFID 244 257 By similarity.
 FT DISULFID 259 274 By similarity.
 FT DISULFID 280 566 By similarity.
 FT DISULFID 441 467 By similarity.
 FT DISULFID 639 666 By similarity.
 FT CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 530 530 Missing (in Ref. 1).
 SQ SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;

Query Match 85.8%; Score 1113; DB 1; Length 674;
 Best Local Similarity 82.8%; Pred. No. 9.6e-84;
 Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKNGSPYTKNGSFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFFCLCKAGWG 60

Db 87 PRYQCVKRYGRPEKNPDPFAKCVQNLDPQCTPNPCDKKGTTHICQDLWGNFFCVCTDGGW 146
 QY 61 GRLCDKDVNCSQNGCGLQICHNKPGSFCHSGFELSSDGRTCQDIDECADSEACGE 120
 Db 147 GRLCDKDVNCSQNGCGLQICHNKPGSFCHSGFELSSDGRTCQDIDECADSEACGE 206
 QY 121 ARCKNLPGSYSCLCDEGFAYSSOFKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
 Db 207 ARCKNLPGSYSCLCDEGYTSSKEKTCQDVEQDRCETCVNSPGSYTCHCDGRGLK 266
 QY 181 LSQDMDTCEDILPCVPFSAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
 Db 267 LSPDMDTCEDILPCVPFSAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313
 RESULT 5
 Q6PAE0
 ID Q6PAE0 PRELIMINARY; PRT; 668 AA.
 AC Q6PAE0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC68463 protein.
 GN Name=MGC68463;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX Klein S., Strausberg R.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL; BC060355; AAH060355.1; -.
 DR HSSP; P00743; IAP0.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO: GO:0005198; F:structural molecule activity; IEA.

DR InterPro: IPR0007155; P:cell adhesion; IEA.

DR InterPro: IPR000152; Asx hydroxyl S.

DR InterPro: IPR000985; ConA like lec_gl.

DR InterPro: IPR000742; EGF 2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR002383; GLA blood.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR001791; Laminin G.

DR InterPro: IPR003129; TSP N.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam: PF00008; EGF; 1.

DR Pfam: PF07645; EGF_CA; 3.

DR Pfam: PF00594; Gla; 1.

DR Pfam: PF02210; Laminin G 2; 1.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00181; EGF; 4.

DR SMART: SM00179; EGF_CA; 4.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00282; LamG; 2.

DR PROSITE: PS00010; ASX HYDROXYL; 3.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 3.

DR PROSITE: PS00026; EGF_3; 2.

DR PROSITE: PS01187; EGF_CA; 2.

DR PROSITE: PS00011; GLA_1; 1.

DR PROSITE: PS00025; LAM_G_DOMAIN; 2.

KW EGF-like domain.

SEQUENCE 668 AA; 74905 MW; 8BEE5232F4EF3916 CRC64;

Query Match 62.5%; Score 810; DB 2; Length 669;

Best Local Similarity 60.1%; Pred. No. 1e-58;

Matches 137; Conservative 33; Mismatches 56; Indels 2; Gaps 2;

QY 1 PRYLDCKNGSPYTKNSGFATCVQNLDPQCTNPNCDKRGTCACODLMGNFCLCKAGWG 60

DB 84 PYIECNRRY-RHLNKKOSLTTICRHIPQCSAPCYREGSLHCLDHLGDFCHCKPGWT 142

QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFCHSGFELSSDGRTCQDIDECADS-EACG 119

DB 143 GSKCGTDINECATENGNCSCQICNKGTHQCLSSGYRLHANNKLCIDIDECASFNIG 202

QY 120 EARKNLPGSYCLDEGFPAYSQEKACRDVDECIQRCQVCVNSPGSYTCHDGRGL 179

DB 203 TAQCKNVRSYTVCLCEDGYRDELTKSCQDVDECKEGRCEQTCVNSPGSYTCHDGRGV 262

QY 180 KLSQDMTDCEDILPCVPFVSKVSLYLGRMFSGTPTVIRLFKRLQ 227

DB 263 KLSQNMNTCEDILPCIPFASEKSKNSLYLGRMFSGTPTVIRLFKRLQ 310

RESULT 6

QDFA5 QDFA5 PRELIMINARY; PRT; 669 AA.

AC Q6DFA5;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Gas6-prov protein.

GN Name=gas6-prov;

OC Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxId=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative.";

RN Dev. Dyn. 225:384-391(2002).

RL [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;

RA Klein S., Gerhard D.S.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 EGF-like domain.

DR EMBL; BC076835; AAH76835.1; -.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro: IPR000152; Asx hydroxyl S.

DR InterPro: IPR008985; ConA like lec_gl.

DR InterPro: IPR000742; EGF 2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR002383; GLA blood.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR001791; Laminin G.

DR InterPro: IPR003129; TSP N.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 3.

DR Pfam; PF07645; EGF_CA; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00054; Laminin G 1; 1.

DR Pfam; PF02210; Laminin G 2; 1.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00181; EGF; 4.

DR SMART; SM00179; EGF_CA; 4.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX HYDROXYL; 3.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS00026; EGF_3; 2.

DR PROSITE; PS01187; EGF_CA; 2.

DR PROSITE; PS00011; GLA_1; 1.

DR PROSITE; PS00025; LAM_G_DOMAIN; 1.

KW EGF-like domain.

SEQUENCE 669 AA; 75232 MW; A8DE1E362540F643 CRC64;

Query Match 62.5%; Score 810; DB 2; Length 669;

Best Local Similarity 59.2%; Pred. No. 1e-58;

Matches 135; Conservative 35; Mismatches 56; Indels 2; Gaps 2;

QY 1 PRYLDCKNGSPYTKNSGFATCVQNLDPQCTNPNCDKRGTCACODLMGNFCLCKAGWG 60

DB 84 PYIECNRRY-RHLNKKOSLTTICRHIPQCSAPCYREGSLHCLDHLGDFCHCKPGWT 142

QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFCHSGFELSSDGRTCQDIDECADS-EACG 119

DB 143 GSKCGTDINECATENGNCSCQICNKGTHQCLSSGYRLHANNKLCIDIDECASFNIG 202

QY 120 EARKNLPGSYCLDEGFPAYSQEKACRDVDECIQRCQVCVNSPGSYTCHDGRGL 179

DB 203 TAQCKNVRSYTVCLCEDGYRDELTKSCQDVDECKEGRCEQTCVNSPGSYTCHDGRGV 262

QY 180 KLSQDMTDCEDILPCVPFVSKVSLYLGRMFSGTPTVIRLFKRLQ 227

DB 263 KLSQNMNTCEDILPCIPFASEKSKNSLYLGRMFSGTPTVIRLFKRLQ 310

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Db 85 PKYIECNRRY-RHLNKDSLTTIHNIPDQSSAPCYREGSLHCTDLHGDFCHCKPGWT 143
Qy 61 GRLCDKDVNECSQNGGCLQICHNKPQSFHCSHGSELSDGRTCDIDECADS-EACG 119
Db 144 GKTCRSDINECATENGSHCIINKPGTHQCLCRSGYRLHTNNKLCIDIDECASPNFCG 203
Qy 120 EARCCKNLPGSYCLCDEGFAYSSQKACRDVDECLQGCCEQVVCVNSPGSYTCHCDGRGGL 179
Db 204 TAQCKNLVSTVYCLCEDGTRVDETSKQDIDECCKGRCBQTCVNSPGSYTCHCDGRGGV 263
Qy 180 KLSQMDMTCEDILPCVPFVSAKSVKSLYLGRMFSGTPIVIRLFRKLQP 227
Db 264 KLSQNMTCEDILPCLPFASEKRSNLSYLGRMFSGTPIVIRLFRKQKP 311
RESULT 7
Q7T3H4
ID Q7T3H4 PRELIMINARY; PRT; 648 AA.
AC Q7T3H4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Growth arrest specific 6.
GN ORFNames=zgc:63860;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo.
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo.
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC053117; AAH53117.1; -.
DR HSSP; Q14393; 1H30.
DR ZFIN; ZDB-GENE-030131-7773; zgc:63860.
DR GO; GO:0005578; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR00152; Asx hydroxyl S.
DR InterPro; IPR002453; Beta tubulin.
DR InterPro; IPR008985; ConA-like_lac_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
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DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF02210; Laminin_G; 2.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 648 AA; 72625 MW; E2935F42AF21CF64 CRC64;
Query Match 49.9%; Score 647; DB 2; Length 648;
Best Local Similarity 49.8%; Pred. No. 2.9e-45;
Matches 112; Conservative 31; Mismatches 80; Indels 2; Gaps 2;
Qy 1 PRYLDICINKYGSPTKNSGFATCYQNLPDQCTNPDCRKGTOACODLMGNFFCLCKAGWG 60
Db 79 PKYQACMERFGDSEKKQDLITCVHNIPDQCSNPVCYHYGTVRCEDKKGFECHCFTGWS 138
Qy 61 GRLCDKDVNECSQNGGCLQICHNKPQSFHCSHGSELSDGRTCDIDECADS-EACG 119
Db 139 GATCQNDVDEICSGNGGCEHVCNNTMGSKCSDBGYRLSGH-HSCLDVDECVETPDVCG 197
Qy 120 EARCCKNLPGSYCLCDEGFAYSSQKACRDVDECLQGCCEQVVCVNSPGSYTCHCDGRGGL 179
Db 198 SARCSNLIGGLECLCDGFIYDNISRSCVDDECTHVCEECVNTFGSFCFCDCGRGLGK 257
Qy 180 KLSQMDMTCEDILPCVPFVSAKSVKSLYLGRMFSGTPIVIRLFRKPR 224
Db 258 RLSSDMSCSESIGLDRLDVRNRSRLYLGRMFSGIPVVLRFPR 302
RESULT 8
PRTS MACMU
ID _PRTS MACMU STANDARD; PRT; 649 AA.
AC Q28520;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor (Fragment).
GN Name=PROS1; Synonyms=PROS;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95134217; PubMed=7832752;
RA Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;
RA "Identification of candidate residues for interaction of protein S
RA with C4b binding protein and activated protein C.";
RL Biochem. J. 305:397-403 (1995).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
CC activated protein C in the degradation of coagulation factors Va
CC and VIIa. It help to prevent coagulation and stimulating
CC fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
```

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: L31380; AAA70376.1; ALT_INIT.
 CC HSSP: P00740; 1CFH.
 CC InterPro: IPR000152; Asx hydroxyl S.
 CC InterPro: IPR008985; ConA-like_lec_gl.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001791; Laminin G.
 CC InterPro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00008; EGF; 4.
 CC Pfam: PF00594; Glc; 1.
 CC Pfam: PF00054; Laminin G; 1.
 CC PRINTS: PR00001; GLABLOOD.
 CC PROSITE: PS00010; ASX HYDROXYL; 4.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 3.
 CC PROSITE: PS00026; EGF_3; 4.
 CC PROSITE: PS01187; EGF_Ca; 3.
 CC PROSITE: PS00011; GLA_1; 1.
 CC PROSITE: PS00998; GLA_2; 1.
 CC PROSITE: PS00025; LAM_G_DOMAIN; 2.
 CC Blood coagulation; Calcium; EGF-like domain;
 CC Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
 CC Repeat; Vitamin K; Zymogen.
 CC NON_TER 1
 CC PROREP <1 14
 CC CHAIN 15 649
 CC DOMAIN 15 60
 CC DOMAIN 61 89
 CC DOMAIN 90 128
 CC DOMAIN 130 173
 CC DOMAIN 174 215
 CC DOMAIN 216 236
 CC DOMAIN 272 448
 CC DOMAIN 457 639
 CC MOD_RES 20 20
 CC MOD_RES 21 21
 CC MOD_RES 28 28
 CC MOD_RES 30 30
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 CC MOD_RES 39 39
 CC MOD_RES 40 40
 CC MOD_RES 43 43
 CC MOD_RES 46 46
 CC MOD_RES 50 50
 CC MOD_RES 109 109
 CC DISULFID 94 107
 CC DISULFID 99 116
 CC DISULFID 118 127
 CC DISULFID 134 148
 CC DISULFID 144 157
 CC DISULFID 159 172
 CC DISULFID 178 190
 CC DISULFID 185 199
 CC DISULFID 201 214
 CC DISULFID 220 229
 CC DISULFID 225 238
 CC DISULFID 240 255
 CC CARBOHYD 472 472
 CC CARBOHYD 482 482
 CC CARBOHYD 503 503
 CC SEQUENCE 649 AA; 72402 MW; 5C7C13D31CD7EB6B CRC64;

Query Match 47.0%; Score 609.5; DB 1; Length 649;
 Best Local Similarity 44.0%; Pred. No. 3.7e-42;
 Matches 106; Conservative 39; Mismatches 71; Indels 25; Gaps 5;
 QY 1 PRYLDCKINKYSPYTKNSGFAT-----CVQNLDPDOCTPMPCKRKGTOACOD 46
 Db 56 PKYLVLCLRSF-----QSGLFTAAQSTDAYPDLRSCVNAIPDQCSPDPNEDGYSCKD 109
 QY 47 LMGNFCLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPQSFHSCSHGFBELSSDG 103
 Db 110 GKASFTCTCKPGWQGCERCEFDINECKDPNSINGGCSQICDNTPGSYHCSCKSGFVWLSNK 169
 QY 104 RYCQIDISCA-DSEACGEARKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQGRCEQVC 162
 Db 170 KDKDQVDECSLKNPMCGTAVCKNIPGDFECPEGYRNLKSKSCDVEDCESENCAQLC 229
 QY 163 VNSPGSYTCHCDGRGGLKLSODMDTCEDILPCVPFSVAKSVKSLVLRMFSTPTVLRRF 222
 Db 230 VNYPGGYTCYCDGRKGFKAQDQKSCSAVSVCLPLNLDTKYELLYLABQFAGV-VLYLKF 288
 QY 223 K 223
 Db 289 R 289
 RESULT 9
 Q7Z715 PRELIMINARY; PRT; 497 AA.
 AC Q7Z715
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Protein S (Alpha) (Fragment).
 GN Name=PROS1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY308744; AAP45054.1; -
 DR HSSP: P00740; 1CFH.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR008985; ConA_like_lec_gl.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001791; Laminin G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF07645; EGF_Ca; 2.
 DR Pfam: PF00594; Glc; 1.
 DR Pfam: PF00054; Laminin_G_1; 1.
 DR SMART: SM00179; EGF_CA; 3.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00282; LamG; 1.
 DR PROSITE: PS00010; ASX HYDROXYL; 4.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS00026; EGF_3; 2.
 DR PROSITE: PS01187; EGF_Ca; 3.
 DR PROSITE: PS00011; GLA_1; 1.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 1.
 KW EGF-like domain.
 FT NON_TER 497 497
 FT SEQUENCE 497 AA; 55563 MW; B05828AC43C59903 CRC64;

Query Match 46.4%; Score 601.5; DB 2; Length 497;
Best Local Similarity 43.4%; Pred No. 1.3e-41;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDQCTNPDRKGTQACQDLGMGNFF 52
DB 83 PKYLVLCLRSFQTGLFTAAARQSTNAYPDLRSVNAIPDQCSPLPCNEDGYMCKDGKASFT 142

QY 53 CLCKAGWGRCLDKDVNEC---SQENGCLQICHNKPSPFCSCHSFGELSSDGRTCODI 109
DB 143 CTCKFGWQGEKCFEINECKDPNSINGCSQICDNTPGSYHCXKNGFVNLNKKDCKDV 202

QY 110 DECA--DSEACGEARCNLPKGSVSLCDGFGAYSSOEKACRDVDECLQRCQVQCVNSPGS 168
DB 203 DECSLKPSICGTAVCNKIPGFECECPGYRYNLKSKSCBIIDECSENMCAQLCVNYPGG 262

QY 169 YTHCDGRGLKLSQMDPTEDILPCVPFSPVAKSVKSLYLGRMFSGTPTVIRLPK 223
DB 263 YTCYCDGKGPFLAQDKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKER 316

RESULT 10
PRTS HUMAN
ID PRTS HUMAN STANDARD; PRT; 676 AA.
AC P07225; O15518;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN Name=PROS1; Synonyms=PROS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87092407; PubMed=3467362;
RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
RT "Cloning and characterization of human liver cDNA encoding a protein S
precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353 (1987).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=88005138; PubMed=2820795; DOI=10.1016/0014-5793(87)80217-X;
RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
RA Bertina R.M.;
RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
sequences for the post-translational processing.";
RL FEBS Lett. 222:186-190 (1987).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=91084444; PubMed=2148110;
RA Schmid D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
RT "Organization of the human protein S genes.";
RL Biochemistry 29:7845-7852 (1990).
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91084445; PubMed=2148111;
RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
RT "Intron-exon organization of the active human protein S gene PS alpha
and its pseudogene PS beta: duplication and silencing during primate
evolution.";
RL Biochemistry 29:7853-7861 (1990).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uedlin T.B., Tohiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellin N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E.,
Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN SEQUENCE OF 27-676 FROM N.A.
RX MEDLINE=86313649; PubMed=2944113;
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720 (1986).
RN [7]
RN VARIANT HEERLEN PRO-501.
RX MEDLINE=90335440; PubMed=2143091;
RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A., Coenen J.,
RA Leemhuis M.P., Deutz-Terlouw P.P., van der Linden I.K., Reitsma P.H.;
RT "Heerlen polymorphism of protein S, an immunologic polymorphism due to
dimorphism of residue 460.";
RL Blood 76:538-548 (1990).
RN [8]
RN VARIANT PROS1 DEFICIENCY SER-258.
RA Cooper D.N.;
RL Unpublished observations (SEP-1993).
RN [9]
RN VARIANT PROS1 DEFICIENCY TOKUSHIMA GLU-196.
RX MEDLINE=94129009; PubMed=8298131;
RA Hayashi T., Nishioka J., Shigeakiyo T., Saito S., Suzuki K.;
RT "Protein S Tokushima: abnormal molecule with a substitution of Glu for
Lys-155 in the second epidermal growth factor-like domain of protein
S.";
RL Blood 83:683-690 (1994).
RN [10]
RN VARIANTS PROS1 DEFICIENCY CYS-482; CYS-485 AND GLY-561, AND VARIANTS
PRO-501 AND MET-559.
RX MEDLINE=99374922; PubMed=10447256;
RX DOI=10.1002/(SICI)1098-1004(1999)14:1<30::AID-HUMU4>3.3.CO;2-O;
RA Espinosa-Parzilla Y., Morell M., Souto J.C., Tirado I.,
RA Fontcuberta J., Estivill X., Sala N.;
RT "Protein S gene analysis reveals the presence of a cosegregating
mutation in most pedigrees with type I but not type III PS
deficiency.";
RL Hum. Mutat. 14:30-39 (1999).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
activated protein C in the degradation of coagulation factors Va
and VIIIa. It helps to prevent coagulation and stimulating
fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- DISEASE: Defects in PROS1 are the cause of protein S deficiency
(PROS1 deficiency) [MIM:176880]. It is associated with an
increased risk to develop thrombotic disease (thrombophilia).
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
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DR EMBL; M13044; AAA30757.1; -.
DR EMBL; X12891; CAA31382.1; -.
DR PIR; A24759; KXBOS.
DR HSP; P00740; 1CFH.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 3.
DR PROSITE; PS00026; EGF 3; 3.
DR PROSITE; PS01187; EGF_Ca; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW Blood coagulation; Calcium; Direct protein sequencing;
KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein;
KW Hydroxylation; Plasma; Repeat; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 675
FT DOMAIN 42 87
FT DOMAIN 88 116
FT DOMAIN 117 155
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 665
FT SITE 93 94
FT SITE 111 112
FT MOD_RES 47 47
FT MOD_RES 48 48
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FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
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FT MOD_RES 73 73
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FT MOD_RES 58 63
FT DISULFID 88 113
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FT DISULFID 126 143
FT DISULFID 145 154
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FT DISULFID 186 199
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FT DISULFID 228 241
FT DISULFID 247 256
FT DISULFID 252 265
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FT DISULFID 267 282
FT DISULFID 288 567
FT DISULFID 449 475
FT DISULFID 638 665
FT CARBOHYD 499 499
FT CARBOHYD 509 509
SQ SEQUENCE 675 AA; 75132 MW; CF7EC5BC1C318DEE CRC64;

Query Match 46.0%; Score 596.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 4.5e-41;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

Qy 1 PRYLDCKINKYGSPTKNSGFAT-----CVQNLDPQCTPNPCDRKGTQACQDLMGNNFF 52
Db 83 PKYLGCLGSFRAGLFTFAARLSTNAYPDLRSVCVNAISDCNPLPCNEDGFMTCKDQATFT 142
Qy 53 CLCKAGWGRLCKDKNVNECSQE---NGGCLQICHNKPGSFHCSCHSFEISSDRTQDII 109
Db 143 CICKSGWQEKCESDINECKDPVNINGGCSQICENTPGSYHSCCKNGFVMSLNKKDKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGAYSSQEKACRDVDECLQRCGEQVCNPSGS 168
Db 203 DECVLKPSICGTAVCKNIPGDCECAEGYKYNPVSCKDDVDECAENLCAQLCVNYPGG 262
Qy 169 YTHCDGRGGLKLSQMDTCTEDILPCVPFVSVAKSLSYLGRMFSFGTPVIRLRFK 223
Db 263 YSCYCDGKGFKAQDKSCENPVCLPLDLDDKNYELLYLAEPVGV-VLYLKER 316

RESULT 12
PRTS_MOUSE
ID_PRTS_MOUSE STANDARD; PRT; 675 AA.
AC Q08761; P43483;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DB Vitamin K-dependent protein S precursor.
GN Name=Prosl; Synonyms=Pros;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94198297; Pubmed=8148380; DOI=10.1016/0167-4781(94)90294-1;
RA Chu M.D., Sun J., Bird P.I.;
RT "Cloning and sequencing of a cDNA encoding the murine vitamin K-
dependent protein S.";
RL Biochim. Biophys. Acta 1217:325-328(1994).
RN [2]
RP SEQUENCE OF 33-675 FROM N.A.
RX MEDLINE=94302659; Pubmed=8029814; DOI=10.1016/0049-3848(94)90006-X;
RA Lu D., Schmidel D.K., Long G.L.;
RT "Structure of mouse protein S as determined by PCR amplification and
DNA sequencing of cDNA.";
RL Thromb. Res. Suppl. 74:135-142(1994).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
activated protein C in the degradation of coagulation factors Va
and VIIa. It help to prevent coagulation and stimulating
fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC -----
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CC EMBL; Z25469; CAA80961.1; -
CC EMBL; L27439; AAA40006.1; -
CC PIR; S43504; KXMS.
CC HSSP; P00740; 1CFH.
CC MGI; MGI:1095733; Prosl.
CC InterPro; IPR000152; Asx_hydroxyl_s.
CC InterPro; IPR008985; ConA_like_lec_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR009030; Grow_fac_recept.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF_3.
CC Pfam; PF00594; Gla_1.
CC Pfam; PF00594; Gla_1.
CC PRINTS; PF00054; Laminin_G; 1.
CC PRINTS; PF00001; GLABLOOD.
CC PROSITE; PS00010; ASX_HYDROXYL; 4.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS00026; EGF_3; 4.
CC PROSITE; PS01187; EGF_CA; 3.
CC PROSITE; PS00011; GLA_1; 1.
CC PROSITE; PS00998; GLA_2; 1.
CC PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW Blood coagulation; Calcium; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 By similarity.
FT PROPEP 25 41 By similarity.
FT CHAIN 42 675 Vitamin K-dependent protein S.
FT DOMAIN 42 87 Gla.
FT DOMAIN 88 116 Thrombin-sensitive.
FT DOMAIN 117 135 EGF-like 1.
FT DOMAIN 157 200 EGF-like 2, calcium-binding (Potential).
FT DOMAIN 201 242 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 243 283 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 299 475 Laminin G-like 1.
FT DOMAIN 484 665 Laminin G-like 2.
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 73 73 4-carboxyglutamate (By similarity).
FT MOD_RES 77 77 4-carboxyglutamate (By similarity).
FT MOD_RES 136 136 3-hydroxyaspartate (By similarity).
FT DISULFID 121 134 By similarity.
FT DISULFID 126 143 By similarity.
FT DISULFID 145 154 By similarity.
FT DISULFID 161 175 By similarity.
FT DISULFID 171 184 By similarity.
FT DISULFID 186 199 By similarity.
FT DISULFID 205 217 By similarity.
FT DISULFID 212 226 By similarity.
FT DISULFID 228 241 By similarity.
FT DISULFID 247 256 By similarity.
FT DISULFID 252 265 By similarity.
FT DISULFID 267 282 By similarity.
FT CARBOHYD 499 509 N-linked (GlcNAc...) (Potential).
FT CONFLICT 493 493 F -> L (in Ref. 2).
SQ SEQUENCE 675 AA; 74934 MW; 79D51203E85AF31F CRC64;
Query Match 45.6%; Score 591.5; DB 1; Length 675;
Best Local Similarity 44.7%; Pred. No. 1.2e-40;

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Matches 105; Conservative 35; Mismatches 82; Indels 13; Gaps 5;
QY 1 PRYLDCKINKY--GSPYTKNSG-----FATCVQNLDPDOCTNPDCRKGTOACQDLMGNNFF 52
DB 83 PKYLGLGAFRVGSGFHAARQSANAYPDLRSVCVKAISDQCDIPCNEDGYLACQDQQAFT 142
QY 53 CLKAGWGRLCDKDVNEC-----SQENGGLQICHNKPGSFHCSHGSELSDDGRTQDI 109
DB 143 CFCKPGWQDRQCYDVNECKDFSNVNGGCSQICDNTPGSYHCSCKRGFAMLPNKKDKDL 202
QY 110 DECA--DSEACGEARCKNLPGSYGCLDEGFAYSSQEKACRDVDECLQGRQGVQCVNSPGS 168
DB 203 DECALKPSVCGTAVCKNIPGDFECPCDGYRDPSSSKCKDVDESENMCALQCVNFFGG 262
QY 169 YTCXCDGRGGLKLSQMDMTCEDILPCVPFVSVAKSYKSLYLGRMFSGTGVIRLRK 223
DB 263 YSCYCDGKKGFLAQDQKSCGIPVCLSLDLKKNVELLYLAEQFAGV-VLYLKR 316

RESULT 13
PRTS_RABIT
ID PRTS_RABIT STANDARD; PRT; 646 AA.
AC P98118;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor (Fragment).
GN Name=PROS1; Synonyms=PROS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94039141; PubMed=8223642;
RA He X., Dahlback B.;
RT "Molecular cloning, expression and functional characterization of
  rabbit anticoagulant vitamin K-dependent protein S.";
RL Eur. J. Biochem. 217:857-865(1993).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
  activated protein C in the degradation of coagulation factors Va
  and VIIIa. It help to prevent coagulation and stimulating
  fibrinolysis.
CC -!- SUBUNIT: Interacts with C4b-binding protein, a regulator of the
  complex system. In rabbit plasma however, protein S appears to be
  present only in free form.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
  domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC EMBL; Z26485; CAA81259.1; -.
CC PIR; S38819; S38819.
CC HSSP; P00740; 1CFH.
CC InterPro; IPR000152; Asx_hydroxyl_s.
CC InterPro; IPR008985; ConA_like_lec_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR009030; Grow_fac_recept.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR003129; TSP_N.

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DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00098; GLA_2; 1.
DR PROSITE; PS00025; LAM_G DOMAIN; 2.
KW Blood coagulation; Calcium; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Vitamin K; Zymogen.
FT NON_TER 1
FT PROPEP <1 12 Potential.
FT CHAIN 13 646 Vitamin K-dependent protein S.
FT DOMAIN 13 58 Gla.
FT DOMAIN 59 87 Thrombin-sensitive.
FT DOMAIN 88 126 EGF-like 1.
FT DOMAIN 128 171 EGF-like 2, calcium-binding (Potential).
FT DOMAIN 172 213 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 214 254 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 270 446 Laminin G-like 1.
FT DOMAIN 455 636 Laminin G-like 2.
FT MOD_RES 18 18 4-carboxyglutamate (By similarity).
FT MOD_RES 19 19 4-carboxyglutamate (By similarity).
FT MOD_RES 26 26 4-carboxyglutamate (By similarity).
FT MOD_RES 28 28 4-carboxyglutamate (By similarity).
FT MOD_RES 31 31 4-carboxyglutamate (By similarity).
FT MOD_RES 32 32 4-carboxyglutamate (By similarity).
FT MOD_RES 37 37 4-carboxyglutamate (By similarity).
FT MOD_RES 38 38 4-carboxyglutamate (By similarity).
FT MOD_RES 41 41 4-carboxyglutamate (By similarity).
FT MOD_RES 44 44 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 107 107 3-hydroxyaspartate (By similarity).
FT DISULFID 92 105 By similarity.
FT DISULFID 97 114 By similarity.
FT DISULFID 116 125 By similarity.
FT DISULFID 132 146 By similarity.
FT DISULFID 142 155 By similarity.
FT DISULFID 157 170 By similarity.
FT DISULFID 176 188 By similarity.
FT DISULFID 183 197 By similarity.
FT DISULFID 199 212 By similarity.
FT DISULFID 218 227 By similarity.
FT DISULFID 223 236 By similarity.
FT DISULFID 238 253 By similarity.
FT CARBOHYD 470 470 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 646 AA; 71969 MW; 131219C48891B2EC CRC64;

Query Match 45.2%; Score 586.5; DB 1; Length 646;
Best Local Similarity 43.2%; Pred. No. 2.9e-40;
Matches 101; Conservative 39; Mismatches 81; Indels 13; Gaps 5;

Qy 1 PRYLDLCINKYSPY----TKNSG-----FATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFF 52
Db 54 PKYLGLGSLFRKFLTATRRSANGYPDLRSVCNAIPDQCNLPCEGGLNCKDGQATFT 113

Qy 53 CLCKAGWGRLCDKDVNECSOE---NGGCLQICHNKPSPHSCSCHSGFELSSDGRTCODI 109
Db 114 CICKPGWQGEKCEIDINECKDPTNINGCSQICDNTAGSYCHSCSKSGFVMLANEKCKDM 173

Qy 110 DECA-DSBACGEARKNLPGSYSLCDREGFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
Db 174 DECSVKPSVCGTAVCKNTPGDFECCESGYYRNPFAKSCEDIIDECSENWCAQLCVNYPGG 233

Qy 169 YTCHCDRGGGLKLSODMPTCDBILDIPCVFPFSVAKSVKSLYLGRMPSGTPVIRLRF 222
Db 176 CICKAGWGRLCDKDVNEC---SQENGCLQICHNKPSPHSCSCHSGFELSSDGRTCODI 109
Db 117 CTCKPGWQGEKCEIDINECKDPTNINGCSQICDNTFSGYCHSCSKSGFVMLSNKKCKDV 176
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234 YSCYCDGKGFKLAQDKKSCAVPVCLPLDLDKNYQLLYLAEQFVGA-VLYLKF 286

Db 234 YSCYCDGKGFKLAQDKKSCAVPVCLPLDLDKNYQLLYLAEQFVGA-VLYLKF 286

RESULT 14

Q16519 PRELIMINARY; PRT; 650 AA.

AC Q16519; 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Protein S precursor (Fragment).

GN Name=PROS1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86313649; PubMed=2944113;

RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,

RA Stenflo J., Wydro R.;

RT "Isolation and sequence of the cDNA for human protein S, a regulator

RT of blood coagulation.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720 (1986).

DR EMBL; M14338; AAA60181.1; -.

DR HSSP; P00740; 1CFH.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR00152; Asx_hydroxyl_S.

DR InterPro; IPR008985; ConA_like_lec_gl.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_CA.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR001791; Laminin_G.

DR InterPro; IPR003129; TSP_N.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF07645; EGF_CA; 1.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00054; Laminin_G_1; 1.

DR Pfam; PF02210; Laminin_G_2; 1.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00669; GLA_1; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 3.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS00026; EGF_3; 2.

DR PROSITE; PS01187; EGF_CA; 2.

DR PROSITE; PS00011; GLA_1; 1.

DR PROSITE; PS00025; LAM_G DOMAIN; 2.

KW EGF-like domain; Signal.

FT NON_TER 1 1 Potential.

FT SIGNAL <1 15

FT CHAIN 16 650 protein S.

SQ SEQUENCE 650 AA; 72462 MW; 9AB0C044C503BF474 CRC64;

Query Match 45.2%; Score 586.5; DB 2; Length 650;

Best Local Similarity 42.6%; Pred. No. 2.9e-40;

Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

Qy 1 PRYLDLCINKY-----GSPYTKNS--GFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFF 52

Db 57 PKYLGLGSLFRKFLTATRRSANGYPDLRSVCNAIPDQCNLPCEGGLNCKDGQATFT 116

Qy 53 CLCKAGWGRLCDKDVNEC---SQENGCLQICHNKPSPHSCSCHSGFELSSDGRTCODI 109

Db 117 CTCKPGWQGEKCEIDINECKDPTNINGCSQICDNTFSGYCHSCSKSGFVMLSNKKCKDV 176

SEQUENCE	648 AA; 11914 MW; 4BDF9A8B138721336 CRC64;
Query Match	45.1%; Score 585.5; DB *2; Length 648;
Best Local Similarity	43.0%; Pred. No. 3.5e+40;
Matches 101; Conservative	40; Mismatches 81; Indels 13; Gaps 4
QY	1 PRYLDCKNGSPYTKNGSAT-----CQNLDPDQCTPNPCDKGTQACQDLNGHFF 52
DB	56 PAYTACLGFSFAGLFTAAARLSTNAYPVLRSCVNAIPDQCNPLPDSBGFWTKCGAQMPT 115
QY	53 CLCKAGWGGRUCDKDVNECSOEN---GGCIQI CHNKPGSFHCSCHSGFELSSDGRTCODI 109

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Db 116 CICKSGWEKCELNECKOPNPNIIGCSQICDNTPGSYHSCSKSGFIMLSNKKDKCDV 175
Qy 110 DECA-DSEACGEARKNULPGSYSLCDSEGFAYSSQEKACRDVDECLQRCQVGVNPSGS 168
Db 176 DECSVKPSICDITAVCNIPGDFECPCPEGRYRNPFLKSCDVEDCESENMCAQLCVNYPGG 235
Qy 169 YTHCDGRGGGLKLSODMDTCDILPCVPFSAKSVKSLVGLGRMFGTPIVRLRPF 223
Db 236 YSCYCDGRGKFKLAQDKSCAVPCLPLNLDKNLYLLAEQFVG-VLYLKFR 289

RESULT 17
PRTS_RAT
ID _PRTS_RAT STANDARD; PRT; 675 AA.
AC P53813;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN Name=Prosl; Synonyms=ProB;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95332263; PubMed=7608128;
RA Yasuda F., Hayashi T., Tanitame K., Nishioka J., Suzuki K.;
RT "Molecular cloning and functional characterization of rat plasma
protein S.";
RL J. Biochem. 117:374-383(1995).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
activated protein C in the degradation of coagulation factors Va
and VIIa. It help to prevent coagulation and stimulating
fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S78744; AAC60704.1; -.
DR PIR; JC4180; KXRTS.
DR HSP; P00740; 1CFH.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA-like_lect_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR000294; Vitek_dep_GLA.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin G; 1.
DR PRINTS; PR00001; GLABLOD.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF 2; 3.
DR PROSITE; PS00026; EGF 3; 4.
DR PROSITE; PS01187; EGF_Ca; 3.
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DR PROSITE; PS00011; GLA 1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
KW Blood coagulation; Calcium; EGF-like domain;
KW gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 By similarity.
FT PROPEP 25 41 By similarity.
FT CHAIN 42 675 Vitamin K-dependent protein S.
FT DOMAIN 42 87 Gla.
FT DOMAIN 88 116 Thrombin-sensitive.
FT DOMAIN 117 155 EGF-like 1.
FT DOMAIN 157 200 EGF-like 2, calcium-binding (Potential).
FT DOMAIN 201 242 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 243 283 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 299 475 Laminin G-like 1.
FT DOMAIN 484 665 Laminin G-like 2.
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 73 73 4-carboxyglutamate (By similarity).
FT MOD_RES 77 77 4-carboxyglutamate (By similarity).
FT MOD_RES 136 136 3-hydroxyaspartate (By similarity).
FT DISULFID 121 134 By similarity.
FT DISULFID 126 143 By similarity.
FT DISULFID 145 154 By similarity.
FT DISULFID 161 175 By similarity.
FT DISULFID 171 184 By similarity.
FT DISULFID 186 199 By similarity.
FT DISULFID 205 217 By similarity.
FT DISULFID 212 226 By similarity.
FT DISULFID 228 241 By similarity.
FT DISULFID 247 256 By similarity.
FT DISULFID 252 265 By similarity.
FT DISULFID 267 282 By similarity.
FT CARBOHYD 499 499 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 675 AA; 74626 MW; B4338F756B486075 CRC64;

Query Match 45.18; Score 585.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 3.7e-40;
Matches 101; Conservative 41; Mismatches 80; Indels 13; Gaps 5;

Qy 1 PRYLDICNKY-----GSPVTKNS--GFATCVQNLPPQCTPNPCDRKGTQACQDLMGNNF 52
Db 83 PKYLGCGAFRGVGNFSAARQSANAYPDLRCVNAIPDQCDPMPCNEDGYLSCKDQGAFT 142
Qy 53 CLCKAGWGRLCDKDVNEC---SQENGCGCIQICHNKPGSFHCSCHSFELSSDGRTCQDI 109
Db 143 CICKPGWQDKQDFDINECKDPSNNGGCSQTCNTPTGSHYSCCKIGIFAMLTNNKDKCDV 202
Qy 110 DECA-DSEACGEARKNULPGSYSLCDSEGFAYSSQEKACRDVDECLQRCQVGVNPSGS 168
Db 203 DECSLRKPSVCGTAVCKNIPGDFECPCPEGRYRNPFLKSCDVEDCESENMCAQLCVNYPGG 262
Qy 169 YTHCDGRGGGLKLSODMDTCDILPCVPFSAKSVKSLVGLGRMFGTPIVRLRPF 223
Db 263 YSCYCDGRGKFKLAQDKSCAVPCLPLNLDKNLYLLAEQFAGV-VLYLKFR 316

RESULT 18
Q68EF9
ID Q68EF9 PRELIMINARY; PRT; 907 AA.
AC Q68EF9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Db 436 VDRSCEDVNECLNSPCSQE--CANYGYSQYCRRGYQLSDVGVTCEDIDECALPTGG 493
QY 158 --CEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCV 195
Db 494 HICSYRCINIFSPQSCSPCS-SGYRLAPNGRCQIDECV 532

RESULT 20
Q8C9Q4 PRELIMINARY; PRT; 992 AA.
AC Q8C9Q4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630023E24 product:signal peptide, CUB domain, EGF-like
DE 1, full insert sequence.
GN Name=Scubel;
OS Mus musculus. (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK041590; BAC30996.1; -
DR HSSP; P35555; LMJ
DR MGD; MGI:1890616; Scubel.
DR GO; GO:0009897; C:external side of plasma membrane; ISS.
DR GO; GO:0005509; F:calcium ion binding; ISS.
DR GO; GO:0046982; F:protein heterodimerization activity; ISS.
DR GO; GO:0042804; F:protein homooligomerization activity; ISS.
DR GO; GO:0007512; P:adult heart development; ISS.
DR GO; GO:0007596; P:blood coagulation; ISS.
DR GO; GO:0045446; P:endothelial cell differentiation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0009791; P:post-embryonic development; ISS.
DR InterPro; IPR000152; Aex_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001491; Thrombomoduln.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 2.
DR PRINTS; PR00307; THROMBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 992 AA; 108569 MW; 42219D6679791FA1 CRC64;

Query Match 27.6%; Score 358.5; DB 2; Length 992;
Best Local Similarity 38.6%; Pred. No. 3e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY 14 YTKNSGFATCVQNLPDQTPN--PCDRKGTQACQDLMGNFCLCKAGH----GGRLCDKD 67
Db 232 YALHADGRTCIET----CAVNGGCDR----TKDRTATGVRCSGPGFTLPDQDKTC-KD 282
QY 68 VNECSQENGCGCLQICHNKPFGSHCSHGSLSDGRTQDIDECADSEACGEARCKNLP 127
Db 283 INECLMNGGCDHFCRNVTGVSFGCGQKHLLDERTCQDIDECSPFRTCDHI-CINSP 341
QY 128 GSYSLCLDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGGLKLSQD 184
Db 342 GSFQCLCRGYTLTGTH--CGDVDECSMNGSCGQGVNTKGSVEYCVCP--PGRRLHWN 397
QY 185 MDTEDILPCVPFVSVAKSLSYLGRM 211
Db 398 QKDCVEMNGCLSRKSKASQAQQLSCGV 424

RESULT 21
Q6NZL8
ID Q6NZL8 PRELIMINARY; PRT; 1018 AA.
AC Q6NZL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).

```


QY 185 MDTCEIDILCPVPSVAKSVKSLVLRM 211
 DB 398 QKDCVEMNGCLSRKASQAQLSCGKV 424

RESULT 23
 LTB4_MOUSE
 ID LTB4_MOUSE STANDARD; PRT: 1666 AA.
 AC Q8K4G1; Q8K4G0;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Latent transforming growth factor beta binding protein 4 precursor
 DE (LTBP-4).
 GN Name=LTBP4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=22198089; PubMed=12208849; DOI=10.1101/gad.229102;
 RA Sterner-Kock A., Thorey I.S., Koli K., Wempe F., Ote J., Bangsow T.,
 RA Kuhlmeier K., Kirchner T., Jin S., Keski-Oja J., von Weichner H.;
 RT "Disruption of the gene encoding the latent transforming growth
 RT factor-beta binding protein 4 (LTBP-4) causes abnormal lung
 RT development, cardiomyopathy, and colorectal cancer.";
 RL Genes Dev. 16:2264-2273(2002).
 RN [2]
 RP SEQUENCE OF 60-1666 FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May be involved in the assembly, secretion and targeting
 CC of TGFbeta to sites at which it is stored and/or activated. May play
 CC critical roles in controlling and directing the activity of TGFbeta.
 CC May have a structural role in the extra cellular matrix (ECM) (By
 CC similarity).
 CC -!- SUBUNIT: Forms part of the large latent transforming growth factor
 CC beta precursor complex; removal is essential for activation of
 CC complex. Binds to FBNI (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=LTBP4L;
 CC IsoId=Q8K4G1-1; Sequence=Displayed;
 CC Name=2; Synonyms=LTBP4S;
 CC IsoId=Q8K4G1-2; Sequence=VSP_009248, VSP_009250;
 CC Name=3;
 CC IsoId=Q8K4G1-3; Sequence=VSP_009249;
 CC Note=Sequence incomplete.
 CC -!- DOMAIN: Associates covalently with small latent TGF-beta complex
 CC via Repeat C.

CC -!- PTM: Contains hydroxylated asparagine residues (By similarity).
 CC -!- SIMILARITY: Belongs to the LTBP family.
 CC -!- SIMILARITY: Contains 14 EGF-like domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF410798; AAN04661.1; -;
 CC EMBL; AF410799; AAN04662.1; -;
 CC EMBL; BC059016; AAN59016.1; -;
 CC HSSP; P35555; 1EMN.
 CC MGD; MGI:1321395; Ltbp4.
 CC GO; GO:0005578; C:extracellular matrix; ISS.
 CC GO; GO:0005509; F:calcium ion binding; ISS.
 CC GO; GO:0005539; F:glycosaminoglycan binding; ISS.
 CC GO; GO:0005178; F:integrin binding; ISS.
 CC GO; GO:0007275; P:development; ISS.
 CC GO; GO:0030252; P:growth hormone secretion; ISS.
 CC GO; GO:0046879; P:hormone secretion; IMP.
 CC GO; GO:0006457; P:protein folding; ISS.
 CC GO; GO:0045595; P:regulation of cell differentiation; ISS.
 CC GO; GO:0001558; P:regulation of cell growth; ISS.
 CC GO; GO:0030162; P:regulation of proteolysis and peptidolysis; ISS.
 CC GO; GO:0017015; P:regulation of transforming growth factor be...; ISS.
 CC InterPro; IPR000152; Axx_hydroxyl_S.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR002212; Fibril-assoc.
 CC InterPro; IPR009030; Grow_fac_recept.
 CC Pfam; PF00008; EGF; 16.
 CC Pfam; PF00683; TB; 3.
 CC SMART; SM00179; EGF_CA; 16.
 CC PROSITE; PS00010; ASX_HYDROXYL; 14.
 CC PROSITE; PS00022; EGF_1; 2.
 CC PROSITE; PS01186; EGF_2; 12.
 CC PROSITE; PS00026; EGF_3; 16.
 CC PROSITE; PS01187; EGF_CA; 17.
 CC Alternative splicing; EGF-like domain; Glycoprotein;
 CC Growth factor binding; Repeat; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 1666
 CC Latent transforming growth factor beta
 CC binding protein 4.
 CC EGF-like 1.
 CC EGF-like 2, calcium-binding (Potential).
 CC Internal repeat 1.
 CC EGF-like 3.
 CC EGF-like 4, calcium-binding (Potential).
 CC EGF-like 5, calcium-binding (Potential).
 CC EGF-like 6, calcium-binding (Potential).
 CC EGF-like 7, calcium-binding (Potential).
 CC EGF-like 8, calcium-binding (Potential).
 CC EGF-like 9, calcium-binding (Potential).
 CC EGF-like 10, calcium-binding (Potential).
 CC EGF-like 11, calcium-binding (Potential).
 CC EGF-like 12, calcium-binding (Potential).
 CC Internal repeat 2.
 CC EGF-like 13, calcium-binding (Potential).
 CC EGF-like 14, calcium-binding (Potential).
 CC Internal repeat 3.
 CC EGF-like 15.
 CC EGF-like 16.
 CC Pro-rich.
 CC Cys-rich.
 CC Pro-rich.
 CC By similarity.
 CC By similarity.
 CC DISULFID 152 162
 CC DISULFID 156 168

```

170 179 By similarity.
171 360 By similarity.
172 371 By similarity.
173 380 By similarity.
174 385 By similarity.
175 604 By similarity.
176 592 By similarity.
177 613 By similarity.
178 628 By similarity.
179 634 By similarity.
180 641 By similarity.
181 655 By similarity.
182 670 By similarity.
183 688 By similarity.
184 697 By similarity.
185 712 By similarity.
186 718 By similarity.
187 725 By similarity.
188 739 By similarity.
189 750 By similarity.
190 769 By similarity.
191 778 By similarity.
192 793 By similarity.
193 811 By similarity.
194 820 By similarity.
195 835 By similarity.
196 881 By similarity.
197 893 By similarity.
198 902 By similarity.
199 918 By similarity.
200 936 By similarity.
201 945 By similarity.
202 960 By similarity.
203 977 By similarity.
204 986 By similarity.
205 1007 By similarity.
206 1101 By similarity.
207 1116 By similarity.
208 1131 By similarity.
209 1299 By similarity.
210 1312 By similarity.
211 1321 By similarity.
212 1336 By similarity.
213 1354 By similarity.
214 1363 By similarity.
215 1378 By similarity.
216 1590 By similarity.
217 1585 By similarity.
218 1601 By similarity.
219 1614 By similarity.
220 1635 By similarity.
221 1644 By similarity.
222 1659 By similarity.
223 351 N-linked (GlcNAc. .) (Potential).
224 424 N-linked (GlcNAc. .) (Potential).
225 1097 N-linked (GlcNAc. .) (Potential).
226 1242 N-linked (GlcNAc. .) (Potential).
227 1381 N-linked (GlcNAc. .) (Potential).
228 1 Missing (in isoform 2).
229 1 /FTID=VSP_009248.
230 150 KSSRTRACSRVRNPPAKCTGLEGLTPTTSPVSPSPV
231 EKSQVSLNWQPLTLOEARALLQRPRPGFWARALLKRPPH
232 RAPAQARV -> RHEALOPWRAARSCGRCYWCWFSWG
233 RSPYADRESYFACASPLCAACVASTGTPLAPVPRPARPA
234 TPVDGAPGAGNAPGPGFRAF (in isoform 3).
235 /FTID=VSP_009249.
236 150 ASQVRNCPFAKCTGLEGLTPTTSPVSPSPVSKSQVSL
237 NWQPLTLOEARALLQRPRPGFWARALLKRPPHPRAPAGOA
238 RV -> MAGGAQLLVSLVLLVLAQLGQPQVLGRPRRLVR

Query Match 27.4%; Score 356; DB 1; Length 1666;
Best Local Similarity 41.9%; Pred. No. 8.1e-21;
Matches 75; Conservative 25; Mismatches 51; Indels 20; Gaps 9;

29 DOCTPNP--CDKKGTAQCQDLGMGNFCLCKAGGRLCDKDVNECSQENGGC-LQICHNK 85
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
716 DECTQSPGLC---GRGVENLPGRFCVCPAGFRGSACEEDVDECAQQPPGPGRCUNT 772
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

86 PGSHFCHSGHSGFELSSDGRGTQQDIDECADSEA-CGEARCKNLPGSYCLCDGFAYSQOE 144
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```

Db 773 AGSFHCACPAGRSRPGCAPCQDVDECSRSPSCAYGRCENTEGSFKVCVPTGFPQNAAG 832
Qy 145 KACEDVDECLQGR--CE-QVNVSPGSYTC-----HCDGRGGLKLSQDMDTCEDILPC 194
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 833 SECEDVDECE-ENRLACPGQBCVNSPGSQACRACPVGHHLHRG---RCTDVDECSSTGPC 887
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 24
P87363 PRELIMINARY; PRT; 708 AA.
AC P87363;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibrillin-1 (Fragment).
GN Name=FBN1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20152896; PubMed=10691037;
RA Zhou G., Price C.E., Rosenquist T.H., Gadson P.F., Godfrey M.;
RT "Partial cloning and sequencing of chick fibrillin-1 cDNA.";
RL In Vitro Cell. Dev. Biol. Anim. 36:19-25(2000).
DR EMBL; U88872; AAB48531.1; -.
DR HSSP; P35555; ILMJ.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; Abx_hydroxyl_s.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR008209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF07645; EGF_CA; 13.
DR Pfam; PF00683; TB; 2.
DR SMART; SM00179; EGF_CA; 14.
DR PROSITE; PS00010; ASX_HYDROXYL; 13.
DR PROSITE; PS01186; EGF_2; 10.
DR PROSITE; PS00026; EGF_3; 13.
DR PROSITE; PS01187; EGF_CA; 13.
KW EGF-like domain.
FT NON TER 708
SQ SEQUENCE 708 AA; 76163 MW; C247271CLDF73361 CRC64;

Query Match 27.4%; Score 355; DB 2; Length 708;
Best Local Similarity 35.1%; Pred. No. 4.3e-21;
Matches 85; Conservative 25; Mismatches 80; Indels 52; Gaps 11;

Qy 6 CINKYGS-----PYTKNSGFATCVQLPDQCTPNPCD-----RKGTAQCQDLGMGNFF 52
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 152 CINTEGSFRCDCPPGHHSNISACID-----INECDLSTNLCRNG--HCVNLIQYQ 202
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 53 CLCXAGGRLCDR----DVNECSQENGGCLQICHNKPFSHCHSGFELSSDGRTCOD 108
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 203 CACNPGYQS-TADKLHCIDIDECINNGGCENFCFTGSEGSVECSCKQGFALPDHRTCTD 261
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 109 IDECADS-EACGEARCKNLPGSYCLCDGFAYSQBAKRDVDE-----CLOGRCEQ 160
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 262 IDECEDPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLHPNICLSGTCE- 320
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 161 VCVNSPGSYTCHD---GRGGLKLSQDMDTCE-----DILPCVPFSPVAKSVKSLY 207
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 321 ---NTKGSFICHCDMGYSGKKGTGTCTDINECEIGAHCNDRHAVCTNIPGSKFCSCSSGW 377
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 208 IG 209
|:|
Db 378 IG 379
|:|

RESULT 25
Q9VSS89
```

ID AC Q9V889 PRELIMINARY; PRT: 1577 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG7526-PA (CG7526-pb).
GN ORFNames=CG7526;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasmann D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003558; AAF50538.3; --
DR HSSP: P00736; 1APQ.
DR FlyBase: FBgn0035798; CG7526.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR001152; Asx hydroxyl_S.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001181; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR003410; HyalIn.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF07645; EGF_Ca; 10.
DR Pfam: PF00084; Sushi; 3.
DR SMART: SM00032; CCP; 3.
DR SMART: SM00181; EGF; 13.
DR SMART: SM00179; EGF_Ca; 12.
DR PROSITE: PS00010; ASX HYDROXYL; 8.
DR PROSITE: PS01186; EGF_2; 9.
DR PROSITE: PS50026; EGF_3; 4.
DR PROSITE: PS01187; EGF_Ca; 10.
DR PROSITE: PS50825; HYR; 2.
DR PROSITE: PS50923; SUSHI; 1.
KW EGF-like domain.
SQ SEQUENCE 1577 AA; 172605 MW; 716DE6C311263E33 CRC64;
Query Match 27.3%; Score 354.5; DB 2; Length 1577;
Best Local Similarity 32.4%; Pred. No. 1e-20;
Matches 72; Conservative 29; Mismatches 89; Indels 32; Gaps 5;
QY 1 PRYLDCKNGSPYTKSGFATCVQNLPDQCTPNPCDRKGTQACODLWGNFCLCKAGW- 59
DB 610 PGGYGCICAAGYELKLDGIRGYCFDI--DECSQRTGCSQDQMLCNLNGSYTCLCPGYA 668
QY 60 -----GGRLCKDKNVCSQENGCGCLOIChNKPGSFHSCSCH 94
DB 669 IGLDNHIVTSLNSSFITDSTSETPSAHTC-LDIDECSLANGNCSHFQNGPFGQACAP 727
QY 95 SGFELSSDGRTCQDIDECADSEACGEARKNLPGSYSCLCDEGFAYSSQEKACRDVDSCL 154
DB 728 LGYALSDMRTCQDIDECCLDSNGQCSQLCLNQPGGFACACETGFELTDPGFGCADIDCS 787
QY 155 Q--GCEQVCVNSPGSYTCHCDGRGLKLSQDMTDCEDILPC 194
DB 788 QDYGNCSIDICNLGLGTHACACE--RGVELAKDKLSCLDVDEC 827
RESULT 26
000508
ID 000508 PRELIMINARY; PRT: 1587 AA.
AC 000508;

DT	01-JUL-1997	(TrEMBLrel. 04, Created)
DT	01-JUL-1997	(TrEMBLrel. 04, Last sequence update)
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE	Latent TGF-beta binding protein-4.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID=9606;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=97415399; PubMed=9271198; DOI=10.1016/S0014-5793(97)00685-6;	
RA	Gilkey R., Kostka G., Timpl R.;	
RT	"Sequence and expression of a novel member (LTBP-4) of the family of	
RL	latent transforming growth factor-beta binding proteins.";	
RL	FEBS Lett. 411:164-168(1997).	
DR	EMBL; Y13622; CAA73944.1; ..	
DR	HSPB; P22064; LKSO.	
DR	Genew; HGNC:6717; LTBP4.	
DR	GO; GO:0005578; C:extracellular matrix (sensu Metazoa); ISS.	
DR	GO; GO:0005509; F:calcium ion binding; ISS.	
DR	GO; GO:0005539; F:glycosaminoglycan binding; ISS.	
DR	GO; GO:0005178; F:integrin binding; ISS.	
DR	GO; GO:0005515; F:protein binding; TAS.	
DR	GO; GO:0007275; F:development; ISS.	
DR	GO; GO:0030352; F:growth hormone secretion; ISS.	
DR	GO; GO:0006457; P:protein folding; ISS.	
DR	GO; GO:0045595; P:regulation of cell differentiation; ISS.	
DR	GO; GO:001558; P:regulation of cell growth; ISS.	
DR	GO; GO:0030625; P:regulation of proteolysis and peptidolysis; ISS.	
DR	GO; GO:0017015; P:regulation of transforming growth factor be.. ; ISS.	
DR	InterPro; IPR000152; Asx hydroxy_l_S.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR002212; FibriI-asoc.	
DR	InterPro; IPR003018; GAP.	
DR	Pfam; PF00008; EGF; 3.	
DR	Pfam; PF07645; EGF_CA; 16.	
DR	Pfam; PF00683; TB; 4.	
DR	SMART; SM00179; EGF_CA; 16.	
DR	SMART; SM00065; GAF; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 14.	
DR	PROSITE; PS00022; EGF_1; UNKNOWN_2.	
DR	PROSITE; PS01186; EGF_2; 12.	
DR	PROSITE; PS00026; EGF_3; 13.	
DR	PROSITE; PS01187; EGF_CA; 17.	
KW	EGF-like domain.	
SQ	SEQUENCE 1587 AA; 57A832P95FA0AE46 CRC64;	
	Query Match 27.3%; Score 354.5; DB 2; Length 1587;	
	Best Local Similarity 43.3%; Pred. No. 1e-20;	
	Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;	
Qy	29 DQCTPNP--CDRKGTQTACQDLMGNFPCLCXAGWGRIICDKVNPESQNGGC-IQICHNK 85	
Db	636 DECTQSPLCLGRGG---CKNLPGSFRCVCPAGFRGSACEVDVDECAEQPPPCGPGRCNDT 692	
Qy	86 PGSHFCSCHGFSLSDGRTCODTDDECADS-EAGEARCKNLPGSYSLCDEGFAYSQEE 144	
Db	693 AGSFHCACPAGFRSGFGAPCCQGVDECARSPPTCYGRCENTGESFCQVCMPGPNTAG 752	
Qy	145 KACRDVDECIQG-RCE-QVCVNSPGSYTCH-CDGRGGILKLSQ--DMDTCED-ILPCVP 196	
Db	753 SECDVDEECENHLACPGQECVNSFGSQCRTCPSGHLLHRCRGTDDDECSSGAPCGP 810	
RESULT 27		
QJUSO		
ID	QJUSO PRELIMINARY; PRT; 997 AA.	
AC	QJUSO;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	

RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008960; EAA10730.2; --
 DR HSSP; P00736; IAPQ.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR003410; Hyalin.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF000008; EGF; 2.
 DR Pfam; PF07645; EGF_CA; 12.
 DR Pfam; PF02494; HYR; 1.
 DR Pfam; PF00084; Sushi; 2.
 DR PRINTS; PR00907; THROMBOMODULN.
 DR PROSITE; PS00010; ASX_HYDROXYL; 13.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS00026; EGF_3; 6.
 DR PROSITE; PS01187; EGF_CA; 11.
 DR PROSITE; PS00825; HYR; 2.
 DR PROSITE; PS00923; SUSHI; 1.
 DR EGF-like domain.
 KW NON_TER
 FT NON_TER 1222 1222
 SQ SEQUENCE 1222 AA; 134789 MW; DECD795CCFF7D740 CRC64;

Query Match 27.3%; Score 353.5; DB 2; Length 1222;
 Best Local Similarity 35.4%; Pred. No. 9.6e-21;
 Matches 73; Conservative 24; Mismatches 66; Indels 43; Gaps 10;
 QY 22 TCQNLPDOCT---PNPDRKGTQACQDLGNFFCLCKAGW-----GRLCDKDVNEC--- 71
 DB 452 TCVDR--DECANARGGGCDHN-----CHNTAGSYCTCHAGYKLAENARTC-MDVNDCCSP 504
 QY 72 -----SQBNGCGLQICHNKGPSFHCSCHSGLSSDGRTCODIDE 111
 DB 505 KGFQLDSEHQKTCVDVDECAISRGNGGCSHECVNSPGSYECPCPDGYELRHRHACQDVDE 564
 QY 112 C-ADSEACGEACKNLPGSYCLCDGFGAYSSQEKACRDVDECLQGR--CEQVCVNSPGS 168
 DB 565 CIVENGNCNSNI-CINLPGGRHCACEIGYSLQDDQRTCSVDVDECNQDTHDCSHHCNVNPGA 623
 QY 169 YTHCDGRGGLKLSQDMTDCEDILPC 194
 DB 624 YECECP--AGFKLGRNLSCEDVDEC 647

RESULT 29
 O75412 PRELIMINARY; PRT; 1511 AA.
 ID O75412
 AC O75412
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Latent transforming growth factor-beta binding protein 4S.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=98325059; PubMed=9660815; DOI=10.1074/jbc.273.29.18459;
 RA Saharinen J., Taipale J., Monni O., Keski-Oja J.;

RT "Identification and characterization of a new latent transforming
 RT growth factor--binding protein, LTBP-4.";
 RL J. Biol. Chem. 273:18459-18469(1998).
 DR EMBL; AF051344; AAC39879.1; --
 DR HSSP; P35555; LEWN.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005509; F:calcium ion binding; NAS.
 DR GO; GO:0005539; F:glycosaminoglycan binding; NAS.
 DR GO; GO:0005178; F:integrin binding; NAS.
 DR GO; GO:0050431; F:transforming growth factor beta binding; IEA.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0030252; P:growth hormone secretion; TAS.
 DR GO; GO:0008457; P:protein folding; TAS.
 DR GO; GO:0045595; P:regulation of cell differentiation; TAS.
 DR GO; GO:0001558; P:regulation of cell growth; TAS.
 DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IEA.
 DR GO; GO:0017015; P:regulation of transforming growth factor be...; TAS.
 DR InterPro; IPR00152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF07645; EGF_CA; 16.
 DR Pfam; PF00883; TB; 4.
 DR SMART; SM00179; EGF_CA; 16.
 DR PROSITE; PS00010; ASX_HYDROXYL; 14.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
 DR PROSITE; PS01186; EGF_2; 12.
 DR PROSITE; PS00026; EGF_3; 13.
 DR PROSITE; PS01187; EGF_CA; 17.
 KW EGF-like domain.
 SQ SEQUENCE 1511 AA; 161157 MW; C61AB757B256958D CRC64;
 Query Match 27.3%; Score 353.5; DB 2; Length 1511;
 Best Local Similarity 43.3%; Pred. No. 1.2e-20;
 Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;
 QY 29 DOCTNP--CDRKGTAQCDLGNFFCLCKAGWGRGLCDKDVNECSQENGCG-LQICHNK 85
 DB 560 DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEEDVDECAQBPPCPGRCNDT 616
 QY 86 PSFHCSCHSGLSSDGRTCODIDECAADS--BACGEACKNLPGSYCLCDGFGAYSSQE 144
 DB 617 AGSFHCACPAGFRSGPAGCPQDVDECARSPPTCYGRCENTEGSFQCVCPMGFPQNAAG 676
 QY 145 KACRDVDECLQGR--RCE--QVCVNSPGSYTCH--CDGRGGLKLSQ--DMTDCED--ILPCVP 196
 DB 677 SECDVDECNHLCAPGQECVNSPGSFQCRACPSGHHLHRCRTDVEDCSGAPCGP 734
 RESULT 30
 O88840 PRELIMINARY; PRT; 3857 AA.
 ID O88840
 AC O88840
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mutant fibrillin-1.
 GN Name=Fbni;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B10.D2;
 RX MEDLINE=98069008; PubMed=9405934;
 RA Bona C.A., Murai C., Casares S., Kasturi K., Nishimura H., Honjo T.,
 RA Matsuda F.;
 RT "Structure of the mutant fibrillin-1 gene in the tight skin (TSK)
 RT mouse.";
 RL DNA Res. 4:267-271(1997).


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DR EMBL; AF007248; AAC62317.1; -.
DR HSP; P35555; 1LWJ.
DR MGD; MGI:95489; Fbn1.
DR GO; GO:0001527; C:micr fibril; TAG.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR002557; Chitin_bind_PeRA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00608; EGF_Ca; 59.
DR Pfam; PF00683; TB_12.
DR SMART; SM00494; ChtBD2; 5.
DR SMART; SM00179; EGF_Ca; 60.
DR PROSITE; PS00010; ASX HYDROXYL; 61.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 50.
DR PROSITE; PS50026; EGF_3; 56.
DR PROSITE; PS01187; EGF_Ca; 61.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 3857 AA; 418303 MW; 5BC0618BC527E04C CRC64;

Query Match 27.1%; Score 351.5; DB 2; Length 3857;
Best Local Similarity 33.2%; Pred. No. 4.3e-20;
Matches 83; Conservative 26; Mismatches 94; Indels 47; Gaps 8;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAG 58
DB 2115 CHNTEGSRCEPCPGHQLSPNISACIDINECELSANLCPH---GRCVNLIGKYCACNPG 2171
QY 59 W---GGRLCDKDVNCSQENGGLQICHNKPGSFHCSGFSFELSSDQRTQDIDECADS 115
DB 2172 YHPHTRDLFCVDIDECISIMNGGCFTCTNSDGSYECSCQPGFALMPDQRSCTDIDECEDN 2231
QY 116 -EAGEARCKNLPGSYCLDCEGFAYSSQEKACRDVDE-----CLOGRCEQVCVNSPG 167
DB 2232 PNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNICLSGTCE----NTKG 2287
QY 168 SYTHCHD---GRGGLKLSQMDTCE-----DILPCVPFSSVAKSVKS 205
DB 2288 SFICHCDMGYSKKGKGTCTDINECEIGAHNCDRHAVCTNTAGSKFCSQPGWIGDGKIC 2347
QY 206 LYLGRMFSGT 215
DB 2348 TDLDECSST 2357

RESULT 31
Q9WUH8 PRELIMINARY; PRT; 2872 AA.
AC Q9WUH8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibrillin-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9032689; PubMed=9815129;
RA Kanwar Y.S.; Ota K.; Yang Q.; Kumar A.; Wada J.; Kashiwara N.;
RA Peterson D.R.;
RT "Isolation of rat fibrillin-1 cDNA and its relevance in metanephric
RT development."
RL Am. J. Physiol. 275:F710-F723 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96132851; PubMed=8557636; DOI=10.1074/jbc.271.28.16662;
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RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135059; AAD34438.1; -.
DR HSP; P35555; 1APJ.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR011398; Fibrillin.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF07645; EGF_Ca; 41.
DR Pfam; PF00683; TB_9.
DR SMART; PIRSF036312; Fibrillin; 1.
DR SMART; SM00179; EGF_Ca; 41.
DR PROSITE; PS00010; ASX HYDROXYL; 42.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS50026; EGF_3; 38.
DR PROSITE; PS01187; EGF_Ca; 41.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 2872 AA; 312069 MW; 0C4F7F3B87A80280 CRC64;

Query Match 27.0%; Score 350.5; DB 2; Length 2872;
Best Local Similarity 36.9%; Pred. No. 3.9e-20;
Matches 76; Conservative 24; Mismatches 77; Indels 29; Gaps 7;

QY 6 CINKYG-----SPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAG 58
DB 1130 CHNTEGSRCEPCPGHQLSPNISACIDINECELSANLCPH---GRCVNLIGKYCACNPG 1186
QY 59 W---GGRLCDKDVNCSQENGGLQICHNKPGSFHCSGFSFELSSDQRTQDIDECADS 115
DB 1187 YHPHTRDLFCVDIDECISIMNGGCFTCTNSDGSYECSCQPGFALMPDQRSCTDIDECEDN 1246
QY 116 -EAGEARCKNLPGSYCLDCEGFAYSSQEKACRDVDE-----CLOGRCEQVCVNSPG 167
DB 1247 PNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNICLSGTCE----NTKG 1302
QY 168 SYTHCHD---GRGGLKLSQMDTCE 189
DB 1303 SFICHCDMGYSKKGKGTCTDINECE 1328

RESULT 32
PBN1_BOVIN STANDARD; PRT; 2871 AA.
AC P98133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 1 precursor (MP340).
GN Name=PBN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RX MEDLINE=95137597; PubMed=7835900;
RA Tilstra D.J.; Potter K.A.; Byers P.H.;
RT "Sequence of the coding region of the bovine fibrillin cDNA and
RT localization to bovine chromosome 10."
RL Genomics 23:480-485 (1994).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=96132851; PubMed=8557636; DOI=10.1074/jbc.271.28.16662;
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FT DISULFID 1097 1111 By similarity.
FT DISULFID 1117 1129 By similarity.
FT DISULFID 1124 1138 By similarity.
FT DISULFID 1140 1153 By similarity.
FT DISULFID 1159 1171 By similarity.
FT DISULFID 1166 1180 By similarity.
FT DISULFID 1182 1195 By similarity.
FT DISULFID 1201 1212 By similarity.
FT DISULFID 1208 1221 By similarity.
FT DISULFID 1223 1236 By similarity.
FT DISULFID 1242 1254 By similarity.
FT DISULFID 1249 1263 By similarity.
FT DISULFID 1265 1278 By similarity.
FT DISULFID 1284 1296 By similarity.
FT DISULFID 1291 1305 By similarity.
FT DISULFID 1307 1320 By similarity.
FT DISULFID 1326 1339 By similarity.
FT DISULFID 1333 1348 By similarity.
FT DISULFID 1350 1361 By similarity.
FT DISULFID 1367 1380 By similarity.
FT DISULFID 1374 1389 By similarity.
FT DISULFID 1391 1402 By similarity.
FT DISULFID 1408 1420 By similarity.
FT DISULFID 1415 1429 By similarity.
FT DISULFID 1431 1444 By similarity.
FT DISULFID 1450 1461 By similarity.
FT DISULFID 1456 1470 By similarity.
FT DISULFID 1472 1485 By similarity.
FT DISULFID 1491 1502 By similarity.
FT DISULFID 1497 1511 By similarity.
FT DISULFID 1513 1526 By similarity.

Query Match 26.9%; Score 349.5; DB 1; Length 2871;
Best Local Similarity 35.9%; Pred. No. 4.7e-20;
Matches 78; Conservative 21; Mismatches 67; Indels 51; Gaps 9;

QY 6 CLNKSGPYTKNSGFATCVQNLPDQCTP-----NPKDRKGTQA-----CQDL 47
DB 1129 CLNTGSG-----YRC-----ECFCHQLAPNISACIDINECELSAHLCPHRCVNL 1174
QY 48 MNFFCLCKAGWG---RLCDKDVNECSQNGGLQIQIHNKPGSFHCSHGFFELSSDGR 104
DB 1175 IGKYCACNPGYHSTPDLRFCDVIDECSIMNGCETFTCTNSGSEYECSCQPGFALMPDQR 1234
QY 105 TCQDIDECADS-EAGEARCKNLPGSYCLDEGFAYSSQEKACRDVDE-----CLOG 156
DB 1235 SCTDIDECEDPNICDGGQCTNIPGEYRCLCYDGFMASEDMMKTCVDVNECDLNPNICLSG 1294
QY 157 RCEQVCVNSPGSYTCHCD---GRGLKLSQDMDTCE 189
DB 1295 TCE---NTKGSFICHCDMGYSKGKGTCTDINECE 1327

RESULT 33
Q81WY4
ID Q81WY4 PRELIMINARY; PRT; 988 AA.
AC Q81WY4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Signal peptide-CUB-EGF-like domain containing protein 1.
GN Name=SCUBE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22336413; PubMed=12270931; DOI=10.1074/jbc.M207410200;
RA Yang R.-B., Ng C.K.D., Wasserman S.M., Colman S.D., Shenoy S.,
RA Mehraban F., Komuves L.G., Tomlinson J.E., Topper J.N.;
RT "Identification of a novel family of cell-surface proteins expressed
RT in human vascular endothelium.";

RL J. Biol. Chem. 277:46364-46373 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang R.-B., Ng C.K.D., Wasserman S.M., Colman S.D., Shenoy S.,
RA Mehraban F., Komuves L., Tomlinson J.E., Topper J.N.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525689; AAAT7133.1; -.
DR HSSP; P01130; 1428.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0046982; F:protein heterodimerization activity; IDA.
DR GO; GO:0042804; F:protein homooligomerization activity; IPI.
DR GO; GO:0007512; P:adult heart development; NAS.
DR GO; GO:0007596; P:blood coagulation; NAS.
DR GO; GO:0045446; P:endothelial cell differentiation; NAS.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR GO; GO:0009791; P:post-embryonic development; NAS.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR00859; CUB.
DR InterPro; IPR00742; EGF 2.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR01491; Thrombomodulin.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 4.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF 2; 7.
DR PROSITE; PS00026; EGF 3; 2.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 988 AA; 107900 MW; 1BF57BEF7780C9C1 CRC64;

Query Match 26.9%; Score 349; DB 2; Length 988;
Best Local Similarity 37.7%; Pred. No. 1.8e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;

QY 14 YTKNSGFATCVQNLPDQCTP---PCDRKGTQAQODLMGNFFCLCKAGW---GGRLCDKD 67
DB 232 YAPHSRGRTCIET---CAVNGGCDR---TKDTATGVKSCFVGTLPDQKTC-KD 282
QY 68 VNECSQNGGLQIQIHNKPGSFHCSHGFFELSSDGTCDIDECADSEAGEARCKNLP 127
DB 283 INECLVNGGCDHFCRNTVGSFEGCGKRGYKLLTDETCQDIDECFERTCDHI-CINSP 341
QY 128 GSYSLCLDEGF-AYSQEKACRDVDEC---LQRCQECVQVNSPGSYTCHCDGRGLKLSQD 184
DB 342 GSPQCLCHRGYLYGTH---CGDVDECSMNGSCDQGVNTKGSYECVCP---PGRRLHWN 397
QY 185 MDTCEDILPC-----VPFSVAKSVKSLYL 208
DB 398 RKDCVETGKCLSRKTSPTRAQLSCSKAGGVESCF 432

RESULT 34
Q75N88
ID Q75N88 PRELIMINARY; PRT; 1365 AA.
AC Q75N88;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibrillin 1.
GN Name=FBN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RA Yoneda T., Takahashi T., Eto S., Sato T., Xu G., Kanazaki R., Toki T.,
RA Yonekawa S., Ito E.;
RT "Three novel mutations of the fibrillin-1 gene and ten single
RT nucleotide polymorphisms of the fibrillin-3 gene in Marfan syndrome
RT patients.";
RL J. Hum. Genet. 49:404-407(2004).
CC -1- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AB177802; BAD16738.1; -;
DR HSP; P00736; IAPQ.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_2.
DR InterPro; IPR001438; EGF_1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF07645; EGF_CA; 17.
DR Pfam; PF00683; TB; 5.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 22.
DR SMART; SM00179; EGF_CA; 19.
DR PROSITE; PS00010; ASX-HYDROXYL; 18.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 15.
DR PROSITE; PS00026; EGF_3; 18.
DR PROSITE; PS01187; EGF_CA; 18.
KW EGF-like domain.
SQ SEQUENCE 1365 AA; 147448 MW; ED83FB79C1B2BD48 CRC64;

Query Match 26.9%; Score 348.5; DB 2; Length 1365;
Best Local Similarity 42.9%; Pred. No. 2.8e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLGNFFCLKAGWG---RLCDKDVNCSQENGGLQICHNKGSFCHSCHSFELS 100
DB 1171 CVNLKGYQCACNPGYHSTPDRFLFCVDIDECSTFMNGCCTFTNSGSEYECSCQPGFALM 1230
QY 101 SDGRTQDIDECADS-EAGCEARCKNLPGSYSLCDGEGFAYSSQERACRDVDS----- 152
DB 1231 PDGRTCTDIDECEDNPNICDGGCTWPGYRCLCYDGFNASEDMKTCVDVNECDLNPNI 1290
QY 153 CLGRCQEVNCSFGSYTCHD----GRGGLKLSQMDTCE 189
DB 1291 CLSGTCE---NTKGSFICHGDMGYSSKKGKGTCTDINECE 1327

RESULT 35
FBN1_HUMAN STANDARD; PRT; 2871 AA.
AC P3555;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 1 precursor.
GN Names=FBN1; Synonyms=FBN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
TX TISSUE=Placenta;
RX MEDLINE=93372850; PubMed=8364578;
RA Ferreira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
RA Pangillan T., Bonadio J.;
RT "Genomic organization of the sequence coding for fibrillin, the
RT defective gene product in Marfan syndrome.";
RL Hum. Mol. Genet. 2:961-968(1993).
RN [2]
RP SEQUENCE OF 1-932 FROM N.A.

RC TISSUE=Fibroblast, and Placenta;
RX MEDLINE=94010947; PubMed=7691719;
RA Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;
RT "Fibrillin binds calcium and is coded by cDNAs that reveal a
RT multidomain structure and alternatively spliced exons at the 5' end.";
RL Genomics 17:476-484(1993).
RN [3]
RP SEQUENCE OF 899-2871 FROM N.A.
RX MEDLINE=91304568; PubMed=1852207; DOI=10.1038/352334a0;
RA Maslin C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;
RT "Partial sequence of a candidate gene for the Marfan syndrome.";
RL Nature 352:334-337(1991).
RN [4]
RP SEQUENCE OF 813-1313 FROM N.A.
RX MEDLINE=91304567; PubMed=1852206; DOI=10.1038/352334a0;
RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
RA Tsipouras P., Ramirez F., Hollister D.W.;
RT "Linkage of Marfan syndrome and a phenotypically related disorder to
RT two different fibrillin genes.";
RL Nature 352:330-334(1991).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=91317849; PubMed=1860873;
RA Sakai L.Y.; Keene D.R.; Glanville R.W., Bachinger H.P.;
RT "Purification and partial characterization of fibrillin, a cysteine-
RT rich structural component of connective tissue microfibrils.";
RL J. Biol. Chem. 266:14763-14770(1991).
RN [6]
RP STRUCTURE BY NMR OF 2054-2125.
RX MEDLINE=98031893; PubMed=9362480; DOI=10.1093/emboj/16.22.6659;
RA Yuan X., Downing A.K., Knott V., Handford P.A.;
RT "Solution structure of the transforming growth factor beta-binding
RT protein-like module, a domain associated with matrix fibrils.";
RL EMBO J. 16:6659-6666(1997).
RN [7]
RP STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=96144829; PubMed=8568689; DOI=10.1006/jmbi.1996.0003;
RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;
RT "Calcium binding properties of an epidermal growth factor-like domain
RT pair from human fibrillin-1.";
RL J. Mol. Biol. 255:22-27(1996).
RN [8]
RP STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=9622301; PubMed=8653794; DOI=10.1016/S0092-8674(00)81259-3;
RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
RA Handford P.A.;
RT "Solution structure of a pair of calcium-binding epidermal growth
RT factor-like domains: implications for the Marfan syndrome and other
RT genetic disorders.";
RL Cell 85:597-605(1996).
RN [9]
RP REVIEW ON MFS VARIANTS.
RX MEDLINE=96174615; PubMed=8594563; DOI=10.1093/nar/24.1.137;
RA Colod G., Beroud C., Soussi T., Junien C., Boileau C.;
RT "Software and database for the analysis of mutations in the human FBN1
RT gene.";
RL Nucleic Acids Res. 24:137-141(1996).
RN [10]
RP REVIEW ON MFS VARIANTS.
RX MEDLINE=97169383; PubMed=9016526; DOI=10.1093/nar/25.1.147;
RA Colod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
RA Richards R.I., Wang W., Junien C., Boileau C.;
RT "Marfan Database (second edition): software and database for the
RT analysis of mutations in the human FBN1 gene.";
RL Nucleic Acids Res. 25:147-150(1997).
RN [11]
RP REVIEW ON VARIANTS.
RX MEDLINE=98062175; PubMed=9401003;
RX DOI=10.1002/(SICI)1098-1004(1997)10:6<415::AID-HUMU1>3.3.CO;2-2;
RA Hayward C., Brock D.J.H.;
RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
RT fibrillinopathies.";

RL Hum. Mutat. 10:415-423 (1997).
[12]
RP REVIEW ON MFS.
RX PubMed=10633129;
RA Robinson P.N., Godfrey M.;
RT "The molecular genetics of Marfan syndrome and related
microfibrilopathies.";
J. Med. Genet. 37:9-25 (2000).
[13]
RP REVIEW ON VARIANTS.
RX PubMed=12203987; DOI=10.1002/humu.10113;
RA Robinson P.N., Booms P., Katze S., Ladewig M., Neumann L., Palz M.,
Pregla R., Tiecke F., Rosenberg T.;
RT "Mutations of FBNI and genotype-phenotype correlations in Marfan
syndrome and related fibrillinopathies.";
Hum. Mutat. 20:153-161 (2002).
[14]
RP VARIANT MFS PRO-1137.
RX MEDLINE=91304569; PubMed=1852208; DOI=10.1038/352337a0;
RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,
Curristin S.M., Stetten G., Meyers D.A., Francomano C.A.;
RT "Marfan syndrome caused by a recurrent de novo missense mutation in
the fibrillin gene.";
Nature 352:337-339 (1991).
[15]
RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.
RX MEDLINE=93250834; PubMed=1301946;
RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;
RT "Clustering of fibrillin (FBNI) missense mutations in Marfan syndrome
patients at cysteine residues in EGF-like domains.";
Hum. Mutat. 1:366-374 (1992).
[16]
RP VARIANT MFS SER-2307.
RX MEDLINE=92232590; PubMed=1569206;
RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,
Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;
RT "Marfan phenotype variability in a family segregating a missense
mutation in the epidermal growth factor-like motif of the fibrillin
gene.";
J. Clin. Invest. 89:1674-1680 (1992).
[17]
RP VARIANTS MFS ILE-548 AND ALA-723.
RX MEDLINE=94010946; PubMed=8406497;
RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
Pyeritz R.B., Francomano C.A.;
RT "Four novel FBNI mutations: significance for mutant transcript level
and EGF-like domain calcium binding in the pathogenesis of Marfan
syndrome.";
Genomics 17:468-475 (1993).
[18]
RP VARIANT MFS SER-2144.
RX MEDLINE=93278402; PubMed=8504310;
RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
RT "A novel fibrillin mutation in the Marfan syndrome which could disrupt
calcium binding of the epidermal growth factor-like motif.";
Hum. Mol. Genet. 2:475-477 (1993).
[19]
RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
ALA-1148.
RX MEDLINE=94108431; PubMed=8281141;
RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gaerner C.,
Berg M.A., Miller D.C., Francke U.;
RT "Mutation screening of complete fibrillin-1 coding sequence: report of
five new mutations, including two in 8-cysteine domains.";
Hum. Mol. Genet. 2:1813-1821 (1993).
[20]
RP VARIANTS MFS GLY-217 AND ARG-2627.
RX MEDLINE=95067970; PubMed=7977366;
RA Karttunen L., Ragnath M., Lomqvist L., Peltonen L.;
RT "A compound-heterozygous Marfan patient: two defective fibrillin
alleles result in a lethal phenotype.";
Am. J. Hum. Genet. 55:1083-1091 (1994).

RP VARIANT EL LYS-2447.
RX MEDLINE=94245249; PubMed=8189302;
RA Lomqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
Peltonen L.;
RT "A novel mutation of the fibrillin gene causing ectopia lentis.";
Genomics 19:573-576 (1994).
[22]
RP VARIANT MFS CYS-627.
RX MEDLINE=94272487; PubMed=8004112;
RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
RT "Two novel mutations and a neutral polymorphism in EGF-like domains of
the fibrillin gene (FBNI): SSCP screening of exons 15-21 in Marfan
syndrome patients.";
Hum. Mol. Genet. 3:373-375 (1994).
[23]
RP VARIANT MFS CYS-122.
RX MEDLINE=94314977; PubMed=8040326;
RA Stahl-Hallengren C., Ukonen T., Kainulainen K., Kristofersson U.,
Saxne T., Torngvist K., Peltonen L.;
RT "An extra cysteine in one of the non-calcium-binding epidermal growth
factor-like motifs of the FBNI polypeptide is connected to a novel
variant of Marfan syndrome.";
J. Clin. Invest. 94:709-713 (1994).
[24]
RP VARIANT MFS TYR-1223.
RX MEDLINE=94351682; PubMed=8071963;
RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;
RT "A new missense mutation of fibrillin in a patient with Marfan
syndrome.";
J. Med. Genet. 31:338-339 (1994).
[25]
Query Match 26.9%; Score 348.5; DB 1; Length 2871;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;
Qy 44 CQDLGNFFCLCKAGWG---RLCKDVNEQSGGCLQICHKNKPGSFHCSHSGFELS 100
Db 1171 CVNLIGKYQACNPGYHSTPDLFCVDIDECISVNGGCTFTCTNSEGSEYSCQPGFALM 1230
Qy 101 SDGRTCDQIDECADS-EACGEARCNKLPFGSYSLCDEGFAYSSOEKACRDYDE----- 152
Db 1231 PDQRSCTDIDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNI 1290
Qy 153 CLQGRQVQVNSPGSYTCHCD----GRGLKLSQDMDTCE 189
Db 1291 CLSGTCE----NTKGSFICHDMGYSKGKGTCTDINECE 1327
RESULT 36
Q75N87 PRELIMINARY; PRT; 2871 AA.
ID Q75N87
AC Q75N87; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibrillin 1.
GN Name=FBNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Uyeda T., Takahashi T., Bto S., Sato T., Xu G., Kanazaki R., Toki T.,
Yonesaka S., Ito E.;
RT "Three novel mutations of the fibrillin-1 gene and ten single
nucleotide polymorphisms of the fibrillin-3 gene in Marfan syndrome
patients.";
J. Hum. Genet. 49:404-407 (2004).
CC -!- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AB177803; BAD16739.1; -.

DR HSP; P35555; 1APU.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002212; Fibril-assoc.
 DR InterPro; IPR011398; Fibrillin.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF000008; EGF_3.
 DR Pfam; PF07645; EGF_CA; 42.
 DR Pfam; PF06683; TB; 9.
 DR SMART; SM00181; EGF; 47.
 DR SMART; PIRSP036312; Fibrillin; 1.
 DR SMART; SM00179; EGF_CA; 44.
 DR PROSITE; PS00010; ASX_HYDROXYL; 42.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 38.
 DR PROSITE; PS00026; EGF_3; 39.
 DR PROSITE; PS01187; EGF_CA; 42.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 KW EGF-like domain.
 SQ SEQUENCE 2871 AA; 312219 MW; C3D044A80321E082 CRC64;
 Query Match 26.9%; Score 348.5; DB 2; Length 2871;
 Best Local Similarity 42.9%; Pred.No. 5.7e-20;
 Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;
 QY 44 CQDLMGNFCLCKAGWG---RLCDKDVNECSQENGGLQICHNKPFSCHSGFELS 100
 DB 1171 CYNLICKYQCACNPGYHSTPDLFCVDIDECSTMGCGCTFTCTNSGSEYECSCQPGFALM 1230
 QY 101 SGRTQCDIDECADS-EAGEARCKNLPGSYCLDEGFAYSSQEKACRDVDE----- 152
 DB 1231 PQRSCTDIDECBDNPNICDGGQCTNPGEYRCLCYDGFMASEDMDKTCVDVNECDLNPNI 1290
 QY 153 CLQGRCEQVNSPGSYVTCHCD---GRGGLKLSQDMDTCE 189
 DB 1291 CLSGTCE---NTKGSFICHDMGYSGKKGKTCTDINECE 1327
 RESULT 37
 Q6ZW11 PRELIMINARY; PRT; 971 AA.
 ID Q6ZW11
 AC Q6ZW11
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ41044.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukusumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Ho Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isogai T.;
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK123039; BAC85521.1; --
 DR HSP; P00736; 1APU.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_4.

DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF07645; EGF_CA; 3.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 10.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS00010; ASX_HYDROXYL; 6.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS00026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW EGF-like domain.
 SQ SEQUENCE 971 AA; 106744 MW; 6213C2EED74BD428 CRC64;
 Query Match 26.6%; Score 345; DB 2; Length 971;
 Best Local Similarity 38.1%; Pred.No. 3.9e-20;
 Matches 75; Conservative 28; Mismatches 74; Indels 20; Gaps 10;
 QY 27 LPDQCTPN--PCDRKGTOACQDLMGNFCLCKAGW---GGRLCDKDVNECSQENGGLQ 80
 DB 282 LMETCAVNVGCDR---TCKDTSTGVHCSCVPVGTQLQLDGKTC-KDIDECOTRNGGCDH 336
 QY 81 ICHNKPFSCHSGFELS DGRTCQDIDECADSEACGEARCKNLPGSYCLDEGFA- 139
 DB 337 FCNIVGSGFCCKGFKLLTDEKSCQDVDECSLORTCDHS-CINHPGTFFACACNRGYTL 395
 QY 140 YSSQKACRDVDECL--QGRCEQVNSPGSYVTCHCDGRGGLKLSQDMDTCSDDLPCVPF 197
 DB 396 YGFTH--CGDTNECSINNGCCQVCVNTVGSYECOC--HPGYKLHWNKKDCVEVKGLLPT 451
 QY 198 SVAKSVKSLYLGRMPSG 214
 DB 452 SVSPRV-SLHCGKSGG 467
 RESULT 38
 Q9NQ36 PRELIMINARY; PRT; 999 AA.
 ID Q9NQ36
 AC Q9NQ36
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CEGP1 protein.
 GN Name=CEGP1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21418998; PubMed=11528127;
 RA Amid C., Bahr A., Mujica A., Sampson N., Bikar S.E., Winterpacht A.,
 RA Zabel B., Hankeln T., Schmidt E.R.;
 RT "Comparative genomic sequencing reveals a strikingly similar
 RT architecture of a conserved syntenic region on human chromosome
 RT 1p15.3 (including gene STS) and mouse chromosome 7.";
 RL Cytogenet. Cell Genet. 93:284-290(2001).
 DR EMBL; AJ400877; CAB92285.1; --
 DR HSP; P35555; 1EMN.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF07645; EGF_CA; 3.

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DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 999 AA; 109956 MW; 61334844A053095 CRC64;

Query Match      26.6%; Score 345; DB 2; Length 999;
Best Local Similarity 38.1%; Pred. No. 4e-20;
Matches 75; Conservative 28; Mismatches 74; Indels 20; Gaps 10;

QY 27 LPDQCTPN--PCDRKGTQACQDLNMGNFCLCKAGW----GGFLCDKDYNECSQENGGLQ 80
DB 282 LMETCAVNGGCDR---TCKDTSTGVHCSCVPVGLTLDGKTC-KDIDECQTRNGGCDH 336

QY 81 ICHNKPFGSPHCSHSGFELSSDGRTCQDIDECADSEAGCEARCKNLPGSYSLCDEGFA- 139
DB 337 FCENIVGSFDCGCKGFKLLTDEKSCQDVDESLDRTCDHS-CINHPGTFACACNGYTL 395

QY 140 YSSQBKACRDVDECL--QGRCEQVCNPSGSYTCHCDGRGGGKJUSQDMDTCEDLPCVPF 197
DB 396 YGFTH--CGDTNECSINNGGCGQVCNTVGSVEQCQ--HPGYKLFHWKKDCVVEVKGLLPT 451

QY 198 SVAKSVKSLYLGRMPSG 214
DB 452 SVSPRV-SLHCKSGGG 467

RESULT 39
PEN1_MOUSE
ID FBN1_MOUSE STANDARD; PRT; 2871 AA.
AC Q61554; Q60826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 1 precursor.
GN Name=Fbn1; Synonyms=Fbn-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=95130561; PubMed=7829516; DOI=10.1074/jbc.270.4.1798;
RA Yin W., Germiller J., Sanguinetti C., Smiley E., Pangillan T.,
RA Pereira L., Ramirez F., Bonadio J.;
RT "Primary structure and developmental expression of Fbn-1, the mouse
  fibrillin gene.";
RL J. Biol. Chem. 270:1798-1806 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
RL Submitted (APR-1995) to the EMBL/GenBank/DDAJ databases.
CC -!- FUNCTION: Structural component of connective tissue microfibrils
  that binds calcium. Fibrillin-1-containing microfibrils provide
  long-term force bearing structural support.
CC -!- PTM: Forms intermolecular disulfide bonds either with other
  fibrillin-1 molecules or with other components of the microfibrils
  (By similarity).
CC -!- SIMILARITY: Belongs to the fibrillin family.
CC -!- SIMILARITY: Contains 47 EGF-like domains.
CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
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  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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EMBL; L29454; AAA56840.1; -.
EMBL; U22493; AAA64217.1; -.
PIR; A55624; A55624.
HSSP; P35555; LAPJ.
MGD; MGI:95489; Fbn1.
InterPro; IPR000152; Asx_hydroxyl_s.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_CA.
InterPro; IPR006209; EGF-like.
InterPro; IPR002212; Fibril-assoc.
Pfam; PF00008; EGF; 45.
Pfam; PF00683; TB; 9.
PIRSF; PIRSF016312; Fibrillin; 1.
SMART; SM00179; EGF_CA; 42.
PROSITE; PS00010; ASX_HYDROXYL; 43.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 38.
PROSITE; PS00026; EGF_3; 45.
PROSITE; PS01187; EGF_CA; 43.
KW Calcium-binding; EGF-like domain; Extracellular matrix; Glycoprotein;
  Multigene family; Repeat; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 2871 Fibrillin 1.
FT DOMAIN 81 112 EGF-like 1.
FT DOMAIN 115 146 EGF-like 2.
FT DOMAIN 147 178 EGF-like 3.
FT DOMAIN 246 287 EGF-like 4, calcium-binding.
FT DOMAIN 288 329 EGF-like 5, calcium-binding.
FT DOMAIN 330 401 TGFBP 1.
FT DOMAIN 402 446 Pro-rich.
FT DOMAIN 449 489 EGF-like 6.
FT DOMAIN 490 529 EGF-like 7, calcium-binding.
FT DOMAIN 530 571 EGF-like 8, calcium-binding.
FT DOMAIN 572 612 EGF-like 9, calcium-binding.
FT DOMAIN 613 653 EGF-like 10, calcium-binding.
FT DOMAIN 656 721 TGFBP 2.
FT DOMAIN 723 764 EGF-like 11, calcium-binding.
FT DOMAIN 765 806 EGF-like 12, calcium-binding.
FT DOMAIN 807 846 EGF-like 13, calcium-binding.
FT DOMAIN 910 951 EGF-like 14, calcium-binding.
FT DOMAIN 952 1018 TGFBP 3.
FT DOMAIN 1028 1069 EGF-like 15, calcium-binding.
FT DOMAIN 1070 1112 EGF-like 16, calcium-binding.
FT DOMAIN 1113 1154 EGF-like 17, calcium-binding.
FT DOMAIN 1155 1196 EGF-like 19, calcium-binding.
FT DOMAIN 1197 1237 EGF-like 19, calcium-binding.
FT DOMAIN 1238 1279 EGF-like 20, calcium-binding.
FT DOMAIN 1280 1321 EGF-like 21, calcium-binding.
FT DOMAIN 1322 1362 EGF-like 22, calcium-binding.
FT DOMAIN 1363 1403 EGF-like 23, calcium-binding.
FT DOMAIN 1404 1445 EGF-like 24, calcium-binding.
FT DOMAIN 1446 1486 EGF-like 25, calcium-binding.
FT DOMAIN 1487 1527 EGF-like 26, calcium-binding.
FT DOMAIN 1528 1559 TGFBP 4.
FT DOMAIN 1560 1647 EGF-like 27, calcium-binding.
FT DOMAIN 1648 1688 EGF-like 28, calcium-binding.
FT DOMAIN 1689 1758 TGFBP 5.
FT DOMAIN 1759 1807 EGF-like 29, calcium-binding.
FT DOMAIN 1808 1848 EGF-like 30, calcium-binding.
FT DOMAIN 1849 1890 EGF-like 31, calcium-binding.
FT DOMAIN 1891 1929 EGF-like 32, calcium-binding.
FT DOMAIN 1930 1972 EGF-like 33, calcium-binding.
FT DOMAIN 1973 2012 EGF-like 34, calcium-binding.
FT DOMAIN 2013 2054 EGF-like 35, calcium-binding.
FT DOMAIN 2055 2121 TGFBP 6.
FT DOMAIN 2127 2165 EGF-like 36, calcium-binding.
FT DOMAIN 2166 2205 EGF-like 37, calcium-binding.
FT DOMAIN 2206 2246 EGF-like 38, calcium-binding.
FT DOMAIN 2247 2290 EGF-like 39, calcium-binding.
FT DOMAIN 2291 2332 EGF-like 40, calcium-binding.
FT DOMAIN 2333 2400 TGFBP 7.
```

FT	DOMAIN	2402	2443	EGF-like 41, calcium-binding.	FT	DISULFID	1367	1380	By similarity.
FT	DOMAIN	2444	2484	EGF-like 42, calcium-binding.	FT	DISULFID	1374	1389	By similarity.
FT	DOMAIN	2485	2523	EGF-like 43, calcium-binding.	FT	DISULFID	1391	1402	By similarity.
FT	DOMAIN	2524	2566	EGF-like 44, calcium-binding.	FT	DISULFID	1408	1420	By similarity.
FT	DOMAIN	2567	2606	EGF-like 45, calcium-binding.	FT	DISULFID	1415	1429	By similarity.
FT	DOMAIN	2607	2647	EGF-like 46, calcium-binding.	FT	DISULFID	1431	1444	By similarity.
FT	DOMAIN	2648	2687	EGF-like 47, calcium-binding.	FT	DISULFID	1450	1461	By similarity.
FT	DISULFID	85	94	By similarity.	FT	DISULFID	1456	1470	By similarity.
FT	DISULFID	89	100	By similarity.	FT	DISULFID	1472	1485	By similarity.
FT	DISULFID	102	111	By similarity.	FT	DISULFID	1491	1502	By similarity.
FT	DISULFID	119	129	By similarity.	FT	DISULFID	1497	1511	By similarity.
FT	DISULFID	123	134	By similarity.	FT	DISULFID	1513	1526	By similarity.
FT	DISULFID	136	145	By similarity.	FT	DISULFID	1610	1622	By similarity.
FT	DISULFID	150	160	By similarity.	FT	DISULFID	1617	1631	By similarity.
FT	DISULFID	154	166	By similarity.	Query Match 26.6%; Score 345; DB 1; Length 2871;				
FT	DISULFID	168	177	By similarity.	Best Local Similarity 38.6%; Pred No. 1,1e-19;				
FT	DISULFID	250	262	By similarity.	Matches 71; Conservative 23; Mismatches 68; Indels 22; Gaps 6;				
FT	DISULFID	257	271	By similarity.	QY 21 ATCVQLPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGW---GGRLCDKDVNCSQENG 77				
FT	DISULFID	273	286	By similarity.	Db 1151 SACIDINECELSANLCPH---GRCVNLIGKYQACNPGVHPHTRDLFCVDIDECSIMNGG 1207				
FT	DISULFID	292	304	By similarity.	QY 78 CLQICHNKPFGSCHSGFELSSDGRTCODIDECADS-EACGEARCKNLPKSYSLCDE 136				
FT	DISULFID	299	313	By similarity.	Db 1208 CETFCTNSDGSYECSCQCFALMPDQRCTDIDQEDNPNICDGGCTNPGEYRCLCYD 1267				
FT	DISULFID	315	328	By similarity.	QY 137 GPAYSSQSKACRDVDE-----CLOGRCEQVCVNSPGSYTCHCD---GRGGLKLSQDM 185				
FT	DISULFID	453	465	By similarity.	Db 1268 GFMASEDNKTCDVNECDLNPNICLSGTCE-----NTKGSFICHDMGYSGKKGKTGCTDI 1323				
FT	DISULFID	460	474	By similarity.	QY 186 DTFCE 189				
FT	DISULFID	476	488	By similarity.	Db 1324 NCECE 1327				
FT	DISULFID	494	504	By similarity.	RESULT 40				
FT	DISULFID	499	513	By similarity.	ID FBLL CAEEL STANDARD; PRT; 798 AA.				
FT	DISULFID	515	528	By similarity.	AC 077459; O18026; 077474; Q20903; Q95NZ3; Q9T2S1;				
FT	DISULFID	534	546	By similarity.	DT 16-OCT-2001 (Rel. 40, Created)				
FT	DISULFID	541	555	By similarity.	DT 28-FEB-2003 (Rel. 41, Last sequence update)				
FT	DISULFID	557	570	By similarity.	DT 25-OCT-2004 (Rel. 45, Last annotation update)				
FT	DISULFID	576	587	By similarity.	DE Fibulin-1 precursor.				
FT	DISULFID	582	596	By similarity.	GN Name=fbl-1; Synonyms=fbln1; ORFNames=F56H11.1;				
FT	DISULFID	598	611	By similarity.	OC Caenorhabditis elegans.				
FT	DISULFID	617	628	By similarity.	OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;				
FT	DISULFID	623	637	By similarity.	OC Rhabditidae; Feloderinae; Caenorhabditis.				
FT	DISULFID	639	652	By similarity.	OX NCBI_TaxID=6239;				
FT	DISULFID	727	739	By similarity.	RN [1]				
FT	DISULFID	734	748	By similarity.	RP SEQUENCE FROM N.A. (ISOFORMS A AND B).				
FT	DISULFID	750	763	By similarity.	RC STRAIN=CB1489;				
FT	DISULFID	769	781	By similarity.	RX MEDLINE=99120531; PubMed=9923656; DOI=10.1016/S0945-053X(98)90114-7;				
FT	DISULFID	776	790	By similarity.	RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;				
FT	DISULFID	792	805	By similarity.	RT "Identification of chicken and C. elegans fibulin-1 homologs and				
FT	DISULFID	811	821	By similarity.	RL Matrix Biol. 17:635-646(1998).				
FT	DISULFID	832	845	By similarity.	RN [2]				
FT	DISULFID	866	880	By similarity.	RP SEQUENCE FROM N.A.				
FT	DISULFID	914	926	By similarity.	RC STRAIN=Bristol N2;				
FT	DISULFID	921	935	By similarity.	RX MEDLINE=99069613; PubMed=9851916;				
FT	DISULFID	937	950	By similarity.	RT The C. elegans sequencing consortium;				
FT	DISULFID	1032	1044	By similarity.	RL "Genome sequence of the nematode C. elegans: a platform for				
FT	DISULFID	1039	1053	By similarity.	RN [3]				
FT	DISULFID	1055	1068	By similarity.	RP REVISIONS, AND ALTERNATIVE SPLICING.				
FT	DISULFID	1074	1086	By similarity.	RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
FT	DISULFID	1081	1095	By similarity.	CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.				
FT	DISULFID	1097	1111	By similarity.	CC May play a role in cell adhesion and migration along protein				
FT	DISULFID	1117	1129	By similarity.	CC fibers within the extracellular matrix (ECM). Could be important				
FT	DISULFID	1124	1138	By similarity.	CC for certain developmental processes and contribute to the				
FT	DISULFID	1140	1153	By similarity.					
FT	DISULFID	1159	1171	By similarity.					
FT	DISULFID	1166	1180	By similarity.					
FT	DISULFID	1182	1195	By similarity.					
FT	DISULFID	1201	1212	By similarity.					
FT	DISULFID	1208	1221	By similarity.					
FT	DISULFID	1223	1236	By similarity.					
FT	DISULFID	1242	1254	By similarity.					
FT	DISULFID	1249	1263	By similarity.					
FT	DISULFID	1265	1278	By similarity.					
FT	DISULFID	1284	1296	By similarity.					
FT	DISULFID	1291	1305	By similarity.					
FT	DISULFID	1307	1320	By similarity.					
FT	DISULFID	1326	1339	By similarity.					
FT	DISULFID	1333	1348	By similarity.					
FT	DISULFID	1350	1361	By similarity.					

CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes.
 CC -!- SUBUNIT: Interacts with itself and with various extracellular
 CC matrix components (By similarity).
 CC -!- SURCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=C;
 CC IsoId=O77469-1; Sequence=Displayed;
 CC Name=a; Synonyms=C;
 CC IsoId=O77469-2; Sequence=VSP_001387, VSP_001388, VSP_001389;
 CC Name=b; Synonyms=D;
 CC IsoId=O77469-3; Sequence=VSP_001387, VSP_001388, VSP_001389,
 CC VSP_001390;
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 9 EGF-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF051403; AAC28323.1; -;
 CC EMBL; AF051403; AAC28324.1; -;
 CC EMBL; AF051401; AAC28321.1; -;
 CC EMBL; AF051402; AAC28322.1; -;
 CC EMBL; AF070477; AAC24035.1; -;
 CC EMBL; Z68219; CAA92483.1; -;
 CC EMBL; Z68749; CAA92483.1; JOINED.
 CC EMBL; Z68219; CAC35826.1; -;
 CC EMBL; Z68749; CAC35826.1; JOINED.
 CC EMBL; Z68219; CAC35827.1; -;
 CC EMBL; Z68749; CAC35827.1; JOINED.
 CC EMBL; Z68219; CAA92962.1; -;
 CC EMBL; Z68219; CAA92962.1; JOINED.
 CC EMBL; Z68749; CAC35817.1; -;
 CC EMBL; Z68219; CAC35817.1; JOINED.
 CC EMBL; Z68749; CAC35818.1; -;
 CC EMBL; Z68219; CAC35818.1; JOINED.
 CC PIR; T22793; T22793.
 CC PIR; T42760; T42760.
 CC PIR; T42990; T42990.
 CC HSP; P16109; 1FSB.
 CC IntAct; O77469; -;
 CC WormBase; WBGene0001403; fbl-1.
 CC WormPep; F56H11.1a; CE26701.
 CC WormPep; F56H11.1b; CE26702.
 CC WormPep; F56H11.1c; CE16142.
 CC InterPro; IPR000020; Anaphylatoxin.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR009030; Grow_fac_recept.
 CC Pfam; PF01821; ANATO; 2.
 CC Pfam; PF00008; EGF; 5.
 CC SMART; SM00179; EGF_CA; 4.
 CC PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 4.
 CC PROSITE; PS01186; EGF_2; 5.
 CC PROSITE; PS00026; EGF_3; 4.
 CC PROSITE; PS01187; EGF_CA; 8.
 CC Alternative splicing; Calcium-binding; EGF-like domain;
 CC Extracellular matrix; Glycoprotein; Repeat; Signal.
 CC SIGNAL 1 17 Potential.
 CC CHAIN 18 798 Fibulin-1.

FT	DOMAIN	23	64	Anaphylatoxin-like 1.
FT	DOMAIN	65	96	Anaphylatoxin-like 2.
FT	DOMAIN	97	129	Anaphylatoxin-like 3.
FT	DOMAIN	155	194	EGF-like 1.
FT	DOMAIN	195	280	EGF-like 2, calcium-binding (Potential).
FT	DOMAIN	281	345	EGF-like 3, calcium-binding (Potential).
FT	DOMAIN	346	436	EGF-like 4, calcium-binding (Potential).
FT	DOMAIN	437	476	EGF-like 5, calcium-binding (Potential).
FT	DOMAIN	477	520	EGF-like 6, calcium-binding (Potential).
FT	DOMAIN	521	561	EGF-like 7, calcium-binding (Potential).
FT	DOMAIN	562	606	EGF-like 8, calcium-binding (Potential).
FT	DOMAIN	607	652	EGF-like 9, calcium-binding (Potential).
FT	DISULFID	23	49	By similarity.
FT	DISULFID	24	56	By similarity.
FT	DISULFID	37	57	By similarity.
FT	DISULFID	66	94	By similarity.
FT	DISULFID	79	95	By similarity.
FT	DISULFID	97	121	By similarity.
FT	DISULFID	98	128	By similarity.
FT	DISULFID	111	129	By similarity.
FT	DISULFID	159	168	By similarity.
FT	DISULFID	164	178	By similarity.
FT	DISULFID	180	279	By similarity.
FT	DISULFID	285	298	By similarity.
FT	DISULFID	292	307	By similarity.
FT	DISULFID	313	339	By similarity.
FT	DISULFID	350	363	By similarity.
FT	DISULFID	357	372	By similarity.
FT	DISULFID	394	406	By similarity.
FT	DISULFID	400	415	By similarity.
FT	DISULFID	422	435	By similarity.
FT	DISULFID	441	451	By similarity.
FT	DISULFID	446	460	By similarity.
FT	DISULFID	462	475	By similarity.
FT	DISULFID	481	495	By similarity.
FT	DISULFID	489	504	By similarity.
FT	DISULFID	506	519	By similarity.
FT	DISULFID	525	536	By similarity.
FT	DISULFID	532	545	By similarity.
FT	DISULFID	547	560	By similarity.
FT	DISULFID	566	581	By similarity.
FT	DISULFID	577	590	By similarity.
FT	DISULFID	592	605	By similarity.
FT	DISULFID	611	623	By similarity.
FT	DISULFID	616	632	By similarity.
FT	DISULFID	637	651	By similarity.
FT	VARSPPLIC	193	278	Missing (in isoform a and isoform b). /FTid=VSP_001387. and isoform b).
FT	VARSPPLIC	326	345	NNCPLIIINNTFNCKYFFVE -> CR (in isoform a and isoform b). /FTid=VSP_001388. Y -> CTSITCPNGYYPKNGMCND (in isoform a and isoform b). /FTid=VSP_001389.
FT	VARSPPLIC	390	390	RCNQPSACGLPEECSSKVPLELTQYFISLARAVPISSHRPA ITLKFVSAPNHADTEVNPFLQLTQTVGAPNVLPAIRANFL LQKGEKNSAVVTLRSDLDGPTVKLQLLLRMSKKGNFT YAANLIVDVAARKHNTVHPFLMKIR -> QIADGYSCKIV CSTEDTECLGNHTREVLVQFRAVPSLTKITIIPIEVSRIVTH MGVPFSDYNDLDYVQQRHFRIVQERNIGIVOLVPIGPTV ETIKVNIHTKSRGTGVILAFNEAIIIEISVSKYPF (in isoform b). /FTid=VSP_001390.
FT	VARSPPLIC	650	798	Query Match 26.6%; Score 344.5; DB 1; Length 798; Best Local Similarity 34.2%; Pred. No. 3.5e-20; Matches 77; Conservative 26; Mismatches 89; Indels 33; Gaps 8;
QY	5 DCINKYGS-----PYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLMGNFF 52			
DB	405 ECVNTPGSFRCCQGNLCAHGYEVNGATGFCED--VNECQGVVC---GSMECINLPGYK 459			
FT	CHAIN	18	798	Fibulin-1.

QY 53 CLKACW----GRLCDKDNVCSQENGGLQI---CHNKPQSFHCSHGSELSGDRT 105
Db 460 CKGPGYEFNDARKCE-DVDECIKFAHVCIDLSAEICINTIGSCFECKRPGQLASDGR 518
QY 106 CODIDECADSEACGEARCKNLPGSYCLDEGFAYSSQEKACRDVDECL-----QGRCE 159
Db 519 CEDVNECTGIAACEKQCNVPGSYOCIDRGFALGPDGTKEDIDECISWAGSNDLCM 578
QY 160 QVCNVPSPGYTHCDGRGGLKLSQMDTCEIDLPCVPFVSVAKSVK 204
Db 579 GGCINTKGSYLQCP--PGYKIQPDGRTCDVDECAMGECAGSDK 621

RESULT 41
FBN3 HUMAN
ID FBN3 HUMAN STANDARD; PRT; 2809 AA.
AC Q75N90; Q75N91; Q75N92; Q75N93; Q86SJS; Q96JP8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 3 precursor.
GN Name=FBN3; Synonyms=KIAA1776;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=14962672; DOI=10.1016/j.ygeno.2003.08.023;
RA Corson G.M., Charbonneau N.L., Keene D.R., Sakai L.Y.;
RT "Differential expression of fibrillin-3 adds to microfibril variety in human and avian, but not rodent, connective tissues."; Genomics 83:461-472(2004).
RL [2]
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS GLN-473; LEU-935; PHE-938; TRP-1083; GLY-1614; IYS-1863; PRO-1904 AND GLU-2610.
RX PubMed=15221638; DOI=10.1007/s10039-004-0168-x;
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Kanezaki R., Toki T., Yonesaka S., Ito E.;
RT "Three novel mutations of the fibrillin-1 gene and ten single nucleotide polymorphisms of the fibrillin-3 gene in Marfan syndrome patients."; J. Hum. Genet. 0:0-0(2004).
RL [3]
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-1326; GLY-1614 AND GLN-1806.
RC TISSUE=Brain;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 8:85-95(2001).
RL [3]
CC -!- FUNCTION: Structural component of connective tissue microfibrils that binds calcium. Fibrillin-containing microfibrils provide long-term force bearing structural support.
CC -!- SUBCELLULAR LOCATION: Secreted; component of extracellular matrix.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in connective tissues such as skeletal muscle, tendon, skin, perichondrium and periosseum. Highly expressed in fetal lung, brain, kidney.
CC Expressed at low level in prostate, testis, mammary gland, uterus, ovary, placenta, bladder, adrenal gland, thyroid, fetal thymus, fetal liver, liver, fetal heart and heart.
CC -!- PTM: Probably forms intermolecular disulfide bonds either with other FBN3 molecules or with other components of the microfibrils (by similarity).
CC -!- SIMILARITY: Belongs to the fibrillin family.
CC -!- SIMILARITY: Contains 44 EGF-like domains.
CC -!- SIMILARITY: Contains 9 TGF-beta binding protein (TGFBP) domains.
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CC
CC
CC
CC
DR EMBL; AY155863; AAO18145.1; -
DR EMBL; AY155864; AAO18146.1; -
DR EMBL; AY155865; AAO18147.1; -
DR EMBL; AB177797; BAD16733.1; -
DR EMBL; AB177798; BAD16734.1; -
DR EMBL; AB177799; BAD16735.1; -
DR EMBL; AB177800; BAD16736.1; -
DR EMBL; AB053450; BAB47408.1; -
DR HSSP; F35555; LLMJ.
DR Genew; HGNC:18794; FBN3.
DR MIM; 608529; -
DR InterPro; IPR00152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 42.
DR Pfam; PF00683; TB; 9.
DR PIRSF; PIRSF036312; Fibrillin; 1.
DR SMART; SM00179; EGF_CA; 41.
DR PROSITE; PS00010; ASX HYDROXYL; 41.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 36.
DR PROSITE; PS00026; EGF_3; 44.
DR PROSITE; PS01187; EGF_CA; 40.
KW Calcium-binding; EGF-like domain; Extracellular matrix; Glycoprotein; Multigene family; Polymorphism; Repeat; Signal.
FT SIGNAL 1 31
FT CHAIN 32 2809
FT DOMAIN 147 179 EGF-like 1.
FT DOMAIN 194 236 TGFBP 1.
FT DOMAIN 247 288 EGF-like 2, calcium-binding.
FT DOMAIN 302 345 TGFBP 2.
FT DOMAIN 408 448 EGF-like 3.
FT DOMAIN 449 488 EGF-like 4, calcium-binding.
FT DOMAIN 489 530 EGF-like 5, calcium-binding.
FT DOMAIN 531 571 EGF-like 6, calcium-binding.
FT DOMAIN 572 612 EGF-like 7, calcium-binding.
FT DOMAIN 627 669 TGFBP 3.
FT DOMAIN 682 723 EGF-like 8, calcium-binding.
FT DOMAIN 724 765 EGF-like 9, calcium-binding.
FT DOMAIN 766 805 EGF-like 10, calcium-binding.
FT DOMAIN 819 862 TGFBP 4.
FT DOMAIN 869 910 EGF-like 11, calcium-binding.
FT DOMAIN 924 965 TGFBP 5.
FT DOMAIN 986 1027 EGF-like 12, calcium-binding.
FT DOMAIN 1028 1070 EGF-like 13, calcium-binding.
FT DOMAIN 1071 1112 EGF-like 14, calcium-binding.
FT DOMAIN 1113 1154 EGF-like 15, calcium-binding.
FT DOMAIN 1156 1195 EGF-like 16, calcium-binding.
FT DOMAIN 1196 1237 EGF-like 17.
FT DOMAIN 1238 1279 EGF-like 18, calcium-binding.
FT DOMAIN 1280 1320 EGF-like 19, calcium-binding.
FT DOMAIN 1321 1361 EGF-like 20, calcium-binding.
FT DOMAIN 1362 1403 EGF-like 21, calcium-binding.
FT DOMAIN 1404 1444 EGF-like 22, calcium-binding.
FT DOMAIN 1445 1485 EGF-like 23, calcium-binding.
FT DOMAIN 1504 1545 TGFBP 6.
FT DOMAIN 1563 1604 EGF-like 24, calcium-binding.
FT DOMAIN 1605 1646 EGF-like 25, calcium-binding.
FT DOMAIN 1659 1702 TGFBP 7.
FT DOMAIN 1721 1762 EGF-like 26, calcium-binding.
FT DOMAIN 1763 1804 EGF-like 27, calcium-binding.
FT DOMAIN 1805 1846 EGF-like 28.
FT DOMAIN 1847 1885 EGF-like 29, calcium-binding.
FT DOMAIN 1886 1928 EGF-like 30, calcium-binding.
FT DOMAIN 1929 1968 EGF-like 31, calcium-binding.
FT DOMAIN 1969 2010 EGF-like 32, calcium-binding.

FT	DOMAIN	2024	2067	TGFBP 8.	QY	11	GSPYTKNSGFATCQVNLPLDQCTP-NPCDRKGTQACQDL-----MGNF 51
FT	DOMAIN	2084	2125	EGF-like 33, calcium-binding.	Db	1084	GGTCTNTDGSYKC-----QCPGHETAKGT-ACEDIDECSLSDGLCPHGQCVNVIGAF 1136
FT	DOMAIN	2126	2165	EGF-like 34, calcium-binding.	QY	52	FCLCKAGWGG---RLCDKDVNECSQENGGLQICHNKPFGSFHCSHGFEISSDGRTCQD 108
FT	DOMAIN	2207	2251	EGF-like 36, calcium-binding.	Db	1137	QCSCHAGFQSTPDRQGVGVDINECRVQNGGCDVHCINTEGSRVCSGCGQSYSLMPDGRACAD 1196
FT	DOMAIN	2252	2293	EGF-like 37, calcium-binding.	QY	109	IDECADS-EACGEARCKNLPGSYSLCDEGFPAYSSQEKACDVDE-----CLOGRCEQ 160
FT	DOMAIN	2307	2350	TGFBP 9.	Db	1197	VDECEENPRVCDQGHCTNMPGGHRCCLCYDGMATPDMRTCTVDVDECDLNPHCILHGDCGE- 1255
FT	DOMAIN	2363	2404	EGF-like 38, calcium-binding.	QY	161	VCVNSPGSYTCHCD---GRGGLKLSQDDMTCE 189
FT	DOMAIN	2405	2445	EGF-like 39, calcium-binding.	Db	1256	---NTKGSFVCHCOLGYMVRKGTGCSDDVDECE 1285
FT	DOMAIN	2484	2484	EGF-like 40, calcium-binding.	RESULT 42		
FT	DOMAIN	2485	2527	EGF-like 41, calcium-binding.	PBL1_CHICK STANDARD; PRT; 704 AA.		
FT	DOMAIN	2528	2567	EGF-like 42, calcium-binding.	ID_FBL1_CHICK STANDARD; PRT; 704 AA.		
FT	DOMAIN	2568	2609	EGF-like 43, calcium-binding.	AC 073775; 073774; Rel. 40, Created		
FT	DOMAIN	2610	2649	EGF-like 44, calcium-binding.	DT 16-OCT-2001 (Rel. 42, Last sequence update)		
FT	DISULFID	151	161	By similarity.	DT 05-JUL-2004 (Rel. 44, Last annotation update)		
FT	DISULFID	155	167	By similarity.	DE Fibulin-1 precursor.		
FT	DISULFID	169	178	By similarity.	GN Name=FBLN1;		
FT	DISULFID	251	263	By similarity.	OS Gallus gallus (Chicken).		
FT	DISULFID	258	272	By similarity.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
FT	DISULFID	274	287	By similarity.	OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
FT	DISULFID	412	424	By similarity.	OC Gallus.		
FT	DISULFID	419	433	By similarity.	OX NCBI_TaxID=90311;		
FT	DISULFID	435	447	By similarity.	RN [1]		
FT	DISULFID	453	463	By similarity.	RP TISSUE=Embryo;		
FT	DISULFID	458	472	By similarity.	RC MEDLINE=99120531; PubMed=9923656; DOI=10.1016/S0945-053X(98)90114-7;		
FT	DISULFID	474	487	By similarity.	RA Barth J.L., Argreaves K.M., Roark E.F., Little C.D., Argreaves W.S.;		
FT	DISULFID	493	505	By similarity.	RT Identification of chicken and C. elegans fibulin-1 homologs and		
FT	DISULFID	500	514	By similarity.	RL Matrix Biol. 17:635-646(1998).		
FT	DISULFID	516	529	By similarity.	CC -! FUNCTION: Incorporated into fibronectin-containing matrix fibers.		
FT	DISULFID	535	546	By similarity.	CC May play a role in cell adhesion and migration along protein		
FT	DISULFID	541	555	By similarity.	CC fibers within the extracellular matrix (ECM). Could be important		
FT	DISULFID	557	570	By similarity.	CC for certain developmental processes and contribute to the		
FT	DISULFID	576	587	By similarity.	CC supramolecular organization of ECM architecture, in particular to		
FT	DISULFID	582	596	By similarity.	CC those of basement membranes.		
FT	DISULFID	598	611	By similarity.	CC -! SUBUNIT: Interacts with itself and with various extracellular		
FT	DISULFID	666	698	By similarity.	CC matrix components (By similarity).		
FT	DISULFID	693	707	By similarity.	CC -! SUBCELLULAR LOCATION: Secreted; extracellular matrix.		
FT	DISULFID	709	722	By similarity.	CC -! ALTERNATIVE PRODUCTS:		
FT	DISULFID	728	740	By similarity.	CC Name=D;		
FT	DISULFID	735	749	By similarity.	CC IsoId=073775-2; Sequence=Displayed;		
FT	DISULFID	751	764	By similarity.	CC Name=C;		
FT	DISULFID	770	780	By similarity.	CC IsoId=073775-1; Sequence=VSP_007378;		
FT	DISULFID	775	789	By similarity.	CC -! SIMILARITY: Belongs to the fibulin family.		
FT	DISULFID	791	804	By similarity.	CC -! SIMILARITY: Contains 3 anaphylatoxin-like domains.		
FT	DISULFID	873	885	By similarity.	CC -! SIMILARITY: Contains 9 EGF-like domains.		
FT	DISULFID	880	894	By similarity.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration		
FT	DISULFID	896	909	By similarity.	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -		
FT	DISULFID	990	1002	By similarity.	CC the European Bioinformatics Institute. There are no restrictions on its		
FT	DISULFID	997	1011	By similarity.	CC use by non-profit institutions as long as its content is in no way		
FT	DISULFID	1013	1026	By similarity.	CC modified and this statement is not removed. Usage by and for commercial		
FT	DISULFID	1032	1044	By similarity.	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/		
FT	DISULFID	1039	1053	By similarity.	CC or send an email to license@isb-sib.ch).		
FT	DISULFID	1055	1069	By similarity.	CC -----		
FT	DISULFID	1075	1087	By similarity.	CC EMBL; AF051399; AAC05387.1; -		
FT	DISULFID	1082	1096	By similarity.	CC EMBL; AF051400; AAC05388.1; -		
FT	DISULFID	1098	1111	By similarity.	CC HSPF; P01130; 1H28.		
FT	DISULFID	1117	1129	By similarity.	CC InterPro; IPR000020; Anaphylatoxin.		
FT	DISULFID	1124	1138	By similarity.	CC InterPro; IPR000152; Asx_hydroxyl_S.		
FT	DISULFID	1140	1153	By similarity.	CC InterPro; IPR000742; EGF_2.		
FT	DISULFID	1159	1170	By similarity.			
FT	DISULFID	1166	1179	By similarity.			
FT	DISULFID	1181	1194	By similarity.			
FT	DISULFID	1200	1212	By similarity.			
FT	DISULFID	1207	1221	By similarity.			
FT	DISULFID	1223	1236	By similarity.			
FT	DISULFID	1242	1254	By similarity.			
FT	DISULFID	1249	1263	By similarity.			
FT	DISULFID	1265	1278	By similarity.			
FT	DISULFID	1284	1297	By similarity.			

Query Match 26.4%; Score 342.5; DB 1; Length 2809;
Best Local Similarity 36.2%; Pred. No. 1.8e-19;
Matches 77; Conservative . 21; Mismatches 70; Indels 45; Gaps 9;

DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF01821; ANATO; 2.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 5.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW Alternative splicing; Calcium-binding; EGF-like domain;
 KW Extracellular matrix; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 25 704 Fibrulin-1.
 FT DOMAIN 33 74 Anaphylatoxin-like 1.
 FT DOMAIN 75 109 Anaphylatoxin-like 2.
 FT DOMAIN 110 142 Anaphylatoxin-like 3.
 FT DOMAIN 177 216 EGF-like 1.
 FT DOMAIN 217 262 EGF-like 2, calcium-binding (Potential).
 FT DOMAIN 263 308 EGF-like 3, calcium-binding (Potential).
 FT DOMAIN 309 356 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 357 399 EGF-like 5, calcium-binding (Potential).
 FT DOMAIN 400 441 EGF-like 6, calcium-binding (Potential).
 FT DOMAIN 442 481 EGF-like 7, calcium-binding (Potential).
 FT DOMAIN 482 525 EGF-like 8, calcium-binding (Potential).
 FT DOMAIN 526 579 EGF-like 9, calcium-binding (Potential).
 FT DOMAIN 357 441 Self-association and FNI-binding (By similarity).
 FT DISULFID 33 59 By similarity.
 FT DISULFID 34 66 By similarity.
 FT DISULFID 47 67 By similarity.
 FT DISULFID 76 107 By similarity.
 FT DISULFID 89 108 By similarity.
 FT DISULFID 110 134 By similarity.
 FT DISULFID 111 141 By similarity.
 FT DISULFID 124 142 By similarity.
 FT DISULFID 181 191 By similarity.
 FT DISULFID 187 200 By similarity.
 FT DISULFID 202 215 By similarity.
 FT DISULFID 221 234 By similarity.
 FT DISULFID 228 243 By similarity.
 FT DISULFID 249 261 By similarity.
 FT DISULFID 267 280 By similarity.
 FT DISULFID 274 289 By similarity.
 FT DISULFID 295 307 By similarity.
 FT DISULFID 313 326 By similarity.
 FT DISULFID 320 335 By similarity.
 FT DISULFID 342 355 By similarity.
 FT DISULFID 361 374 By similarity.
 FT DISULFID 368 383 By similarity.
 FT DISULFID 385 398 By similarity.
 FT DISULFID 404 416 By similarity.
 FT DISULFID 412 425 By similarity.
 FT DISULFID 427 440 By similarity.
 FT DISULFID 446 455 By similarity.
 FT DISULFID 451 464 By similarity.
 FT DISULFID 466 480 By similarity.
 FT DISULFID 486 499 By similarity.
 FT DISULFID 495 508 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 530 543 By similarity.
 FT DISULFID 537 552 By similarity.
 FT DISULFID 557 578 By similarity.
 FT CARBOHYD 96 96 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 568 704 VLEKTDTRICKSCRPDNCVLPDPVHTVISHVLSLTPFR
 ETRPPEITFLRAITPTYPANQADIFDITEGNLRESFDII
 KRYMDGMTGVVRQVRPIVGPFFHAIKLEMMNVVGGVWSHR

FT FT NIVNHIIFVSEWTF -> RCERLPCNENKECOSLRLITYY
 FT HLSFTNIOVPTDIFRMGSPNAVPGDKILLSIISGNQEGFF
 FT TTKVNNHSGIYVMQRIETPRDLTLITQMLTRHGTVNTF
 FT IAKLFVFS AOL (in isoform C).
 FT /FTID=VSP 007378.
 SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;
 Query Match 26.4%; Score 342; DB 1; Length 704;
 Best Local Similarity 36.9%; Pred. No. 5e-20;
 Matches 79; Conservative 29; Mismatches 74; Indels 32; Gaps 12;
 QY 6 CINKYGS-----PYTKNSGFATCQNLDPQCTPN--PCDRKGTQACQDLMGNF 51
 DB 326 CINTDGSVTCORISPSGGRVHLNEDGTRCVD--VDECSSSDQPCGE--GHVCINGPGNY 381
 QY 52 FCLCKAGMG---GRLCDKDVNECSQENG--CLQICHNKPGSFHCSHGFSLSDDGRTC 106
 DB 382 RCEKSGVSVFVISRT--IDINECRYPGRCAHKCENTPGSYCTCTGCTGFKLSDDGRSC 440
 QY 107 QDIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEK--ACRDVDECLQGR----CEQV 161
 DB 441 EDLNEC-ESSPCSQ--ECANVYGSYQCYCRGFQSLSDIDGISCEDIDECALPTGHCISPR 498
 QY 162 CVNSGSGYTCDCGRGGLKLSQDMTCEDILPCV 195
 DB 499 CINIPEGSPQCTCPST--GYRLAPNARNQCQIDECV 531
 RESULT 43
 Q8NBH6 PRELIMINARY, PRT; 638 AA.
 AC Q8NBH6;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein PSEC0266.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
 RA Nagahari K., Sugano S., Isoigai T.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK075566; BAC11705.1;
 DR HSSP; P01330; 1HJ7.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF07645; EGF_CA; 8.
 DR SMART; SM00179; EGF_CA; 7.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW EGF-like domain.
 SQ SEQUENCE 638 AA; 70577 MW; EBCODE3147A7621F CRC64;
 Query Match 26.1%; Score 339; DB 2; Length 638;
 Best Local Similarity 37.3%; Pred. No. 8.1e-20;
 Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;
 QY 6 CINKYGSPTKNSGFATCQNLDP-----DOCTP--NPCDRKGTQACQ 45
 DB 260 CINTEGS-----YTCQKNVPCGRGYHLNEGTCTVDVDECAPPAEPCG--KG--HRCV 309


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DR SMART; SM00179; EGF_CA; 9.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 9.
KW EGF-like domain.
SQ SEQUENCE 1174 AA; 126460 MW; 8D628AC710FBA6B8 CRC64;

Query Match          26.1%; Score 339; DB 2; Length 1174;
Best Local Similarity 36.6%; Pred.No.1.5e-19;
Matches 78; Conservative 27; Mismatches 68; Indels 40; Gaps 11;

QY 6 CLINKYS-----PYTKSGPATCVQLPQDCTPNPCD-----RKGT-QACQDLIM 48
DB 817 CINTVGSYTCQRNPLVCGRGYHANESEGCVD-----VNECEFGVHRCGEGQLCYNLP 869

QY 49 GNFFCLCKAGWG---GRLCDKDVNECSQENG-GLQICHNKPGSFHCSHGFSLSDDG 103
DB 870 GSYRCDCRPGFORDAFGRTC-IDVNECWSPGLCHQHTCENTPGSYRSCAGFLLAAGD 928

QY 104 RTCODIDECADSEACGEARCKNLPGSYCLDCDEGFAYSSQEKACRDVDECIQGR---CEQ 160
DB 929 KHCEDVNEC-ETRRCSQ-ECANIYGSQCYCRQGYQLAEDGHTCTDIDECAGGAGILCTF 986

QY 161 VCVNSPFGSYTCHCDRGGLKLS-----QDMDC 188
DB 987 RCNVNPGSYQCACPEQGYTMANGRSCKDLDEC 1019

RESULT 46
FBL2_MOUSE
ID FBL2_MOUSE STANDARD; PRT; 1221 AA.
AC P37889; Q9WUI2;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibulin-2 precursor.
GN Name=Fbln2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC TISSUE=Fibroblast;
RX MEDLINE=94064787; PubMed=82451330; DOI=10.1083/jcb.123.5.1269;
RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT "Structure and expression of fibulin-2, a novel extracellular matrix
RT protein with multiple EGF-like repeats and consensus motifs for
RT calcium binding.";
RL J. Cell Biol. 123:1269-1277 (1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99337686; PubMed=10406956;
RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT characterization.";
RL Eur. J. Biochem. 263:471-477 (1999).
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=97003230; PubMed=8850569;
RX DOI=10.1002/(SICI)1097-0177(199603)205:3<348::AID-AJAL3>3.0.CO;2-0;
RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT developing mouse embryo.";
RL Dev. Dyn. 205:348-364 (1996).
RN [4]
RP BINDING TO LAMA2.
RX MEDLINE=99146904; PubMed=10022829; DOI=10.1093/emboj/18.4.863;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
perlecan to heparin, sulfatides, alpha-dystroglycan and several
extracellular matrix proteins.";
EMBO J. 18:863-870 (1999).
[5]
DOWN-REGULATION BY GLUCOCORTICOIDS.
MEDLINE=21600963; PubMed=11737251;
Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
"Glucocorticoids down-regulate the extracellular matrix proteins
fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
Eur. J. Haematol. 67:176-184 (2001).
CC -!- FUNCTION: Its binding to fibronectin and some other ligands is
calcium dependent.
CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=P37889-1; Sequence=Displayed;
Name=2; Synonyms=EGF3-less;
IsoId=P37889-2; Sequence=VSP_001391;
CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
connective tissues.
CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
family contributes to the formation of molecularly distinct
extracellular matrices already during early developmental stages
of a large number of tissues.
CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
synthesis.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 11 EGF-like domains.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; X75285; CAA53040.1; -.
EMBL; AF135253; AAD34456.1; -.
EMBL; AF135239; AAD34456.1; JOINED.
EMBL; AF135240; AAD34456.1; JOINED.
EMBL; AF135241; AAD34456.1; JOINED.
EMBL; AF135242; AAD34456.1; JOINED.
EMBL; AF135243; AAD34456.1; JOINED.
EMBL; AF135244; AAD34456.1; JOINED.
EMBL; AF135245; AAD34456.1; JOINED.
EMBL; AF135246; AAD34456.1; JOINED.
EMBL; AF135247; AAD34456.1; JOINED.
EMBL; AF135248; AAD34456.1; JOINED.
EMBL; AF135249; AAD34456.1; JOINED.
EMBL; AF135250; AAD34456.1; JOINED.
EMBL; AF135251; AAD34456.1; JOINED.
EMBL; AF135252; AAD34456.1; JOINED.
PIR; A49457; A49457.
HSSP; P00736; 1APQ.
MGD; MGI:95488; Fbln2.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR009030; Grow_fac_recept.
Pfam; PF01821; ANATO; 2.
Pfam; PF00008; EGF; 5.
SMART; SM00104; ANATO; 3.
SMART; SM00179; EGF_CA; 9.
PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
```


[illegible]

FT	CONFLICT	507	507	Q -> QQ (in Ref. 2).
FT	CONFLICT	1102	1102	Q -> E (in Ref. 2).
SEQ	SEQUENCE	1221	AA; 131818 MW; 87DB2A10A8FDC45F CRC64;	
	Query Match	26.1%;	Score 339; DB 1; Length 1221;	
	Best Local Similarity	36.6%;	Pred. No. 1.5e-19;	
	Matches	78; Conservative	27; Mismatches 68; Indels 40; Gaps 11;	
Qy	6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTNPDC-----RKGTVHRCGEQQLCNLP 48			
Db	864 CINTVGSYTCQRNPLVCGRYHANESECDV-----VNECETGVHRCGEQQLCNLP 916			
Qy	49 GNPFCLCKAGWG----GRLCDKDVNCSQBNNG-CLQICHNKPSPHCSHGSELSSDG 103			
Db	917 GSYRCDCKPGFORDAFGRTCT-IDVNECWSPGRGLCQHTCENTPGSYRCSCAAGFLLAADG 975			
Qy	104 RTCODIDECADSEACGEARCNLPGPSYSLCDRGFPAYSGQEKACRDVDECLQGR---CBQ 160			
Db	976 KHCEVDNVEC-ETRRCSQ-ECANIYGSYQCYCRQYQLAEDGHTCTDIDCAQAGILCTF 1033			
Qy	161 VCVNPSGYSYCHDGRGGLKLS-----QDMDTCT 188			
Db	1034 RCNVPGSYQACPEQGYTMMANGRSCKLDEC 1066			
RESULT	47			
QY9Y3V7	PRELIMINARY;	PRT;	576 AA.	
ID	QY9Y3V7			
AC	QY9Y3V7;			
DT	01-NOV-1999 (T-EMBLrel. 12, Created)			
DT	01-NOV-1999 (T-EMBLrel. 12, Last sequence update)			
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)			
DE	Hypothetical protein DKF2p586A1519 (Fragment).			
GN	Name=DKF2p586A1519;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RG	TISSUE=Uterus;			
RC	The German cDNA Consortium;			
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,			
RA	Fobo G., Han M., Wiemann S.;			
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL050095; CAB43267.1; -.			
DR	HSP; P00736; IAPQ.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	InterPro; IPR000152; ASx hydroxyl_S.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR001881; EGF_CA.			
DR	InterPro; IPR006209; EGF_like.			
DR	InterPro; IPR009030; Grow_fac_recept.			
DR	Pfam; PF07645; EGF CA; 9.			
DR	SMART; SM00179; EGF CA; 8.			
DR	PROSITE; PS00010; ASX HYDROXYL; 4.			
DR	PROSITE; PS01186; EGF_2; 4.			
DR	PROSITE; PS00026; EGF_3; 2.			
DR	PROSITE; PS01187; EGF CA; 9.			
KW	EGF-like domain; Hypothetical protein.			
FT	NON TER			
SEQ	SEQUENCE	576 AA; 63274 MW; FF2F0E9B185D8AC3 CRC64;		
	Query Match	26.1%;	Score 338; DB 2; Length 576;	
	Best Local Similarity	38.0%;	Pred. No. 8.8e-20;	
	Matches	79; Conservative	31; Mismatches 74; Indels 24; Gaps 12;	
Qy	6 CINKYGSPTKNSGFATCVQ-NLPDQCTP-----NPCD-----RKGTVHRCGEQQLCNLP 54			
Db	219 CINTVGS-YTCQRNPLICARGHASDGGTKVDVNECETGVHRCGEQQLCNLP 277			
Qy	55 CRAAGWG----GRLCDKDVNCSQBNNG-CLQICHNKPSPHCSHGSELSSDGRTCDQI 109			

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Db      278 CKAGQRFDAFRGC-IDVNECWASPERLCQHTCENTILSYRCSCASGFLAADGKRCDV 336
Qy      110 DECADESAGEARCKNLPGSYSLCDEGFAYVSQEKACRDVDECLQGR---CEQVCVNSP 166
Db      337 NEC-EAQRCSQ-ECANIYGSYQCYCRQGYQAEDGHTCTDIDECAQAGAILCTFRCLNVP 394
Qy      167 GSYTCHCDRGGLKLSQMDTDCEDILPC 194
Db      395 GSYQCACPEQ-GYTTWANGRSCKVDDEC 421

RESULT 48
FBL2_HUMAN
ID FBL2_HUMAN STANDARD; PRT; 1184 AA.
AC P98035;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fbulin-2 precursor.
GN Name=FBLN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=95104855; PubMed=7806230;
RA Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,
RA Chu M.-L.;
RT "Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
RT of the gene on human and mouse chromosomes.";
RL Genomics 22:425-430(1994).
RN [2]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=96301678; PubMed=8737292;
RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
RT early human embryo.";
RL Histochem. J. 28:109-116(1996).
CC -!- FUNCTION: Its binding to fibronectin and some other ligands is
CC calcium dependent.
CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
CC connective tissues. Expressed in heart, placenta and ovary.
CC -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic
CC development. Primarily detected within the neuroepithelium, spinal
CC ganglia and peripheral nerves.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 11 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X82494; CAA57876.1; -.
DR FIR; A55184; A55184.
DR HSP; P00736; LAPO.
DR Genew; HGNC:3601; FBLN2.
DR MIM; 135821; -.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR InterPro; IPR000020; F:extracellular matrix structural constituent; TAS.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF_2.

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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 5.
DR SMART; SMO0104; ANATO; 3.
DR SMART; SMO0179; EGF_CA; 9.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 9.
KW Calcium-binding; EGF-like domain; Extracellular matrix; Glycoprotein;
KW Plasma; Repeat; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 1184 Fibulin-2.
FT DOMAIN 28 444 N.
FT DOMAIN 28 177 Subdomain NA (Cys-rich).
FT DOMAIN 178 444 Subdomain NB (Cys-free).
FT DOMAIN 445 480 Anaphylatoxin-like 1.
FT DOMAIN 488 519 Anaphylatoxin-like 2.
FT DOMAIN 521 553 Anaphylatoxin-like 3.
FT DOMAIN 604 645 EGF-like 1, calcium-binding.
FT DOMAIN 679 718 EGF-like 2.
FT DOMAIN 719 763 EGF-like 3, calcium-binding.
FT DOMAIN 764 809 EGF-like 4, calcium-binding.
FT DOMAIN 810 857 EGF-like 5, calcium-binding.
FT DOMAIN 858 900 EGF-like 6, calcium-binding.
FT DOMAIN 901 942 EGF-like 7, calcium-binding.
FT DOMAIN 943 981 EGF-like 8, calcium-binding.
FT DOMAIN 982 1024 EGF-like 9, calcium-binding.
FT DOMAIN 1025 1069 EGF-like 10, calcium-binding.
FT DOMAIN 1070 1184 Domain III.
FT DISULFID 445 472 By similarity.
FT DISULFID 446 479 By similarity.
FT DISULFID 459 480 By similarity.
FT DISULFID 489 518 By similarity.
FT DISULFID 502 519 By similarity.
FT DISULFID 521 545 By similarity.
FT DISULFID 522 552 By similarity.
FT DISULFID 535 553 By similarity.
FT DISULFID 608 620 By similarity.
FT DISULFID 616 629 By similarity.
FT DISULFID 631 644 By similarity.
FT DISULFID 683 693 By similarity.
FT DISULFID 689 702 By similarity.
FT DISULFID 704 717 By similarity.
FT DISULFID 723 736 By similarity.
FT DISULFID 730 745 By similarity.
FT DISULFID 751 762 By similarity.
FT DISULFID 768 781 By similarity.
FT DISULFID 775 790 By similarity.
FT DISULFID 796 808 By similarity.
FT DISULFID 814 827 By similarity.
FT DISULFID 821 836 By similarity.
FT DISULFID 831 856 By similarity.
FT DISULFID 862 875 By similarity.
FT DISULFID 886 899 By similarity.
FT DISULFID 905 917 By similarity.
FT DISULFID 913 926 By similarity.
FT DISULFID 928 941 By similarity.
FT DISULFID 947 956 By similarity.
FT DISULFID 952 965 By similarity.
FT DISULFID 967 980 By similarity.
FT DISULFID 986 998 By similarity.
FT DISULFID 994 1007 By similarity.
FT DISULFID 1009 1023 By similarity.
FT DISULFID 1029 1042 By similarity.
FT DISULFID 1036 1051 By similarity.
FT DISULFID 1056 1069 By similarity.

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FT CARBOHYD 180 180 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1035 1035 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 1184 AA; 126543 MW; CA48490A55F9EC5D CRC64;

Query Match 26.0%; Score 337; DB 1; Length 1184;
 Best Local Similarity 36.4%; Pred. No. 2.2e-19;
 Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCD-----RKGT-QACQDILM 48
 DB 827 CINTVGSYTCQNRPLICARGYHASDDGAKCVD-----VNECETGVHRCGEGQVCHNLP 879

QY 49 GNFFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPGSFHCSHGFSLSDDG 103
 DB 880 GSYRCDCKAGFQDAFGRGC-IDVNECWASPGRLCQHTCENTLGSYRCSASCAGFLAADG 938

QY 104 RTCQDIDECADSEACGEARKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGR---CEQ 160
 DB 939 KRCEVDNEC-EAQRCSQ-ECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAGAGILCTF 996

QY 161 VCVNSPGSYTCHDGRGGLKLSQDMDCEDILPC 194
 DB 997 RCLNVPGSYQCACPEQ-GYTMANGRSCKDVDEC 1029

RESULT 49
 Q86V58 PRELIMINARY; PRT; 1184 AA.
 AC Q86V58;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fibulin 2.
 GN Name=FBLN2;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051690; AAH51690.1; --
 DR HSSP; P00736; IAPQ.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF01821; ANATO; 2.
 DR Pfam; PF07645; EGF_CA; 9.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS50026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW EGF-like domain.
 SQ SEQUENCE 1184 AA; 126507 MW; 4240CD6ADBB9EC5D CRC64;

Query Match 26.0%; Score 337; DB 2; Length 1184;
 Best Local Similarity 36.4%; Pred. No. 2.2e-19;
 Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCD-----RKGT-QACQDILM 48
 DB 827 CINTVGSYTCQNRPLICARGYHASDDGAKCVD-----VNECETGVHRCGEGQVCHNLP 879

QY 49 GNFFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPGSFHCSHGFSLSDDG 103
 DB 880 GSYRCDCKAGFQDAFGRGC-IDVNECWASPGRLCQHTCENTLGSYRCSASCAGFLAADG 938

QY 104 RTCQDIDECADSEACGEARKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGR---CEQ 160
 DB 939 KRCEVDNEC-EAQRCSQ-ECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAGAGILCTF 996

QY 161 VCVNSPGSYTCHDGRGGLKLSQDMDCEDILPC 194
 DB 997 RCLNVPGSYQCACPEQ-GYTMANGRSCKDVDEC 1029

RESULT 50
 Q8UIU0 PRELIMINARY; PRT; 1231 AA.
 ID Q8UIU0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fibulin 2.
 GN Name=FBLN2;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li D., Marian A.J., Roberts R.;
 RT "Identification of a novel alternatively spliced isoform of human
 fibulin-2 gene abundantly expressed in heart and genetic evaluation in
 patients with ARVD."
 RT (In) Unknown A. (eds.);
 RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN
 GENETICS., pp.323-0, Unknown Publisher (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li D., Roberts R.;
 RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY130459; AAN05436.1; --
 DR HSSP; P00736; IAPQ.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF07645; EGF_CA; 10.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 9.
KW EGF-like domain.
SQ SEQUENCE 1231 AA; 131789 MW; 95D69EB2082952A7 CRC64;

Query Match 26.0%; Score 337; DB 2; Length 1231;
Best Local Similarity 36.4%; Pred. No. 2.2e-19;
Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCYQNLPDQCTPNPCD----RKGT-QACQDLM 48
DB 874 CINTVGSYTCQNRNPLICARGYHASDDGAKVD-----VNECETGVHRCGEGQVCHNLP 926

QY 49 GNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPSSFHCSCHSGFELSSDG 103
DB 927 GSYRCDCKAGFQDAFGRCC-IDVNECWASPGRLCQHTCENTLGSYRCSGFLAARDG 985

QY 104 RTCQDIDECADSEACGEARCKNLPGSYCLDEGFAYSQEKACRDVDECIQGR---CEQ 160
DB 986 KRCEQVNEC-EAQRCSQ-ECANIYGSYQCYCRQYQLAEDGHTCTDIDECAGAGILCTF 1043

QY 161 VCVNSPGSYTCHCDGRGGGLKLSQDMDCEDILPC 194
DB 1044 RCLNVPGSYQCACPEQ-GYTMANGRSCKVDDEC 1076

Search completed: July 7, 2005, 09:39:25
Job time : 322.706 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:53:50 ; Search time 61.1154 Seconds
(without alignments)
357.377 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PVLDCINKYSPYTNNGF.....LGRMFGTPIRLRFRLQ 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: PIR:79.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1297	100.0	678	2 B48089	growth arrest-spec
2	1117	86.1	674	2 I55476	growth potentiatin
3	1113	85.8	673	2 A48089	growth arrest-spec
4	609.5	47.0	642	2 S53434	plasma protein S p
5	601.5	46.4	676	1 KXHUS	plasma protein S p
6	596.5	46.0	675	1 KXBOS	plasma protein S p
7	593.5	45.8	642	2 S53433	plasma protein S p
8	591.5	45.6	675	1 KXMS	plasma protein S p
9	586.5	45.2	646	2 S38819	plasma protein S p
10	585.5	45.1	675	1 KXRTS	plasma protein S p
11	362	27.9	685	2 S78040	fibulin, splice fo
12	362	27.9	705	2 S34968	fibulin, splice fo
13	349.5	26.9	2871	2 A55567	fibillin I - bovi
14	348.5	26.9	3002	2 A47221	fibillin-1 precu
15	345	26.6	2871	2 A55624	fibillin-1 precu
16	344.5	26.6	589	2 T43210	fibulin-1D precu
17	344.5	26.6	689	2 T42760	fibulin, splice fo
18	344.5	26.6	712	2 T42990	fibulin 1, splice
19	344.5	26.6	798	2 T22793	hypothetical prote
20	339	26.1	601	2 B36346	fibulin 1 precu
21	339	26.1	683	2 C36346	fibulin 1 precu
22	339	26.1	1221	2 A49457	fibulin-2 precu
23	337	26.0	1184	2 A55184	fibulin-2 precu
24	331.5	25.6	2918	2 A5105	transforming growt
25	330.5	25.5	1394	2 A35626	transforming growt
26	326.5	25.2	2907	2 A57278	fibillin-2 precu
27	321	24.7	387	2 I38449	extracellular prot
28	320.5	24.7	1820	2 A55494	latent transformin
29	320	24.7	493	2 JC5621	epidermal growth f

30	319.5	24.6	1251	2 A57293	latent transformin
31	319.5	24.6	1620	2 T27283	hypothetical prote
32	319.5	24.6	1712	2 A38261	masking protein pr
33	315.5	24.3	741	2 T46488	hypothetical prote
34	312	24.1	886	2 A57172	probable hormone r
35	310.5	23.9	1574	2 T13954	MEGF6 protein - ra
36	299.5	23.1	2321	2 S78549	notch3 protein - h
37	291.5	22.5	2318	2 S45306	notch3 protein - h
38	278	21.4	3507	2 T34513	hypothetical prote
39	275.5	21.2	1408	2 S16148	gene serrate prote
40	274	21.1	2555	2 A40043	notch protein homo
41	272	21.0	2703	1 A24420	notch protein - fr
42	271.5	20.9	1220	2 A56136	jagged protein pre
43	270.5	20.9	1203	2 A49175	Notch B protein -
44	270.5	20.9	2352	2 T30201	Notch homolog prot
45	270	20.8	2437	2 S42612	transmembrane prot
46	266	20.5	1964	2 T09059	notch4 - mouse
47	265.5	20.5	2471	2 A49128	cell-fate determin
48	264	20.4	2139	2 A35672	crumbs protein - f
49	264	20.4	2531	2 T31070	notch homolog - se
50	263.5	20.3	3623	2 T08618	intrinsic factor-B
51	262.5	20.2	1081	2 T31329	receptor tyrosine
52	262.5	20.2	2524	2 A35844	Xotch protein - Af
53	262.5	20.2	2531	2 A46019	notch-1 protein -
54	259.5	20.0	1084	2 A40136	fibropellin Ia - s
55	259.5	20.0	2531	2 S18188	notch protein homo
56	257	19.8	577	2 A60501	thrombomodulin pre
57	251.5	19.4	1106	2 T18739	hypothetical prote
58	251	19.4	1247	1 MMHND	nidogen precursor
59	251	19.4	1376	2 G00043	osteonidogen - hum
60	249.5	19.2	1245	1 MMSND	nidogen precursor
61	249	19.2	575	1 THHUB	thrombomodulin pre
62	248.5	19.2	511	2 T17298	hypothetical prote
63	246	19.0	3871	2 T22812	hypothetical prote
64	244.5	18.9	722	2 I48324	DELTA-like 1 - mou
65	244	18.8	861	2 A48825	Notch homolog Motc
66	237	18.3	3623	2 T09456	intrinsic factor-B
67	234	18.0	570	2 A48836	fibropellin C prec
68	232	17.9	1372	2 T25933	hypothetical prote
69	231	17.8	387	2 B49175	Notch A protein -
70	227.5	17.5	860	1 QRHULD	LDL receptor precu
71	227.5	17.5	1687	2 T30176	EGF repeat transme
72	225.5	17.4	1531	2 T42218	slit-1 protein hom
73	224	17.3	869	1 JC4858	VLID receptor prec
74	224	17.3	1295	2 A32901	glp1 protein precu
75	224	17.3	1847	2 T18308	probable vitellog
76	222	17.1	473	2 A56175	adhesive plaque pr
77	222	17.1	728	2 I50719	C-Delta-1 - chicke
78	221.5	17.1	538	2 T17324	hypothetical prote
79	220.5	17.0	356	2 A25918	thrombomodulin - b
80	220	17.0	1217	1 EGMSMG	epidermal growth f
81	219.5	16.9	996	2 JE0237	apolipoprotein B r
82	218.5	16.8	1207	1 EGHU	epidermal growth f
83	216.5	16.7	1429	2 S06434	homeotic protein l
84	215.5	16.6	1025	2 T42626	secreted leucine-r
85	214	16.5	833	2 S19087	gene Delta protein
86	211	16.3	742	2 I37225	leucocyte antigen
87	211	16.3	832	2 A31246	neurogenic protein
88	211	16.3	880	2 S00670	neurogenic repetit
89	211	16.3	1133	1 EGRT	epidermal growth f
90	209.5	16.2	879	1 QRRTLD	LDL receptor precu
91	209	16.1	854	1 QRHYLD	LDL receptor precu
92	208.5	16.1	810	2 T10756	Nel-homolog protei
93	208	16.0	1984	2 T13171	probable vitellog
94	205	15.8	1069	2 T42681	hypothetical prote
95	205	15.8	1523	2 T13953	MEGF5 protein - ra
96	204.5	15.8	642	1 S52111	uroomodulin precu
97	204	15.7	1722	2 E89753	protein Fl1C7.4 [1
98	203.5	15.7	640	1 A30452	uroomodulin precu
99	201.5	15.5	862	1 QRMSLD	LDL receptor precu
100	201	15.5	4544	1 S02392	alpha-2-macroglobu
101	200	15.4	835	2 JP0076	nel protein - chic
102	200	15.4	909	1 QRXL12	LDL receptor 2 pre

103	199.5	15.4	3051	2	S42373	hypothetical prote	176	157	12.1	1170	1	TSHUP1	thrombospondin 1 p
104	199	15.3	4753	1	A47437	LDL-receptor-relat	177	157	12.1	1584	2	T22674	hypothetical prote
105	198	15.3	293	2	B26637	neurogenic repetit	178	156.5	12.1	1357	2	T16860	hypothetical prote
106	197.5	15.2	644	1	A40212	uromodulin precurs	179	155.5	12.0	915	2	T21773	hypothetical prote
107	197.5	15.2	644	2	I84634	Tamm-Horsfall prot	180	155.5	12.0	927	2	T21772	hypothetical prote
108	197.5	15.2	4543	1	A53102	alpha-2-macroglobu	181	155.5	12.0	3672	2	T23433	hypothetical prote
109	197	15.2	863	1	S51789	VLDL receptor prec	182	155.5	12.0	3704	2	T23716	probable laminin a
110	197	15.2	873	1	I48952	VLDL receptor prec	183	155.5	12.0	5147	1	IGFFTM	cadherin-related t
111	196	15.1	4545	1	S25111	alpha-2-macroglobu	184	155	12.0	1353	1	JH0675	restrictin precurs
112	195	15.0	909	1	QRXL11	LDL receptor 1 pre	185	154.5	11.9	618	2	T00476	probable vacuolar
113	194.5	15.0	837	1	A29512	LDL receptor precu	186	153	11.8	416	1	KFBO	coagulation factor
114	193.5	14.9	308	2	JC7125	epidermal growth f	187	153	11.8	502	2	T20130	hypothetical prote
115	193	14.9	873	1	QRREVD	VLDL receptor prec	188	153	11.8	647	2	A43902	tenascin - eastern
116	191.5	14.8	601	2	T22025	hypothetical prote	189	153	11.8	925	2	T37475	lipoprotein recept
117	191.5	14.8	601	2	D89711	protein F40E10.4 (190	152.5	11.8	661	2	T42754	hypothetical prote
118	190	14.6	873	1	A49729	VLDL receptor prec	191	152	11.7	3635	2	T10053	laminin alpha 5 ch
119	186.5	14.4	4660	2	T42737	gp330 protein prec	192	150	11.6	461	1	KFHU	coagulation factor
120	185.5	14.3	383	2	S53716	delta-like homeoti	193	150	11.6	1107	2	T15884	hypothetical prote
121	185.5	14.3	686	2	JC7569	Delta-4 protein -	194	149.5	11.5	293	2	T09065	hypothetical prote
122	185	14.3	5175	2	T20992	hypothetical prote	195	149	11.5	396	1	KXBOZ	plasma protein 2 -
123	185	14.3	5198	2	T43290	hemiceatin precurs	196	149	11.5	956	2	A57121	thrombospondin 3 p
124	184	14.2	475	1	EXCH	coagulation factor	197	148.5	11.4	4135	2	T42629	tenascin-X - bovin
125	182.5	14.1	685	2	JC7570	Delta-4 protein -	198	148	11.4	626	2	T04895	vacuolar sorting r
126	182	14.0	686	2	S43562	KO8E5.3 protein -	199	147	11.3	956	1	A46016	thrombospondin 3 -
127	181.5	14.0	443	2	I46932	coagulation factor	200	146	11.3	1356	2	A45445	janusin precursor,
128	181	14.0	623	2	T06794	vacuolar sorting r	201	145.5	11.2	2406	2	A54148	odz protein - frui
129	180	13.9	907	2	T27317	hypothetical prote	202	145.5	11.2	2515	2	S47008	tenascin-like prot
130	179.5	13.8	385	2	S53718	homeotic protein d	203	145	11.2	1036	2	T17405	scavenger receptor
131	179.5	13.8	488	1	KFHU	coagulation factor	204	145	11.2	1136	1	S57845	protein-tyrosine k
132	179	13.8	407	1	KFBO7	coagulation factor	205	144.5	11.1	640	2	T19346	hypothetical prote
133	179	13.8	456	1	KXBO	protein C (activat	206	144.5	11.1	2643	2	T29149	hypothetical prote
134	178	13.7	1650	2	S53457	dominant autoantig	207	143.5	11.1	650	2	A34498	glycoprotein antig
135	175.5	13.5	482	1	EXET	coagulation factor	208	143	11.0	491	2	S52920	disintegrin (BC 3.
136	175	13.5	991	2	I49540	procollagen C-endo	209	142.5	11.0	806	2	A46271	integrin beta-7 ch
137	174.5	13.5	986	1	B58788	procollagen C-endo	210	141	10.9	808	2	T23129	hypothetical prote
138	174.5	13.5	1469	2	B36665	slit protein 2 pre	211	141	10.9	972	2	A30363	glycoprotein Gp330
139	174.5	13.5	1480	2	A36665	slit protein 1 pre	212	140	10.8	625	2	F84706	probable vacuolar
140	171.5	13.2	385	2	A54785	preadipocyte facto	213	139	10.7	544	2	S52477	disintegrin (BC 3.
141	169.5	13.1	417	2	T08724	hypothetical prote	214	139	10.7	1125	1	S57846	protein-tyrosine k
142	169.5	13.1	1057	1	A39288	dorsal-ventral pat	215	138	10.6	2195	2	T34264	hypothetical prote
143	169	13.0	1070	2	T31069	colloid-BMP-1 like	216	138	10.6	3566	1	A40701	tenascin-X precurs
144	168.5	13.0	492	1	EXBO	coagulation factor	217	138	10.6	4006	2	T09070	probable tenascin
145	168	13.0	452	1	A30351	hypothetical prote	218	137.5	10.6	955	2	A45441	thrombospondin 4 -
146	168	13.0	1965	2	T33216	hypothetical prote	219	137	10.6	1737	2	T00209	MEGF8 protein - hu
147	167.5	12.9	616	2	T29234	hypothetical prote	220	137	10.6	1808	2	T15099	hypothetical prote
148	167	12.9	459	2	JQ0419	coagulation factor	221	137	10.6	2825	2	T14271	Doc4 protein, stre
149	167	12.9	461	1	JX0210	protein C (activat	222	136.5	10.5	915	2	B48225	probable proprotei
150	167	12.9	623	2	T47542	Spot 3 protein and	223	136.5	10.5	2824	2	T22759	hypothetical prote
151	166	12.8	356	2	T20656	hypothetical prote	224	136	10.5	1798	2	S33869	laminin beta-2 cha
152	165	12.7	466	1	KFHU7	coagulation factor	225	134.5	10.4	2180	2	T29764	hypothetical prote
153	165	12.7	624	2	T00044	vacuolar sorting r	226	134.5	10.4	5376	2	T42215	zonadhesin - mouse
154	164	12.6	461	1	KXHU	protein C (activat	227	134	10.3	680	2	PN0510	integrin beta-3 ch
155	163.5	12.6	1827	2	T34288	hypothetical prote	228	134	10.3	3106	1	S53868	laminin alpha-2 ch
156	163	12.6	628	2	T02604	probable vacuolar	229	133.5	10.3	723	2	PN0509	integrin beta-3 ch
157	163	12.6	1170	2	A40558	thrombospondin 1 p	230	133.5	10.3	1023	2	T30257	IGF Fc binding pro
158	162.5	12.5	372	2	T29359	hypothetical prote	231	133.5	10.3	1168	2	I56985	kalinin B1 - mouse
159	162	12.5	628	2	T02602	vacuolar sorting r	232	133	10.3	748	2	S66129	disintegrin (BC 3.
160	162	12.5	2019	1	JQ1322	tenascin precursor	233	132.5	10.2	429	2	T21113	hypothetical prote
161	161.5	12.5	752	2	T20871	hypothetical prote	234	132.5	10.2	1639	1	MMFFB2	laminin gamma-1 ch
162	161	12.4	461	1	S18994	protein C (activat	235	132	10.2	527	2	JE0373	low density lipopr
163	160.5	12.4	1464	2	S58984	development protei	236	132	10.2	755	2	A44315	cartilage oligomer
164	160	12.3	2201	2	A32160	tenascin-C - human	237	132	10.2	1138	1	S24066	protein-tyrosine k
165	159.5	12.3	422	1	KXHUZ	plasma protein 2 p	238	131.5	10.1	1046	2	A26838	prestalk protein p
166	159.5	12.3	961	1	TSHUP4	thrombospondin 4 p	239	131.5	10.1	1807	2	JC6319	integrin beta-4 ch
167	159	12.3	1746	1	S19694	tenascin precursor	240	131	10.1	753	2	B56268	platelet glycoprot
168	158.5	12.2	767	2	T30018	hypothetical prote	241	131	10.1	778	2	A60798	platelet glycoprot
169	158.5	12.2	838	2	T20125	hypothetical prote	242	131	10.1	788	2	I77349	platelet glycoprot
170	158.5	12.2	3712	2	S18253	laminin alpha-1 ch	243	131	10.1	788	2	I51530	integrin beta-3 su
171	158	12.2	252	2	T46247	hypothetical prote	244	131	10.1	788	2	A26547	platelet glycoprot
172	158	12.2	1111	2	T26972	hypothetical prote	245	131	10.1	1124	2	I58388	protein-tyrosine k
173	157.5	12.1	1810	1	A32230	tenascin precursor	246	131	10.1	1615	2	JE0372	low density lipopr
174	157	12.1	621	1	I38467	low density lipopr	247	131	10.1	1748	1	JN0786	integrin beta-4 ch
175	157	12.1	768	2	A42755	P-selectin precurs	248	131	10.1	1797	2	A55677	laminin beta-2 cha

249	130.5	10.1	3191	2	T22945	hypothetical prote	322	119	9.2	1274	2	T42017	cysteine rich prot
250	130	10.0	782	2	A61625	tenascin-like prot	323	119	9.2	1275	2	A36429	integrin beta-4 ch
251	129.5	10.0	799	2	A38308	integrin beta-5 ch	324	119	9.2	2910	2	T42214	otogelin - mouse
252	129	9.9	1178	1	A39804	thrombospondin pre	325	118.5	9.1	769	2	A41029	integrin beta-8 ch
253	129	9.9	1786	1	MMMSB1	laminin beta-1 cha	326	118.5	9.1	1172	1	TSHP2	thrombospondin 2 p
254	128.5	9.9	915	1	A48225	subtilisin-like pr	327	118.5	9.1	1607	1	MMMSB2	laminin gamma-1 ch
255	128.5	9.9	1134	1	JN0711	protein-tyrosine k	328	118.5	9.1	4391	2	A38096	perlecan precursor
256	128.5	9.9	1548	2	S34583	serine proteinase	329	118	9.1	500	2	S66522	cartilage matrix p
257	128.5	9.9	1790	1	MMFFB1	laminin beta-1 cha	330	118	9.1	577	2	B37057	integrin beta-6 ch
258	128	9.9	699	1	IS4763	Ra-reactive factor	331	118	9.1	1257	2	S28764	neurocan precursor
259	128	9.9	730	1	BMHUI	procollagen C-endo	332	117.5	9.1	781	2	S43534	integrin beta3 - c
260	128	9.9	823	1	A58788	procollagen C-endo	333	117	9.0	883	2	S57553	brevican precursor
261	128	9.9	862	2	S43922	versican - pig-tai	334	117	9.0	933	1	OPHUIT	iodide peroxidase
262	128	9.9	1474	2	D88550	protein ZC84.6 [lim	335	117	9.0	1364	2	T00250	MEGF2 protein - hu
263	128	9.9	2844	2	S28291	hypothetical prote	336	117	9.0	1613	2	JE0272	low density lipopr
264	127.5	9.8	798	2	A40526	hypothetical prote	337	116.5	9.0	152	2	T04140	vacuolar sorting r
265	127.5	9.8	1609	1	MMHUB2	integrin beta-7 ch	338	116.5	9.0	738	2	D86345	hypothetical prote
266	127.5	9.8	1661	2	T31330	laminin gamma-1 ch	339	116	8.9	259	2	T21011	hypothetical prote
267	127.5	9.8	1801	1	MWRTS	head-activator bin	340	116	8.9	883	2	S49126	brevican precursor
268	127.5	9.8	13055	2	T16590	laminin beta-2 cha	341	116	8.9	1122	2	S42337	protein-tyrosine k
269	127	9.8	548	2	T16642	hypothetical prote	342	116	8.9	1123	1	JN0712	protein-tyrosine k
270	127	9.8	2823	2	F87908	hypothetical prote	343	116	8.9	1328	2	T43060	agrin - electric r
271	127	9.8	2823	2	T23064	protein T22A3.8 [i	344	116	8.9	1487	2	G96827	protein F20B17.10
272	127	9.8	3102	2	T43291	hypothetical prote	345	115.5	8.9	3097	2	T00021	DN-cadherin - frui
273	126.5	9.8	610	2	A35046	laminin alpha chai	346	115	8.9	325	2	S68985	exogastula-induci
274	126.5	9.8	656	2	JC2005	E-selectin precurs	347	115	8.9	485	2	S36772	E-selectin - bovin
275	126.5	9.8	3034	2	T14119	integrin beta-5 ch	348	115	8.9	830	2	A30359	P-selectin precurs
276	126	9.7	707	2	JC2218	seven-pass transme	349	114	8.8	213	2	S25647	ookinete surface p
277	125.5	9.7	211	2	T32590	procollagen C-endo	350	114	8.8	253	2	T25768	hypothetical prote
278	125.5	9.7	1643	2	T14274	hypothetical prote	351	114	8.8	626	2	T27319	hypothetical prote
279	125.5	9.7	2409	1	A60979	versican precursor	352	114	8.8	646	2	JN0473	P-selectin precurs
280	125.5	9.7	3381	2	T42389	versican precursor	353	114	8.8	788	2	A37057	integrin beta-6 ch
281	125	9.6	1786	1	MMHUB1	laminin beta-1 cha	354	114	8.8	2476	2	T34022	zonadhesin - pig
282	124.5	9.6	313	2	S44208	extracellular matr	355	113.5	8.8	603	2	S28941	coagulation factor
283	124.5	9.6	513	2	D88991	protein apx-1 [imp	356	113.5	8.8	1955	1	AGCH	agrin precursor -
284	124.5	9.6	612	2	B42755	E-selectin precurs	357	113	8.7	220	2	S29195	antistasin - Hydra
285	124.5	9.6	2397	1	A55535	versican precursor	358	113	8.7	798	2	B27079	fibronectin recept
286	124	9.6	1302	2	T00038	hypothetical prote	359	113	8.7	1125	1	JH0771	protein-tyrosine k
287	123.5	9.5	720	2	E86297	F309.6 protein - A	360	113	8.7	1268	2	S52781	neurocan - mouse
288	123	9.5	643	2	T25473	hypothetical prote	361	113	8.7	1299	2	T43251	furin (EC 3.4.21.7
289	123	9.5	733	2	E86345	hypothetical prote	362	113	8.7	1353	2	T19157	probable metal bin
290	122.5	9.4	560	1	JC4795	plasma hyaluronan-	363	113	8.7	1424	2	T19156	probable metal bin
291	122.5	9.4	574	2	B88465	protein B0244.8 [i	364	113	8.7	1613	2	JE0273	low density lipopr
292	122.5	9.4	1297	2	T30274	proteoliasin - se	365	112.5	8.7	769	1	JC1121	leukocyte adhesion
293	122.5	9.4	2531	2	T16743	hypothetical prote	366	112.5	8.7	899	2	G02428	subtilisin-like pr
294	122	9.4	705	1	C1HURB	complement subcomp	367	112.5	8.7	915	2	JC6148	subtilisin-like pr
295	122	9.4	3562	2	A47171	chondroitin sulfat	368	112.5	8.7	1187	2	T18355	hypothetical prote
296	121.5	9.4	102	2	B55885	chondroitin sulfat	369	112.5	8.7	1506	2	T30886	hypothetical prote
297	121.5	9.4	251	2	A55035	cysteine-rich prot	370	112.5	8.7	2215	2	T00348	integrin beta chai
298	121.5	9.4	551	2	I46709	endothelial leukoc	371	112.5	8.7	2718	2	A23475	integrin beta chai
299	121.5	9.4	914	1	S07047	iodide peroxidase	372	112	8.6	677	2	C42125	integrin unc-52 lim
300	121	9.3	565	2	T16408	hypothetical prote	373	112	8.6	794	2	F88508	angiogenesis inhib
301	121	9.3	3707	2	S18252	heparan sulfate pr	374	112	8.6	1192	2	S69000	protein unc-52 lim
302	120.5	9.3	1104	2	T38889	transcription fact	375	111.5	8.6	933	2	A31930	cytotactin - chick
303	120.5	9.3	1172	2	A42587	thrombospondin 2 p	376	111.5	8.6	1766	2	A42125	trophozoite cystel
304	120	9.3	591	2	T48141	acroggranin - guine	377	111	8.6	294	2	T23682	hypothetical prote
305	120	9.3	732	2	T52588	wall-associated se	378	111	8.6	557	2	A48434	variant-specific s
306	120	9.3	768	2	B41029	integrin beta-8 ch	379	111	8.6	809	2	A57283	integrin beta chai
307	120	9.3	855	2	JC7731	membrane-bound arg	380	111	8.6	846	2	A30889	protein unc-52 lim
308	120	9.3	1193	2	A44018	laminin B2t chain	381	111	8.6	1160	2	F88369	protein unc-52 lim
309	120	9.3	1391	2	T20406	hypothetical prote	382	111	8.6	1444	2	T18856	angiogenesis inhib
310	120	9.3	3084	1	MMMSA	laminin alpha-1 ch	383	111	8.6	2295	2	C88369	hypothetical prote
311	119.5	9.2	768	2	I53821	P-selectin - rat	384	111	8.6	3375	2	T19821	hypothetical prote
312	119.5	9.2	914	1	JN0550	iodide peroxidase	385	110.5	8.5	379	2	A59180	Wnt inhibitory fac
313	119.5	9.2	1113	2	JE0315	low-density lipopr	386	110.5	8.5	690	2	B86296	hypothetical prote
314	119.5	9.2	1115	2	S40241	G protein-coupled	387	110	8.5	354	2	T22274	hypothetical prote
315	119.5	9.2	1895	2	T15881	hypothetical prote	388	110	8.5	589	2	B38128	epithelin/granulin
316	119.5	9.2	13288	2	T03099	mucin, submaxillar	389	110	8.5	596	2	A45664	variant-specific s
317	119	9.2	378	2	B59190	Wnt inhibitory fac	390	110	8.5	686	1	A59271	Ra-reactive factor
318	119	9.2	496	2	A37979	cartilage matrix p	391	110	8.5	799	2	JC4126	integrin beta olig
319	119	9.2	798	2	S01659	integrin beta-1 ch	392	109.5	8.4	482	2	JC5092	E-selectin - pig
320	119	9.2	799	1	JMS545	fibronectin recept	393	109.5	8.4	1188	2	D86236	protein F14N23.5 [
321	119	9.2	964	2	JC5545	integrin beta-4 pr	394	109.5	8.4	1280	2	A39117	170K lectin precur

395	109.5	8.4	1292	2	T09229	galactose binding	468	99	7.6	343	2	S45321	follistatin - mou
396	109	8.4	434	1	A35005	u-plasminogen acti	469	99	7.6	937	2	I53282	gene PACB4 protei
397	109	8.4	493	2	A33809	cartilage matrix p	470	99	7.6	1049	1	I19421	ATP-dependent perm
398	109	8.4	558	2	JC5878	plasma hyaluronan-	471	99	7.6	3133	2	S52093	hemocytin - silkwo
399	108.5	8.4	169	1	S18946	ultra high-sulfur	472	98.5	7.6	601	2	T34396	hypothetical prote
400	108.5	8.4	325	2	A40084	exogastrola-induci	473	98.5	7.6	922	2	T37256	metalloproteinase
401	108.5	8.4	589	2	C38128	epithelin/granulin	474	98	7.6	530	2	G02091	pancreatic zymogen
402	108.5	8.4	1170	2	A53612	laminin B1k chain	475	98	7.6	952	2	T18900	disintegrin and me
403	108.5	8.4	3020	2	A43932	mucin 2 precursor,	476	98	7.6	1283	2	T13799	neurexin IV - frui
404	108	8.3	561	2	T27318	hypothetical prote	477	98	7.6	2109	1	I50421	aggreccan precursor
405	108	8.3	601	2	A27020	DLF-induced presta	478	97.5	7.5	344	1	A27701	follistatin precu
406	108	8.3	770	2	S04847	leukocyte adhesio	479	97.5	7.5	344	2	A32141	follistatin i prec
407	108	8.3	771	2	A45839	leukocyte adhesio	480	97.5	7.5	926	1	OPPGIT	iodide peroxidase
408	108	8.3	2704	2	S09118	G surface protein	481	97.5	7.5	1816	1	S68960	laminin alpha-4 ch
409	108	8.3	2809	2	T30213	G-cadherin - sea u	482	97	7.5	264	2	T16271	hypothetical prote
410	107.5	8.3	272	2	T20591	hypothetical prote	483	97	7.5	615	1	KFHU12	coagulation factor
411	107.5	8.3	733	1	A46373	probable serine/th	484	97	7.5	1599	2	T16210	hypothetical prote
412	107.5	8.3	1101	2	T16840	hypothetical prote	485	97	7.5	1713	2	A55347	adhesive ligand ep
413	107	8.2	217	2	S00769	25k ookinete surfa	486	96.5	7.4	330	2	T46256	brevicain - human
414	107	8.2	217	2	A44966	25k ookinete surfa	487	96.5	7.4	756	2	S47656	TMDC II protein - b
415	107	8.2	769	1	IJRHULM	leukocyte adhesio	488	96.5	7.4	1077	2	T41146	probable cysteine-
416	107	8.2	1557	2	T28811	hypothetical prote	489	96.5	7.4	1416	2	E88550	protein 2C84.1 (im
417	107	8.2	1959	1	AGRT	agrin - rat	490	96.5	7.4	2101	2	S57245	insulin receptor (
418	106.5	8.2	667	2	A48579	trophozoite surfac	491	96.5	7.4	2148	1	A56081	insulin receptor
419	106.5	8.2	3075	2	S14458	laminin alpha-1 ch	492	96.5	7.4	2395	1	S50820	surface protein ty
420	106	8.2	379	2	T16213	APX-1 protein homo	493	96	7.4	527	2	A42032	epidermal growth f
421	106	8.2	402	2	S42367	lag-2 protein - Ca	494	96	7.4	1034	2	JC5598	mucin - rat
422	106	8.2	424	2	S11676	spore coat protein	495	96	7.4	1223	1	TVCHLV	epidermal growth f
423	105.5	8.1	772	2	S32659	integrin beta 2 ch	496	96	7.4	1308	2	A47253	epidermal growth f
424	105.5	8.1	4307	2	T20721	hypothetical prote	497	96	7.4	2233	2	T28669	surface protein 51
425	105	8.1	803	1	IJCH3	integrin, band 3 p	498	95.5	7.4	198	2	T24476	hypothetical prote
426	104.5	8.1	512	2	T37819	probable zinc meta	499	95.5	7.4	212	2	T05936	agglutinin isolect
427	104.5	8.1	1019	2	A38738	coagulation factor	500	95.5	7.4	719	2	T00266	hypothetical prote
428	104.5	8.1	1106	2	T44598	hypothetical prote	501	95	7.3	546	2	T49931	hypothetical prote
429	104.5	8.1	1513	2	A54895	hypothetical prote	502	95	7.3	655	1	A46888	hepatocyte growth
430	104	8.0	295	2	JC5559	mucin 2, intestina	503	95	7.3	670	2	S165967	disintegrin-like m
431	104	8.0	713	2	A35502	lectin-B - Virgini	504	95	7.3	695	1	S05008	complement subcomp
432	104	8.0	932	2	I52527	PACE4A - mouse (fr	505	95	7.3	805	2	T34212	hypothetical prote
433	104	8.0	1142	2	T30272	hypothetical prote	506	95	7.3	212	2	S09623	hypothetical prote
434	104	8.0	1680	2	A43434	furin (EC 3.4.21.7	507	94.5	7.3	293	2	T22919	hypothetical prote
435	104	8.0	2610	2	T20968	hypothetical prote	508	94.5	7.3	370	2	S22124	L-selectin precurs
436	104	8.0	2946	2	T15840	hypothetical prote	509	94	7.2	243	2	T28802	hypothetical prote
437	103.5	8.0	583	2	A29154	complement factor	510	94	7.2	372	1	A32375	L-selectin precurs
438	103.5	8.0	773	2	I46059	beta-1 integrin su	511	94	7.2	372	2	S23936	L-selectin precurs
439	103.5	8.0	1106	2	T13938	gene shuttle craft	512	94	7.2	524	2	S38539	disintegrin-like m
440	103.5	8.0	1700	2	S08167	Balbani ring 3 pr	513	94	7.2	798	2	B28193	integrin beta-1 ch
441	103.5	8.0	1895	2	T06609	disease resistance	514	94	7.2	798	2	B28193	integrin beta-1* c
442	103.5	8.0	2813	1	VWU	von Willebrand fac	515	94	7.2	823	2	S18968	cyristestin precurs
443	103	7.9	606	2	A54665	netrin-1 precursor	516	93.5	7.2	273	2	T16246	hypothetical prote
444	103	7.9	969	1	A39490	subtilisin-like pr	517	93.5	7.2	429	2	T16656	hypothetical prote
445	103	7.9	1373	2	JE0095	gastric mucin MUC5	518	93.5	7.2	2153	2	T30074	hypothetical prote
446	102.5	7.9	1119	2	A88481	protein CL6A3.6 [i	519	93.5	7.2	2533	2	T28675	alpha-5LD immobili
447	102.5	7.9	1296	2	T16859	hypothetical prote	520	93.5	7.2	2533	2	T28674	alpha-5LD immobili
448	102.5	7.9	1321	2	JE0352	mucin MUC5B, trach	521	93	7.2	714	2	F86345	Fl6F4.8 protein - c
449	102	7.9	389	2	T23167	hypothetical prote	522	93	7.2	736	2	S47645	TMDC I protein - c
450	102	7.9	419	2	S69207	vascular endotheli	523	93	7.2	903	2	S60257	meltrin alpha - mo
451	101.5	7.8	237	2	S08073	cyclic nucleotide	524	93	7.2	2155	2	T30197	alpha tectorin - m
452	101.5	7.8	344	2	I57698	cell surface glyco	525	93	7.2	2239	2	T16199	hypothetical prote
453	101	7.8	573	2	A33533	coagulation factor	526	93	7.2	2543	2	T31687	surface antigen - P
454	101	7.8	593	2	S45281	hypothetical prote	527	92.5	7.1	337	2	T14079	follistatin - shee
455	101	7.8	884	2	T18649	hypothetical prote	528	92.5	7.1	397	2	JQ2153	proteinase inhibit
456	101	7.8	1321	2	T00382	hypothetical prote	529	92.5	7.1	409	2	T11743	p847 protein - pig
457	100.5	7.7	581	2	B54655	netrin-2 precursor	530	91.5	7.1	223	2	B38346	ultra-high-sulfur
458	100.5	7.7	593	1	GFU	granulin precursor	531	91.5	7.1	470	2	A40697	63K sperm flagella
459	100.5	7.7	1193	2	T21133	hypothetical prote	532	91.5	7.1	588	2	T33815	hypothetical prote
460	100	7.7	646	2	H96665	protein F22C12.10	533	91.5	7.1	686	2	T25987	hypothetical prote
461	100	7.7	649	2	G86434	protein Fl7F8.23 [534	91.5	7.1	2090	2	T30075	L-selectin precurs
462	100	7.7	707	2	T00204	LDL receptor relat	535	91	7.0	323	1	S09702	hypothetical prote
463	100	7.7	1016	2	G86295	hypothetical prote	536	91	7.0	711	2	D86296	hypothetical prote
464	99.5	7.7	600	2	S07638	spore coat protein	537	91	7.0	732	2	C96719	hypothetical prote
465	99.5	7.7	816	2	C69493	hypothetical prote	538	90.5	7.0	344	2	I45894	follistatin - bovi
466	99.5	7.7	832	2	A42112	mucin-like peptide	539	90.5	7.0	427	2	T74211	follistatin - bovi
467	99.5	7.7	917	2	A54423	brevicain precursor	540	90.5	7.0	711	2	T27358	hypothetical prote

541	90.5	7.0	770	2	T00203	LDL receptor-relat	614	84.5	6.5	789	2	S28259	androgen-regulated
542	90	6.9	291	2	J38037	t-plasminogen acti	615	84.5	6.5	804	2	A86327	protein F18014.11
543	90	6.9	372	2	JC5377	L-selectin precurs	616	84.5	6.5	825	2	S55060	fertilin alpha-11
544	90	6.9	419	2	A59414	metalloproteinase	617	84.5	6.5	893	2	S51603	receptor-like tyro
545	90	6.9	562	1	UKHUT	t-plasminogen acti	618	84.5	6.5	898	2	S47489	receptor tyrosine
546	90	6.9	572	2	T29880	hypothetical prote	619	84.5	6.5	919	2	T29581	hypothetical prote
547	90	6.9	694	2	JC6554	complement subcomp	620	84.5	6.5	1122	2	T42400	epn receptor tyros
548	90	6.9	843	1	A27340	complement C7 prec	621	84.5	6.5	1210	1	GQH05	epidermal growth f
549	90	6.9	985	2	I51549	receptor tyrosine	622	84	6.5	71	2	S39422	metallothionein 20
550	90	6.9	1268	2	B36502	insulin receptor-r	623	84	6.5	92	2	D37057	epithelial cell g1
551	90	6.9	1291	2	T21694	hypothetical prote	624	84	6.5	497	2	T27827	hypothetical prote
552	89.5	6.9	178	2	I49259	cellular nucleic a	625	84	6.5	585	2	I46586	complement compone
553	89.5	6.9	186	2	A28401	agglutinin isolect	626	84	6.5	612	2	JH0799	laminin-related pr
554	89.5	6.9	191	2	I46412	keratin KAP5.4 - s	627	84	6.5	613	2	A88448	protein C4509.6 [1
555	89.5	6.9	320	2	A53119	cell adhesion glyco	628	84	6.5	735	2	I48101	ADAM 6 protein pre
556	89.5	6.9	1607	2	T43212	insulin-like growt	629	84	6.5	918	2	JC4361	scavenger receptor
557	89	6.9	197	2	I46413	keratin KAP5.5 - s	630	84	6.5	981	2	S51604	receptor-like tyro
558	89	6.9	376	2	JC4892	L-selectin precurs	631	84	6.5	1005	2	S49015	receptor tyrosine
559	89	6.9	385	1	A34015	L-selectin precurs	632	84	6.5	1260	1	S05479	neural cell adhesi
560	89	6.9	1323	2	A80257	protein let-23 [im	633	83.5	6.4	117	2	A32416	phospholipase A2 (
561	89	6.9	1374	2	S70712	protein-tyrosine k	634	83.5	6.4	329	2	A48805	insulin-like growt
562	89	6.9	4351	2	T00252	MEGF1 protein - ra	635	83.5	6.4	537	2	B33485	spore coat protein
563	88.5	6.8	230	2	A38346	ultra-high-sulfur	636	83.5	6.4	540	2	B47417	insulin receptor-r
564	88.5	6.8	343	2	S55369	folliculin - chic	637	83.5	6.4	868	2	T20239	hypothetical prote
565	88.5	6.8	712	2	A45638	immunodominant mic	638	83.5	6.4	965	2	S62935	hypothetical prote
566	88.5	6.8	803	2	A47723	P-spondin precurs	639	83.5	6.4	1376	1	JQ1534	E2 glycoprotein pr
567	88.5	6.8	1043	2	T19734	hypothetical prote	640	83	6.4	61	1	SMXK1	metallothionein 1
568	88.5	6.8	1252	2	S36016	ococyst wall protei	641	83	6.4	349	2	D36858	gene G4R protein -
569	88	6.8	826	2	A60385	monocyte surface a	642	83	6.4	360	2	B36470	Wnt-2 protein - mo
570	88	6.8	850	2	S56015	gastric mucin MUC5	643	83	6.4	425	2	T38548	hypothetical zinc-
571	88	6.8	975	2	JC5570	subtilisin-like pr	644	83	6.4	429	2	A42972	coagulation factor
572	88	6.8	1522	2	H88360	protein T22P7.3 [1	645	83	6.4	513	2	S28358	prespore vesicle p
573	87.5	6.7	213	1	ABWT2	agglutinin isolect	646	83	6.4	520	2	G88946	protein T12A7.2 [1
574	87.5	6.7	335	2	T32657	hypothetical prote	647	83	6.4	625	1	KFRU1	coagulation factor
575	87.5	6.7	509	1	A37259	membrane glycoprot	648	83	6.4	655	2	JC7850	disintegrin and me
576	87.5	6.7	509	2	T22238	hypothetical prote	649	83	6.4	925	1	A39216	nucleotide diphosp
577	87.5	6.7	713	1	UMMS	period clock prote	650	83	6.4	1369	2	S70713	protein-tyrosine k
578	87.5	6.7	764	2	C86314	hypothetical prote	651	83	6.4	1450	2	T30273	hypothetical prote
579	87.5	6.7	2120	2	T30243	alpha tectorin - c	652	83	6.4	4550	2	T18440	hypothetical prote
580	87.5	6.7	2150	2	T32497	hypothetical prote	653	82.5	6.4	250	2	T30124	hypothetical prote
581	87.5	6.7	2616	2	A57096	nudel protein prec	654	82.5	6.4	310	2	T32006	hypothetical prote
582	87	6.7	71	2	S47577	metallothionein 20	655	82.5	6.4	531	2	T18741	hypothetical prote
583	87	6.7	425	2	T18592	hypothetical prote	656	82.5	6.4	777	2	I48100	ADAM 5 protein pre
584	87	6.7	570	2	T37314	probable kexin (EC	657	82.5	6.4	942	2	D87803	protein b11-4d [im
585	87	6.7	600	2	T18593	hypothetical prote	658	82.5	6.4	1161	1	S31213	nidogen precursor
586	87	6.7	1371	2	A33837	insulin-like growt	659	82.5	6.4	1385	2	T14158	neurexin IV - mous
587	86.5	6.7	318	2	H87929	protein T22H2.6 [1	660	82	6.3	71	2	S39421	metallothionein 20
588	86.5	6.7	549	2	S48169	metalloproteinase	661	82	6.3	170	2	T06056	hypothetical prote
589	86.5	6.7	609	2	S55270	catrocollastatin p	662	82	6.3	178	2	A23219	high-cysteine chor
590	86.5	6.7	1558	2	C89114	protein C37C3.6a [663	82	6.3	258	2	S23106	pria protein - shi
591	86.5	6.7	2167	2	T34395	hypothetical prote	664	82	6.3	281	2	D88637	protein W09G12.1 [
592	86	6.6	182	2	A36686	ultra-high-sulfur	665	82	6.3	360	1	WMBE2E	membrane-bound com
593	86	6.6	348	2	T28623	hypothetical prote	666	82	6.3	660	2	S71949	metalloproteinase
594	86	6.6	491	2	T21421	hypothetical prote	667	82	6.3	661	2	B96596	hypothetical prote
595	86	6.6	738	2	S40992	hypothetical prote	668	82	6.3	704	2	T31227	tran protein homol
596	86	6.6	739	2	B88553	protein K04H4.2b [669	82	6.3	1019	2	T13039	tyrosine kinase re
597	86	6.6	962	2	JC5571	subtilisin-like pr	670	82	6.3	1162	2	T21557	hypothetical prote
598	86	6.6	1091	1	PL0009	complement C3d/Eps	671	82	6.3	1642	2	T19130	hypothetical prote
599	85.5	6.6	206	2	T24484	hypothetical prote	672	82	6.3	2014	2	I36936	complement recepto
600	85.5	6.6	248	2	T19913	hypothetical prote	673	81.5	6.3	186	2	G89614	protein F15G9.5 [1
601	85.5	6.6	255	2	I38426	lymphocyte activat	674	81.5	6.3	195	2	T04161	trypsin inhibitor
602	85.5	6.6	319	2	A53502	folliculin - Afri	675	81.5	6.3	257	2	T18969	hypothetical prote
603	85.5	6.6	571	2	S24789	Jararagin C precu	676	81.5	6.3	345	2	T25138	hypothetical prote
604	85.5	6.6	813	2	T21192	hypothetical prote	677	81.5	6.3	358	2	T25137	hypothetical prote
605	85	6.6	176	2	T31796	hypothetical prote	678	81.5	6.3	437	2	S05478	properdin - mouse
606	85	6.6	349	2	D72175	G2R protein - vari	679	81.5	6.3	552	2	JC7666	serine-type carbox
607	85	6.6	689	4	S30392	hypothetical RrvL-	680	81.5	6.3	776	2	S28258	androgen-regulated
608	85	6.6	905	2	S55059	fertilin alpha-I -	681	81.5	6.3	957	2	T15976	hypothetical prote
609	85	6.6	1627	2	S65464	pregnancy-associat	682	81.5	6.3	1231	1	NBHUH	complement factor
610	84.5	6.5	265	2	H96785	protein F10A5.22 [683	81.5	6.3	1239	2	T13809	probleme disintegr
611	84.5	6.5	302	1	WMBE1E	secretory compleme	684	81.5	6.3	1751	1	MWHUMH	laminin alpha-2 ch
612	84.5	6.5	463	2	T26555	hypothetical prote	685	81.5	6.3	1846	2	T42047	insulin receptor h
613	84.5	6.5	744	2	A43553	ascites sialoglyco	686	81	6.2	400	2	T46383	hypothetical prote

687	6.2	483	2	T24856	hypothetical prote	760	78	6.0	379	2	A35669	gene CVR61 protein
688	6.2	1260	1	TVRTNU	protein-tyrosine k	761	78	6.0	446	2	T31644	hypothetical prote
689	6.2	1300	2	A36502	insulin receptor-r	762	78	6.0	550	2	T47158	hypothetical prote
690	80.5	375	2	A41428	CEP-10 protein pre	763	78	6.0	725	2	E96596	hypothetical prote
691	80.5	387	2	G88124	protein nhr-16 [lm	764	78	6.0	757	2	T34362	hypothetical prote
692	80.5	401	2	S65138	glycoprotein antig	765	78	6.0	795	2	T34468	hypothetical prote
693	80.5	478	2	J47040	gene Tt52 protein	766	78	6.0	922	2	T23573	hypothetical prote
694	6.2	734	2	SC4861	fertilin beta cha	767	78	6.0	1028	2	A96719	hypothetical prote
695	80.5	780	2	A34102	von Willebrand fac	768	78	6.0	1042	2	A57534	mucin 5AC (clone L
696	80.5	788	2	T25061	hypothetical prote	769	78	6.0	1166	1	S06142	protein-tyrosine k
697	80.5	987	2	I48652	mouse developmenta	770	78	6.0	1438	2	A48216	neurexin iii-alpha
698	80.5	987	2	I48953	eph-related recept	771	78	6.0	1471	2	B48218	neurexin iii-alpha
699	80.5	1013	2	I50615	receptor-type prot	772	78	6.0	1578	2	I48216	neurexin iii-alpha
700	80.5	1092	2	H96509	protein F27P5.23 l	773	78	6.0	1647	2	T32934	hypothetical prote
701	80.5	1131	2	T15787	hypothetical prote	774	78	6.0	2014	2	T21560	hypothetical prote
702	80.5	2214	2	T16305	hypothetical prote	775	78	6.0	2043	2	T18524	scavenger receptor
703	80.5	2415	1	A39086	aggreccan precursor	776	78	6.0	2489	2	I73012	complement C3b/Cab
704	80	6.2	117	A34860	phospholipase A2 (777	78	6.0	3968	2	A44265	trithorax homolog
705	80	6.2	137	T15609	hypothetical prote	778	77.5	6.0	83	2	S07405	proteinase inhibit
706	80	6.2	148	S06019	isotocin 2 / neuro	779	77.5	6.0	94	2	JC2225	Bowman-Birk protei
707	80	6.2	177	A32760	cellular nucleic a	780	77.5	6.0	103	1	TISYC2	proteinase inhibit
708	80	6.2	177	JC3512	cellular nucleic a	781	77.5	6.0	133	1	PSOXG	phospholipase A2 (
709	80	6.2	227	1 LNRZ	lectin precursor -	782	77.5	6.0	141	2	FL1294	trophozoite surfac
710	80	6.2	266	S65778	chitinase class IV	783	77.5	6.0	459	2	A34791	interleukin-7 rece
711	80	6.2	406	A44776	transforming prote	784	77.5	6.0	644	2	T31132	hypothetical prote
712	80	6.2	535	T19706	hypothetical prote	785	77.5	6.0	692	2	T32980	hypothetical prote
713	80	6.2	951	T00017	gene ADAMTS-1 prot	786	77.5	6.0	828	2	T23267	hypothetical prote
714	80	6.2	991	T178843	receptor protein t	787	77.5	6.0	1074	2	JC5928	senaphorin F precu
715	80	6.2	1259	S36126	neural cell adhesi	788	77.5	6.0	1360	2	T33922	hypothetical prote
716	80	6.2	1353	1 JQ2168	E2 glycoprotein pr	789	77.5	6.0	2924	2	T18378	variant-specific s
717	80	6.2	1363	T43220	insulin-like growt	790	77.5	6.0	3343	2	S44887	ZK112.7 protein -
718	80	6.2	1428	T08852	lustrin A - Califo	791	77	5.9	60	1	SMH01A	metallothionein 1A
719	80	6.2	1594	T30549	hensin - rabbit	792	77	5.9	71	2	S39420	metallothionein 20
720	80	6.2	1715	C40228	neurexin II-alpha	793	77	5.9	118	1	PSNKK3	phospholipase A2 (
721	80	6.2	1743	2 T26859	hypothetical prote	794	77	5.9	118	2	C34860	phospholipase A2 (
722	80	6.2	2219	2 T27684	hypothetical prote	795	77	5.9	153	2	A34132	vasotocin / neurop
723	79.5	6.1	72	1 TIMB	trypsin inhibitor	796	77	5.9	155	2	A45293	conopressin precur
724	79.5	6.1	118	1 PSNKK1	phospholipase A2 (797	77	5.9	160	2	T25185	hypothetical prote
725	79.5	6.1	330	2 T25169	hypothetical prote	798	77	5.9	188	2	JC6547	high sulfur protei
726	79.5	6.1	362	2 I64128	2-dehydro-3-deoxy-	799	77	5.9	264	1	ORBOLD	LDL receptor - bov
727	79.5	6.1	461	2 JC4302	tumor necrosis fac	800	77	5.9	375	2	T16248	hypothetical prote
728	79.5	6.1	559	1 A29941	t-plasminogen acti	801	77	5.9	454	1	NMIV	exo-alpha-sialidas
729	79.5	6.1	559	1 A29941	hypothetical prote	802	77	5.9	480	1	A30065	trigramin precurs
730	79	6.1	1603	2 T34098	phospholipase A2 (803	77	5.9	676	1	VCWVPV	env polyprotein pr
731	79	6.1	118	2 H34860	hypothetical prote	804	77	5.9	735	2	G02937	fertilin beta - cr
732	79	6.1	135	2 T15610	hypothetical prote	805	77	5.9	814	2	G02390	disintegrin-like m
733	79	6.1	357	2 S23403	sperm surface prot	806	77	5.9	905	2	T23229	hypothetical prote
734	79	6.1	422	2 D86446	hypothetical prote	807	77	5.9	955	2	T18435	hypothetical prote
735	79	6.1	559	1 A35029	t-plasminogen acti	808	77	5.9	1339	2	JC4387	epidermal growth f
736	79	6.1	615	2 S06546	finger protein (cl	809	77	5.9	1381	2	T31083	paranodin - rat
737	79	6.1	713	2 I65253	disintegrin-like t	810	76.5	5.9	124	2	A31761	high-cysteine chor
738	79	6.1	802	2 T24293	hypothetical prote	811	76.5	5.9	171	2	I48298	cellular nucleic a
739	79	6.1	949	2 T24294	hypothetical prote	812	76.5	5.9	323	2	T24836	hypothetical prote
740	79	6.1	975	2 I48974	receptor-protein t	813	76.5	5.9	328	2	S72647	hypothetical prote
741	79	6.1	1053	2 S46199	probable complemen	814	76.5	5.9	345	2	A05279	surface antigen 51
742	79	6.1	1436	2 A46496	antigen WC1.1 prec	815	76.5	5.9	383	2	D88633	protein F56B3.2 li
743	78.5	6.1	2767	1 UIHU	thyroglobulin prec	816	76.5	5.9	530	1	A38690	membrane glycoprot
744	78.5	6.1	72	2 S39419	metallothionein 10	817	76.5	5.9	724	2	T25700	mechanosensory pro
745	78.5	6.1	169	2 T15611	hypothetical prote	818	76.5	5.9	986	2	S78059	protein-tyrosine k
746	78.5	6.1	230	2 T31722	hypothetical prote	819	76.5	5.9	1051	2	JC4091	glycoprotein A - P
747	78.5	6.1	314	2 T27686	hypothetical prote	820	76.5	5.9	1119	2	T16720	hypothetical prote
748	78.5	6.1	449	1 NBHUHS	complement factor	821	76.5	5.9	1210	2	A53183	epidermal growth f
749	78.5	6.1	616	2 A55796	scarin precursor -	822	76.5	5.9	1537	2	JC4172	DNA (cytosine-5')-
750	78.5	6.1	617	2 S48160	metalloproteinase	823	76.5	5.9	3869	2	A48205	All-1 protein +GTE
751	78.5	6.1	654	2 T30136	hypothetical prote	824	76	5.9	61	2	S89277	metallothionein 1R
752	78.5	6.1	689	2 E89135	coenzyme F420-redu	825	76	5.9	71	2	S47576	metallothionein 20
753	78.5	6.1	843	2 A27131	epidermal growth f	826	76	5.9	118	2	B34860	phospholipase A2 (
754	78.5	6.1	849	2 I50617	protein-tyrosine k	827	76	5.9	119	1	PSNOA5	phospholipase A2 h
755	78.5	6.1	1729	2 T18396	erythrocyte membra	828	76	5.9	121	1	PSSNAM	phospholipase A2 h
756	78	6.0	3078	2 T28432	variant-specific s	829	76	5.9	137	2	S68429	myotoxin precursor
757	78	6.0	160	2 JQ0542	185K secretory pro	830	76	5.9	171	2	S57894	laminin - Hydra vu
758	78	6.0	179	2 T25841	hypothetical prote	831	76	5.9	249	2	T46404	hypothetical prote
759	78	6.0	250	2 T29866	hypothetical prote	832	76	5.9	256	2	B32393	T-cell antigen 4-1
759	78	6.0	335	2 T31559	hypothetical prote							

833	76	5.9	335	2	T31561	hypothetical prote	906	74.5	5.7	312	2	T19675	hypothetical prote
834	76	5.9	335	2	T31560	hypothetical prote	907	74.5	5.7	343	2	JC7958	galaxin precursor
835	76	5.9	449	2	T48199	hypothetical prote	908	74.5	5.7	351	2	F83033	vanillate O-demeth
836	76	5.9	600	2	I49281	feritin alpha pre	909	74.5	5.7	416	2	A37877	hemorrhagic protei
837	76	5.9	688	1	C1HUS	complement subcomp	910	74.5	5.7	427	2	JC4915	agg protein precu
838	76	5.9	760	2	A40195	neprin A (EC 3.4.2	911	74.5	5.7	548	2	D82175	probable trypsin V
839	76	5.9	764	1	BBHU	complement factor	912	74.5	5.7	568	2	S42225	major envelope gly
840	76	5.9	767	2	T07693	hypothetical prote	913	74.5	5.7	664	2	T20420	hypothetical prote
841	76	5.9	817	2	T24063	hypothetical prote	914	74.5	5.7	807	2	A38152	F-spondin - rat
842	76	5.9	898	2	T14764	hypothetical prote	915	74.5	5.7	915	1	A55144	autotaxin precursor
843	76	5.9	1003	1	PVZAM	spheroidin precurs	916	74.5	5.7	1526	2	T19473	hypothetical prote
844	76	5.9	1122	2	F71606	probable multiple	917	74.5	5.7	2165	2	T21371	metallothionein IG
845	76	5.9	1172	2	F84572	probable cadmium-t	918	74	5.7	61	1	SMHUIG	metallothionein II
846	76	5.9	1711	2	C71625	variant-specific s	919	74	5.7	61	1	SMHY2C	metallothionein I
847	76	5.9	1717	1	A45558	epidermal growth f	920	74	5.7	61	1	SMMK2	metallothionein 2
848	76	5.9	2153	2	T14893	scavenger receptor	921	74	5.7	61	1	SMRT1	metallothionein I
849	76	5.9	2588	2	T14342	NSD1 protein - mou	922	74	5.7	61	1	S18403	metallothionein II
850	75.5	5.8	72	2	S39417	metallothionein 10	923	74	5.7	61	2	S00810	metallothionein IC
851	75.5	5.8	246	2	B25528	trypsin (EC 3.4.21	924	74	5.7	61	2	I48116	metallothionein II
852	75.5	5.8	249	2	T32060	hypothetical prote	925	74	5.7	118	2	S01801	phospholipase A2 (
853	75.5	5.8	255	2	A40969	folate-binding pro	926	74	5.7	118	2	S29653	textilotoxin chain
854	75.5	5.8	324	2	JC2395	Fas antigen precu	927	74	5.7	127	2	A49269	phospholipase A2 h
855	75.5	5.8	396	2	T23767	hypothetical prote	928	74	5.7	138	2	F48188	phospholipase A2 (
856	75.5	5.8	409	2	T29517	hypothetical prote	929	74	5.7	140	2	T04904	hypothetical prote
857	75.5	5.8	456	2	T17887	lysine/proline-ric	930	74	5.7	153	2	PN0564	von Willebrand fac
858	75.5	5.8	461	1	GQRTT1	tumor necrosis fac	931	74	5.7	170	2	A55499	zinc finger protei
859	75.5	5.8	464	2	C69356	conserved hypothet	932	74	5.7	170	2	I48297	hypothetical nucleic a
860	75.5	5.8	594	2	T04783	hypothetical prote	933	74	5.7	222	2	T27939	hypothetical prote
861	75.5	5.8	649	2	T18063	DNA binding protei	934	74	5.7	242	2	T29699	hypothetical prote
862	75.5	5.8	986	2	I78844	receptor protein-t	935	74	5.7	346	2	T30069	hypothetical prote
863	75.5	5.8	1042	2	T26644	hypothetical prote	936	74	5.7	448	1	H69032	polyferredoxin 2 -
864	75.5	5.8	1208	2	T27822	hypothetical prote	937	74	5.7	464	2	T32401	hypothetical prote
865	75.5	5.8	1372	2	A34157	insulin receptor p	938	74	5.7	470	2	D41977	retinoid receptor
866	75.5	5.8	1376	1	VGIHJ2	B2 glycoprotein p	939	74	5.7	477	1	JQ5089	endo-1,4-beta-xyla
867	75.5	5.8	1383	2	A36080	insulin receptor p	940	74	5.7	610	2	JC8056	halyase - Glycidu
868	75.5	5.8	1507	2	A40228	neurexin I-alpha p	941	74	5.7	640	2	T45924	protein kinase-lik
869	75.5	5.8	1530	2	I45944	neurexin I-alpha -	942	74	5.7	661	1	KFH013	coagulation factor
870	75	5.8	61	2	I46602	metallothionein -	943	74	5.7	689	2	T52060	protein MEDEA limp
871	75	5.8	75	2	S17156	metallothionein -	944	74	5.7	732	2	I52361	testicular metallo
872	75	5.8	118	2	JK0223	phospholipase A2 (945	74	5.7	748	2	S24134	endopeptidase 2 (E
873	75	5.8	118	2	G34860	phospholipase A2 (946	74	5.7	905	1	A27410	nucleotide diphosp
874	75	5.8	122	2	S46979	phospholipase A2 -	947	74	5.7	1014	2	T30545	major surface gly
875	75	5.8	176	2	T22110	hypothetical prote	948	74	5.7	1056	2	A53767	mucin WUCSB, trach
876	75	5.8	186	2	A45910	ultra-high-sulfur	949	74	5.7	1257	1	A41060	neural cell adhesi
877	75	5.8	297	2	S06267	B cell-associated	950	74	5.7	1361	2	S29998	surface protein -
878	75	5.8	305	2	A46476	int-l-like protein	951	74	5.7	2386	1	FNHU	fibronectin precu
879	75	5.8	360	2	S00834	trithorax homolog	952	73.5	5.7	146	2	S09415	proteinase inhibit
880	75	5.8	366	2	I53035	transmembrane prot	953	73.5	5.7	177	2	S37650	high-sulfur kerati
881	75	5.8	380	2	G01639	hypothetical prote	954	73.5	5.7	272	2	I48700	gene ox40 protein
882	75	5.8	383	2	T21946	hypothetical prote	955	73.5	5.7	325	2	B43692	T2 protein - myxom
883	75	5.8	463	1	A36479	milk fat globule m	956	73.5	5.7	326	1	GOVZML	T2 protein - myxom
884	75	5.8	474	2	S18452	variant surface gl	957	73.5	5.7	385	2	T22822	hypothetical prote
885	75	5.8	549	2	T17525	proline-rich prote	958	73.5	5.7	494	2	S57539	probable membrane
886	75	5.8	575	2	C88346	protein P42G4.3a l	959	73.5	5.7	538	2	E84863	hypothetical prote
887	75	5.8	576	2	T18067	hypothetical prote	960	73.5	5.7	710	2	T21339	hypothetical prote
888	75	5.8	584	1	C8H0A	complement C8 alph	961	73.5	5.7	987	2	A54092	protein-tyrosine k
889	75	5.8	585	2	S43572	C05B5.5 protein (c	962	73.5	5.7	1206	1	GVVURV	M polyprotein - Ri
890	75	5.8	585	2	E88571	protein C05B5.5 [i	963	73.5	5.7	1472	2	A84470	hypothetical prote
891	75	5.8	603	2	T22111	hypothetical prote	964	73.5	5.7	1566	2	T20058	hypothetical prote
892	75	5.8	706	2	S33761	transferrin precu	965	73.5	5.7	1914	2	T42635	tenascin Y precu
893	75	5.8	976	2	A36355	protein-tyrosine k	966	73	5.6	61	1	SMHUIB	metallothionein IE
894	75	5.8	984	1	A34076	protein-tyrosine k	967	73	5.6	61	1	SMHUIB	metallothionein 2
895	75	5.8	1025	1	A43526	complement C3d/Eps	968	73	5.6	119	1	PSNOAT	phospholipase A2 (
896	75	5.8	1362	2	A37474	surface glycoprote	969	73	5.6	122	2	S62780	phospholipase A2 (
897	75	5.8	1490	2	JC5145	DNA (cytosine-5)-	970	73	5.6	133	1	TIRZBR	trypsin inhibitor
898	75	5.8	1797	2	T21889	hypothetical prote	971	73	5.6	180	2	A45810	glycoprotein anti
899	75	5.8	1805	2	T21888	hypothetical prote	972	73	5.6	204	2	T08072	proteinase inhibit
900	75	5.8	2098	2	T18397	protein CTRP - mal	973	73	5.6	242	2	JC4360	riboflavin-binding
901	74.5	5.7	125	2	S65624	phospholipase A(2)	974	73	5.6	252	2	B88637	protein W09G12.4 l
902	74.5	5.7	138	1	PSRSB2	phospholipase A2 (975	73	5.6	310	2	G84809	hypothetical prote
903	74.5	5.7	145	2	T15608	hypothetical prote	976	73	5.6	377	2	T05354	hypothetical prote
904	74.5	5.7	251	2	B40369	folate-binding pro	977	73	5.6	470	2	S04801	exo-alpha-sialidase
905	74.5	5.7	292	2	T23966	hypothetical prote	978	73	5.6	579	2	A56740	sperm-egg recognit

979 73 5.6 597 2 S71352 metalloproteinase
980 73 5.6 669 2 S65551 factor H - bovine
981 73 5.6 687 1 B39045 protein-glutamine
982 73 5.6 730 2 H86295 hypothetical prote
983 73 5.6 885 1 A55453 nucleotide diphosp
984 73 5.6 1348 2 S27812 probable epidermal
985 73 5.6 1348 2 A43917 probable epidermal
986 73 5.6 2225 2 T26063 hypothetical prote
987 73 5.6 2265 1 FNBO fibronectin - bovl
988 72.5 5.6 72 2 S39418 metallothionein 10
989 72.5 5.6 119 1 PSB2H phospholipase A2 (
990 72.5 5.6 119 2 A34816 anticonagulant prot
991 72.5 5.6 136 2 S31695 alpha-1-thionin -
992 72.5 5.6 138 1 I51381 phospholipase A2 (l
993 72.5 5.6 138 1 PSR8BT phospholipase A2 (l
994 72.5 5.6 152 2 A32669 vasotocin 1 / neur
995 72.5 5.6 235 2 AEO877 endonuclease I [lm
996 72.5 5.6 247 1 TRDG trypsin (EC 3.4.21
997 72.5 5.6 263 1 C36938 complement control
998 72.5 5.6 263 2 T28450 hypothetical prote
999 72.5 5.6 264 2 T22380 hypothetical prote
1000 72.5 5.6 302 1 GEMSN osteonectin precur

ALIGNMENTS

RESULT 1
B48089 growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: B48089
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: B48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:Cross-references: UNIPROT:Q14393; GB:L13720; NID:9401766; PIDN:AAA58494.1; PID:9401767
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:41-92/Domain: Gla domain homology #status atypical <GLA>
F:120-153/Domain: EGF homology <EG1>
F:160-195/Domain: EGF homology <EG2>
F:201-236/Domain: EGF homology <EG3>
F:242-277/Domain: EGF homology <EG4>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 3e-88;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRYLDCKNGKSPYTKNSGFATCVQNLDPQCTNPDRKGTQACQDLGMGNFCLCKAGWG 60
DB 90 PRYLDCKNGKSPYTKNSGFATCVQNLDPQCTNPDRKGTQACQDLGMGNFCLCKAGWG 149
QY 61 GRLCDKDVNCSQENGCGCLQICHNKPGSFHCSHGFSLSGRTCCQIDECADSEACGE 120
DB 150 GRLCDKDVNCSQENGCGCLQICHNKPGSFHCSHGFSLSGRTCCQIDECADSEACGE 209
QY 121 ARCKNLPGSYCLDGEFGAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHDGRGGLK 180
DB 210 ARCKNLPGSYCLDGEFGAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHDGRGGLK 269
QY 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 270 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 316

RESULT 2
I55476 growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55476
R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.;
J. Biol. Chem. 270, 5702-5705, 1995
A:Title: Vascular smooth muscle cell-derived, Gla-containing growth-potentiating factor I
A:Reference number: I55476; MUID:95197586; PMID:7890695
A:Accession: I55476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-674 <REG>
A:Cross-references: UNIPROT:O63772; GB:D42148; NID:91526567; PIDN:BAA07719.1; PID:9893402
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:129-89/Domain: Gla domain homology <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 86.1%; Score 1117; DB 2; Length 674;
Best Local Similarity 82.8%; Pred. No. 5.1e-75;
Matches 188; Conservative 17; Mismatches 22; Indels 0; Gaps 0;
QY 1 PRYLDCKNGKSPYTKNSGFATCVQNLDPQCTNPDRKGTQACQDLGMGNFCLCKAGWG 60
DB 87 PRYQCEMKRYGRPEDKNPNFATCVKNLPDQCTNPDRKGTQACQDLGMGNFCLCKAGWG 146
QY 61 GRLCDKDVNCSQENGCGCLQICHNKPGSFHCSHGFSLSGRTCCQIDECADSEACGE 120
DB 147 GRLCDKDVNCSQENGCGCGVCHNKPGSFQACHSGLQSDNKSQDIDECTSDTCDG 206
QY 121 ARCKNLPGSYCLDGEFGAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHDGRGGLK 180
DB 207 ARCKNLPGSYCLDCKGVTYSSEKTCQDVDEQDCEQTCVNSPGSYTCHCNGRGLK 266
QY 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 267 LSPDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 3
A48089 growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: A48089; S37437
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of t
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: A48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:Cross-references: UNIPROT:O61592; GB:X59846; NID:9407060; PIDN:CAA42507.1; PID:9407061
A>Note: authors translated the codon CCC for residue 424 as Ile
C:Genetics:
A:Gene: gas6
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:38-89/Domain: Gla domain homology #status atypical <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

C;Complex: in plasma forms a complex with C4b binding protein

C;Function:
A;Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage dest
C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-41/Domain: propeptide #status predicted <PRO>
F;26-85/Domain: Gla domain homology <GLA>
F;42-676/Product: plasma protein S #status predicted <MAT>
F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG4>
F;315-667/Domain: sex hormone-binding globulin homology <SHB>
F;325-478/Domain: laminin G repeat homology <LGR>
F;47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2
F;111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;499,509,530/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 46.4%; Score 601.5; DB 1; Length 676;
Best Local Similarity 43.4%; Pred. No. 4.3e-37;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCINKY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFF 52
DB 83 PKYLCLGSRFQTLTAARQSTNAYPDLRSVCVNAIPDQCSPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGRRLCKDVNEC---SOENGGCLQICHNKPFGSHCSHGFSLSGRTGRTCODI 109
DB 143 CTCKPQWQKCFEDINECKDPNNGGCSQICDNTPGSYHSCNGFVWLSNKKDKDV 202
QY 110 DECA-DSEACGEARCNLPGSYSCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPISICGTAVCKNIPGDFECPEGYRYNLSKSCDIEDCSENNCAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMTCDILPCVPFSPVSKVSLYLGRMFSGTPVIRLRFK 223
DB 263 YTCYCDGKGFKLQADQKSCVSVCLPLNLDTKYELLYLAQFAGV-VLYLKER 316

RESULT 6
KXBS
plasma protein S precursor - bovine
N;Alternate names: vitamin K-dependent protein S
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Aug-1987 #sequence_revision K:PIDN:2940598
C;Accession: A24759; A23888
R;Dahlback, B.; Lundwall, A.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986
A;Title: Primary structure of bovine vitamin K-dependent protein S.
A;Reference number: A24759; MUID:86233400; KPID:2940598
A;Accession: A24759
A;Molecule type: mRNA
A;Residues: 1-675 <DAH>
A;Cross-references: UNIPROT:P07224; GB:M13044; NID:g163697; PIDN:AAA30757.1; PID:g163698
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Dahlback, B.; Lundwall, A.; Stenflo, J.
J. Biol. Chem. 261, 5111-5115, 1986
A;Title: Localization of thrombin cleavage sites in the amino-terminal region of bovine
A;Reference number: A23888; MUID:86158236; PMID:2937785
A;Accession: A23888
A;Molecule type: protein
A;Residues: 42-141 <DA2>
C;Complex: in plasma forms a complex with C4b binding protein

A;Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage dest
C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-41/Domain: propeptide #status predicted <PRO>

F;26-85/Domain: Gla domain homology <GLA>
F;42-675/Product: plasma protein S #status experimental <MAT>
F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG4>
F;315-666/Domain: sex hormone-binding globulin homology <SHB>
F;325-478/Domain: laminin G repeat homology <LGR>
F;47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2
F;111-112/Cleavage site: Arg-Ala (thrombin) #status experimental
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F;499/Binding site: carboxylate (Asn) (covalent) #status experimental
F;509/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 46.0%; Score 596.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 1e-36;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

QY 1 PRYLDCINKYSPYTKNSGFAT-----CVQNLDPQCTPNPCDRKGTQACQDLMGNFF 52
DB 83 PKYLCLGSRFAGLFTAAARLSTNAYPDLRSVCVNAISDQCNPLPCNEDGFMTCKDQATFT 142
QY 53 CLCKAGWGRRLCKDVNECSQE---NGGCLQICHNKPFGSHCSHGFSLSGRTGRTCODI 109
DB 143 CTCKSGWQKCESDINECKDPVNINGGCSQICENTPGSYHSCNGFVWLSNKKDKDV 202
QY 110 DECA-DSEACGEARCNLPGSYSCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECVLKPISICGTAVCKNIPGDFECCEAGYKYNPKSCDDVDECAENLCAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMTCDILPCVPFSPVSKVSLYLGRMFSGTPVIRLRFK 223
DB 263 YTCYCDGKGFKLQADQKSCAVPVCLPLDLDKNYELLYLAQFQGV-VLYLKER 316

RESULT 7
S53433
plasma protein S precursor, vitamin K dependent - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Aug-1995 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: S53433
R;Creengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A;Title: Identification of candidate residues for interaction of protein S with C4b bindi
A;Reference number: S53433; MUID:95134217; PMID:7832752
A;Accession: S53433
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-642 <GRE>
A;Cross-references: UNIPROT:Q29094; EMBL:L31379
A;Experimental source: tissue type liver
C;Genetics:
A;Gene: PROS
C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F;1-51/Domain: Gla domain homology (fragment) <GLA>
F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F;8-642/Product: plasma protein S #status predicted <MAT>
F;87-120/Domain: EGF homology <EG1>
F;127-165/Domain: EGF homology <EG2>
F;171-207/Domain: EGF homology <EG3>
F;213-248/Domain: EGF homology <EG4>
F;281-633/Domain: sex hormone-binding globulin homology <SHB>
F;291-444/Domain: laminin G repeat homology <LGR>

Query Match 45.8%; Score 593.5; DB 2; Length 642;
Best Local Similarity 43.4%; Pred. No. 1.6e-36;
Matches 102; Conservative 40; Mismatches 80; Indels 13; Gaps 4;
QY 1 PRYLDCINKYSPYTKNSGFAT-----CVQNLDPQCTPNPCDRKGTQACQDLMGNFF 52

Db 49 PAYLACGSGFRAGLFTARLSTNAYPDLRSVCNVAIPDQCNPPLPCNEDGFTWCKDQAMFT 108
Qy 53 CLCKAGGRLCDKDVNECSQE---NGGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 109 CICKSGWEGEKELDINECKDPPNINGGCSQICDNTFGSYHCSKSGFIMLSNKKDCKDV 168
Qy 110 DECA-DSEACGEARCKNLPGSYSCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 169 DECVKPSICDVAACKNIPGDFECCEPGYRNPFTLKSCEVDVDECSNMCAQLCVNYPGG 228
Qy 169 YTCDCGRGGLKLSQDMTCDILPCVPPFSVAKSVKSLYLGRMFSGTPVIRLRFK 223
Db 229 YSCYCDGKRGFKLAQDKSCFAVPVCLPLDKNLYELLALAEQFVG-VLYLRFK 282

RESULT 8
KXRTS
Plasma protein S precursor - mouse
N/Alternate names: vitamin K-dependent glycoprotein S
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
A/Accession: S43504; 159616; S35962
R/Chu, M.D.; Sun, J.; Bird, P
Biochim. Biophys. Acta 1217, 325-328, 1994
A/Title: Cloning and sequencing of a cDNA encoding the murine vitamin K-dependent protein
A/Reference number: S43504; MUID:94198297; PMID:8148380
A/Accession: S43504
A/Molecule type: mRNA
A/Residues: 1-675 <CHU>
A/Cross-references: UNIPROT:Q08761; EMBL:Z25469; NID:G396426; PIDN:CAA80961.1; PID:G3964
R/Lu, D.; Schmidt, D.K.; Long, G.L.
Thromb. Res. 74, 135-142, 1994
A/Title: Structure of mouse protein S as determined by PCR amplification and DNA sequencing
A/Reference number: 159616; MUID:94302659; PMID:8029814
A/Accession: 159616
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 33-492, 'L', 494-675 <RES>
A/Cross-references: GB:127439; NID:G487866; PIDN:AAA40006.1; PID:G487867
C/Complex: in plasma forms a complex with C4b binding protein
C/Function:
A/Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage site
C/Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C/Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-41/Domain: propeptide #status predicted <PRO>
F:26-85/Domain: Gla domain homology <GLA>
F:42-675/Product: plasma protein S #status predicted <MAT>
F:121-154/Domain: EGF homology <EG1>
F:161-199/Domain: EGF homology <EG2>
F:205-241/Domain: EGF homology <EG3>
F:247-282/Domain: EGF homology <EG4>
F:315-666/Domain: sex hormone-binding globulin homology <SHB>
F:325-478/Domain: laminin G repeat homology <LGR>
F:47, 48, 55, 57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:58-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241, 2
F:111-112/cleavage site: Arg-Ser (thrombin) #status predicted
F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:137, 219, 258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:479, 509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.6%; Score 591.5; DB 1; Length 675;
Best Local Similarity 44.7%; Pred. No. 2.3e-36;
Matches 105; Conservative 35; Mismatches 82; Indels 13; Gaps 5;

Qy 1 PRYLDICNKY--GSFYTNSG-----FATCVQNLPCQCTPNPCDRKGTAQCQDLMGNFF 52
Db 83 PKYLGLGAFVSGFHAARQSANAYPDLRSVCVAISDQCDIPICNEDGYLACDQGAFT 142

Qy 53 CLCKAGGRLCDKDVNECSQE---SQENGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 143 CFCKPGQGRQRCQYDVNECKDPSNVNGGCSQICDNTFGSYHCSKRGFAMLPNKKDCKDL 202

Qy 110 DECA-DSEACGEARCKNLPGSYSCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECALKPSCGTAVCKNIPGDFECCEPGDYRYPSSKSKXDVDECSNMCAQLCVNYPGG 262
Qy 169 YTCDCGRGGLKLSQDMTCDILPCVPPFSVAKSVKSLYLGRMFSGTPVIRLRFK 223
Db 263 YSCYCDGKRGFKLAQDKSCFAVPVCLPLDKNLYELLALAEQFVG-VLYLRFK 316

RESULT 9
S38819
Plasma protein S - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 18-Feb-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
A/Accession: S38819; S37238
R/He, X.; Dahlbaeck, B.
Eur. J. Biochem. 217, 857-865, 1993
A/Title: Molecular cloning, expression and functional characterization of rabbit anticoag
A/Reference number: S38819; MUID:94039141; PMID:8223642
A/Accession: S38819
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-646 <HEX>
A/Cross-references: UNIPROT:P98118; EMBL:Z26485
R/He, X.; Dahlboock, B.
submitted to the EMBL Data Library, September 1993
A/Description: Molecular Cloning and Expression of Rabbit Anticoagulant Vitamin K-depende
A/Reference number: S37238
A/Accession: S37238
A/Molecule type: mRNA
A/Residues: 1-502, 'L', 504-646 <HE2>
A/Cross-references: EMBL:Z26485; NID:G403306; PIDN:CAA81259.1; PID:G403307
C/Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:1-56/Domain: Gla domain homology (fragment) <GLA>
F:92-125/Domain: EGF homology <EG1>
F:132-170/Domain: EGF homology <EG2>
F:176-212/Domain: EGF homology <EG3>
F:218-253/Domain: EGF homology <EG4>
F:286-637/Domain: sex hormone-binding globulin homology <SHB>
F:296-449/Domain: laminin G repeat homology <LGR>

Query Match 45.2%; Score 586.5; DB 2; Length 646;
Best Local Similarity 43.2%; Pred. No. 5.3e-36;
Matches 101; Conservative 39; Mismatches 81; Indels 13; Gaps 5;

Qy 1 PRYLDICNKYGSFY---TKNSG-----FATCVQNLPCQCTPNPCDRKGTAQCQDLMGNFF 52
Db 54 PKYLGLGSGFRAKLTATRRSANGYPDLRSVCNVAIPDQCNPPLPCSEEGYLNCKDQATFT 113

Qy 53 CLCKAGGRLCDKDVNECSQE---NGGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 114 CICKPGWQGEKCIDINECKDPTNINGGCSQICDNTAGSYHCSKSGFVLANEKCKDM 173

Qy 110 DECA-DSEACGEARCKNLPGSYSCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 174 DECVKPSVCGTAVCKNIPGDFECCEPGYRNPFTAKSCDIDECSENMAQLCVNYPGG 233

Qy 169 YTCDCGRGGLKLSQDMTCDILPCVPPFSVAKSVKSLYLGRMFSGTPVIRLRFK 222
Db 234 YSCYCDGKRGFKLAQDKSCFAVPVCLPLDKNLYELLALAEQFVG-VLYLRFK 286

RESULT 10
KXRTS
Plasma protein S precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
A/Accession: J45180
R/Yasuda, F.; Hayashi, T.; Tanitame, K.; Nishioaka, J.; Suzuki, K.
J. Biochem. 117, 374-383, 1995
A/Title: Molecular cloning and functional characterization of rat plasma protein S.
A/Reference number: J45180; MUID:95332263; PMID:7608128

A;Accession: J04180
A:Molecule type: mRNA
A;Residues: 1-675 <YAS>
A;Cross-references: UNIPROT:P53813; GB:S78744; NID:G1041903; PIDN:AAC60704.1; PID:gl0419
C;Comment: This protein is a vitamin K-dependent plasma glycoprotein that has an anticoagulation of coagulation factors Va and VIIIa. This protein also binds to factor Va and C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat homology; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carboxyl; 1-24/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-41/Domain: propeptide #status predicted <PRO>
F;42-675/Domain: Gla domain homology <GLA>
F;88-116/Domain: thrombin-sensitive #status predicted <THS>
F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG4>
F;315-478/Domain: sex hormone-binding globulin homology <SHB>
F;325-478/Domain: laminin G repeat homology <LGR>
F;47-48, 55, 57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <G>
F;58-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241, 247-258/Modified site: Arg-Ser (thrombin) #status predicted <S>
F;111-112/Cleavage site: Arg-Ser (thrombin) #status predicted <S>
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted <A>
F;177, 219, 258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted <A>
F;499, 509/Binding site: carboxylate (Asn) (covalent) #status predicted <A>

Query Match 45.1%; Score 585.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 6.5e-36;
Matches 101; Conservative 41; Mismatches 80; Indels 13; Gaps 5;

QY 1 PRYLDCINIKY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLGLGAFRCVAFSAQAQANAYPDLRSCVNAIPDQCDPFCNEDGYLSCDKGGQAT 142

QY 53 CLKAGGGRCLDKDVNEC---SQENGGLQICHNPKGSHFCHSGHSGFELSSDGRTCQDI 109
Db 143 CICKGQWQDKQCFDINECKDPNINNGGCSQTCNDTPGSHVCSCKIGFAMLTAKKCKDV 202

QY 110 DECA-DSEACGEARCNLPSCVSLCDEGFAYSSQKACRDVDECLQGRCEQCVNPSGS 168
Db 203 DECLSPKPSVCGTAVCKNIPGDFECPNGRYDPSKSKVDCESENTCAQLCVNYPGG 262

QY 169 YTCHCDGRGLCLSQMDTCDILPCVPFSPVAKSVKSLYLGRMFSGTPVIRLRFK 223
Db 263 YSCYCDGKGFKLAQQRCEGIPVCLSLDLDRNYELLYLAEQFAGV-VLYLKR 316

RESULT 11
S78040
fibulin, splice form C precursor - mouse
N;Alternate names: basement-membrane protein BM-90
C;Species: Mus musculus (house mouse)
C;Date: 24-Jul-1998 #sequence revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S78040; S78560; S36440
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A;Reference number: S34968; MUID:93358897; PMID:8354280
A;Molecule type: mRNA
A;Residues: 1-685 <PAN>
A;Cross-references: UNIPROT:Q08879; EMBL:X70854
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-depe
A;Reference number: S36440
A;Accession: S78560
A;Molecule type: mRNA
A;Residues: 1-685 <CHU>
A;Cross-references: UNIPROT:Q08879; EMBL:X70854
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep
A;Reference number: S36440
A;Accession: S78560
A;Molecule type: mRNA
A;Residues: 1-685 <CHU>
A;Cross-references: EMBL:X70854
C;Genetics:
C;Superfamily: fibulin-1; EGF homology

C;Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-685/Product: fibulin, splice form C #status predicted <MAT>
F;98,537,541/Binding site: carboxylate (Asn) (covalent) #status predicted <A>

Query Match 27.9%; Score 362; DB 2; Length 685;
Best Local Similarity 38.2%; Pred. No. 1.8e-19;
Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 6 CINKYGSPTKNSGFATCVQNLDP-----DQCTP--NPCDRKGTQACQ 45
Db 327 CINTEGS-----YTCQKNVPCNGRGYHLNEEGTRCVDVDECAPPAEPCG-KG-HHCL 376

QY 46 DLMGNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNPKGSHFCHSGHGFELS 100
Db 377 NSPGSFRCCKAGFYFDIGISRTC-VDINECQYPRGLGHKCENTPGSFHSCSAGFRLS 435

QY 101 SDGRTQDIDECADSEACGEARCNLPSCVSLCDEGFAYSSQK-KACRDVDECLQGR-- 157
Db 436 VDRSCEDVNECLNPFCSQKQ--CANVGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 493

QY 158 --CEQVCVNSPGSYTCHCDGRGLKLSQMDTCDILPCV 195
Db 494 HTCSYRCINIPGSHFCHSGHSGFELSSDGRTCQDI 532

RESULT 12
S34968
fibulin, splice form D precursor - mouse
N;Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S34968; S36441; S13814
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A;Reference number: S34968; MUID:93358897; PMID:8354280
A;Accession: S34968
A;Molecule type: mRNA
A;Residues: 1-705 <PAN>
A;Cross-references: UNIPROT:Q08879
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-depe
A;Reference number: S36440
A;Accession: S36441
A;Molecule type: mRNA
A;Residues: 1-39, 'P', 41-705 <PAN>
A;Cross-references: EMBL:X70854; NID:G396820; PIDN:CAA50207.1; PID:G396821
A;Experimental source: cell-line F9 teratocarcinoma
R;Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.
Eur. J. Biochem. 193, 651-659, 1990
A;Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared t
A;Reference number: S13814; MUID:91065369; PMID:2249686
A;Accession: S13814
A;Molecule type: protein
A;Residues: 28:31-49, 'X', 51-53, 'XX', 110-117, 231-240, 'X', 242-243, 339-362, 'S', 364-387, 434-4
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-705/Product: fibulin, splice form D #status predicted <MAT>
F;98,537,541/Binding site: carboxylate (Asn) (covalent) #status predicted <A>

Query Match 27.9%; Score 362; DB 2; Length 705;
Best Local Similarity 38.2%; Pred. No. 1.9e-19;
Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 6 CINKYGSPTKNSGFATCVQNLDP-----DQCTP--NPCDRKGTQACQ 45
Db 327 CINTEGS-----YTCQKNVPCNGRGYHLNEEGTRCVDVDECAPPAEPCG-KG-HHCL 376

QY 46 DLMGNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNPKGSHFCHSGHGFELS 100

J. Biol. Chem. 270, 1798-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene
A;Reference number: A55624; MUID:95130561; PMID:7829516
A;Accession: A55624
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <YIN>
A;Cross-references: UNIPROT:Q61554; GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
C;Genetics:
A;Gene: Fbn-1
C;Superfamily: fibrillin; EGF homology
F;1201-1236/Domain: EGF homology <EGF>

Query Match 26.6%; Score 345; DB 2; Length 2871;
Best Local Similarity 38.6%; Pred. No. 1e-17;
Matches 71; Conservative 23; Mismatches 68; Indels 22; Gaps 6;

Qy 21 ATCVQNLDPDQCTPNPCDRKGTQACODLMGNFFCLCKAGW---GGRLCDKDVNECSQENG 77
Db 1151 SACIDINECELSANLCPH---GRCVNLIGKYQCACNPGYHPTHDRFLFCVDIDBCSIMNG 1207
Qy 78 CLOICHNKPSPHCSHSGFELSDGRTCODIDECADY-EACGEARCKNLPGSYSLCLDE 136
Db 1208 CETFTNSDGSYSCSQPGFALPDQRSCDTIDCEDPNICDGGQCTNIPGEYRCLCYD 1267
Qy 137 GFAYSSQEKACRDVDE-----CLOGRCBOVCVNSPGSYTCHCD---GRGGLKLSQDM 185
Db 1268 GFWASEDMKTCVDVNECDLNPNICLSGTCE---NTKGSFICHCDMGYSKGKTKCTDI 1323
Qy 186 DTCE 189
Db 1324 NECE 1327

RESULT 16
T43210
fibulin-1D precursor - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Apr-2004
C;Accession: T43210
R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, June 1998
A;Description: Identification of chicken and C. elegans fibulin-1 homologs and characterization
A;Reference number: 222337
A;Accession: T43210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-589 <BAR>
A;Cross-references: EMBL:AF070477; PIDN:AAC24035.1
C;Genetics:
A;Note: intron positions not resolved (incomplete sequence)

Query Match 26.6%; Score 344.5; DB 2; Length 589;
Best Local Similarity 34.2%; Pred. No. 3.1e-18;
Matches 77; Conservative 26; Mismatches 89; Indels 33; Gaps 8;

Qy 5 DCINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
Db 219 ECVNTPGSFRCCQKGNLCAHYEVNGATGFCED--VNECQQGVC---GSMCEINLPGT 273
Qy 53 CLCKAGW---GGRLCDKDVNECSQENGGLQI---CHNKPSPHCSHSGFELSDGRT 105
Db 274 CKCGPGYEFNDKKRCE-DVDECIKPAHVCDLSAECINTIGSFCECKKPGQLASDGR 332
Qy 106 CQIDECADSEACGEARCKNLPGSYSLCLDEGFAYSSQEKACRDVDECL-----QGRCE 159
Db 333 CEDVNECTTGIAACEQKCNIPGSYQICDRGFALPGDGTCKCEDIDECISWAGSNDLCM 392
Qy 160 QVCVNSPGSYTCHCDRGGLKLSQDMTDCEDILPCVPFVSVAHSV 204
Db 393 GGCINTKGSYLCOCP--PGYKIQPDGRTCVDDDECAMGECAGSDK 435

RESULT 17
T42760
fibulin, splice form D precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42760
R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998
A;Description: Isolation of chicken and nematode fibulin-1 homologs and characterization
A;Reference number: 222267
A;Accession: T42760
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-689 <BAR>
A;Cross-references: UNIPROT:O77469; EMBL:AF051401; PIDN:AAC28321.1
C;Genetics:
A;Note: FBLN1

Query Match 26.6%; Score 344.5; DB 2; Length 689;
Best Local Similarity 34.2%; Pred. No. 3.5e-18;
Matches 77; Conservative 26; Mismatches 89; Indels 33; Gaps 8;

Qy 5 DCINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
Db 319 ECVNTPGSFRCCQKGNLCAHYEVNGATGFCED--VNECQQGVC---GSMCEINLPGT 373
Qy 53 CLCKAGW---GGRLCDKDVNECSQENGGLQI---CHNKPSPHCSHSGFELSDGRT 105
Db 374 CKCGPGYEFNDKKRCE-DVDECIKPAHVCDLSAECINTIGSFCECKKPGQLASDGR 432
Qy 106 CQIDECADSEACGEARCKNLPGSYSLCLDEGFAYSSQEKACRDVDECL-----QGRCE 159
Db 433 CEDVNECTTGIAACEQKCNIPGSYQICDRGFALPGDGTCKCEDIDECISWAGSNDLCM 492
Qy 160 QVCVNSPGSYTCHCDRGGLKLSQDMTDCEDILPCVPFVSVAHSV 204
Db 493 GGCINTKGSYLCOCP--PGYKIQPDGRTCVDDDECAMGECAGSDK 535

RESULT 18
T42990
fibulin 1, splice form C precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42990
R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998
A;Description: Isolation of chicken and nematode fibulin-1 homologs and characterization
A;Reference number: 222267
A;Accession: T42990
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-712 <BAR>
A;Cross-references: UNIPROT:O77469; EMBL:AF051402; PIDN:AAC28322.1
C;Genetics:
A;Gene: FBLN1
C;Keywords: alternative splicing; basement membrane; extracellular matrix

Query Match 26.6%; Score 344.5; DB 2; Length 712;
Best Local Similarity 34.2%; Pred. No. 3.6e-18;
Matches 77; Conservative 26; Mismatches 89; Indels 33; Gaps 8;

Qy 5 DCINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
Db 319 ECVNTPGSFRCCQKGNLCAHYEVNGATGFCED--VNECQQGVC---GSMCEINLPGT 373
Qy 53 CLCKAGW---GGRLCDKDVNECSQENGGLQI---CHNKPSPHCSHSGFELSDGRT 105
Db 374 CKCGPGYEFNDKKRCE-DVDECIKPAHVCDLSAECINTIGSFCECKKPGQLASDGR 432
Qy 106 CQIDECADSEACGEARCKNLPGSYSLCLDEGFAYSSQEKACRDVDECL-----QGRCE 159
Db 433 CEDVNECTTGIAACEQKCNIPGSYQICDRGFALPGDGTCKCEDIDECISWAGSNDLCM 492

Db 325 CINTGSG-----YTCQKNVPCGRGYHLNBEGTRCVDVDECAPPAEPCG-KG-HRCV 374

QY 46 DLGNPFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSPHCSCHGSFELS 100

Db 375 NSPGSFCECKTYGFDIGSRMC-VDVNECQRPGLRGHKCENTLGSYLCSVSGVGRUS 433

QY 101 SDGRTQDIDECADSEACGEARCKNLPFGSYCLCDGFAFYSOQ-KACRDVDECLQGR-- 157

Db 434 VDRSCEDINECSSSPCSQSE--CANVVGSYQCYCRRGYQLSDVDGVTCEIDECALPTG 491

QY 158 --CEQVNVNPGSYTHCDGRGGLKLSQDMTDCEDILPCV 195

Db 492 HICSYRCINIPGSGFQSCPS-SGYRLAPNRCNQDIDECV 530

RESULT 22

A49457

fibulin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: A49457; S74095

R;Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Paessler, R.; Timpl, R.; Chu, M.L.

J. Cell Biol. 123, 1269-1277, 1993

A:Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with a fibulin-like domain

A:Reference number: A49457; MUID:94064787; PMID:8245130

A:Accession: A49457

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1221 <PAN>

A:Cross-references: UNIPROT:P37889; GB:X75285; NID:9437046; PIDN:CAA53040.1; PID:9437047

R;Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases

A:Reference number: S74094; MUID:96439073; PMID:8841408

A:Accession: S74095

A:Molecule type: protein

A:Residues: 236-238, 'X', 346-361, 'L', 346-361, 405-426, 566-568, 'EM', 569-589

C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer

F;942-978/Domain: EGF homology <EGF>

Query Match 26.1%; Score 339; DB 2; Length 1221;

Best Local Similarity 36.6%; Pred. No. 1.4e-17;

Matches 78; Conservative 27; Mismatches 68; Indels 40; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLPDQCTPNPCD-----RKGT-QACQDLM 48

Db 864 CINTVGSYTCQRNPLVGRGYHANESEGCVD-----VNECETGVHRCGEGQLCYNLP 916

QY 49 GNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSPHCSCHGSFELS 103

Db 917 GSYRCDCKPGFQDAFGRTG-IDVNECWSPGLCQHTCENTPGSYRSCNAGFLLAAG 975

QY 104 RTCQDIDECADSEACGEARCKNLPFGSYCLCDGFAFYSOQKACRDVDECLQGR---CEQ 160

Db 976 KHCEDVNEC-ETRRCSQ-ECANIYGSQCYCRQGYQLAEDGHTCTDIDECACGAGILCTF 1033

QY 161 VCVNSPGSYTHCDGRGGLKLS-----QDMTC 188

Db 1034 RCNVNPGSYQCACPQEGYTMNANGRSCKDLDEC 1066

RESULT 23

A55184

fibulin-2 precursor - human

N;Alternate names: protein DKFP2p56A1519.1

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C:Accession: A55184; T08744

R;Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.

Genomics 22, 425-430, 1994

A:Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping of the gene

A:Reference number: A55184; MUID:95104855; PMID:7806230

A:Accession: A55184

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1184 <ZHA>

A:Cross-references: UNIPROT:P98095; GB:X82494; NID:9575232; PIDN:CAA57876.1; PID:9575233

R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z16471

A:Accession: T08744

A:Molecule type: mRNA

A:Residues: 656-719, 'QDELMGADCSRQFCVNTLGSFYCVNHTVLCADGYILNAHRKCD', 720-853, 'T', 855-111

A:Cross-references: EMBL:AL050095

A:Experimental source: adult uterus; clone DKFP2p56A1519

C:Genetics:

A:Gene: GDB:FBLN2

A:Cross-references: GDB:293037; OMIM:135821

A:Map position: 3p25-3p24

A>Note: DKFP2p56A1519.1

C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C:Keywords: alternative splicing; extracellular matrix

F;1-27/Domain: signal sequence #status predicted <SIG>

F;28-1184/Product: fibulin-2 protein #status predicted <MAT>

F;905-941/Domain: EGF homology <EGF>

Query Match 26.0%; Score 337; DB 2; Length 1184;

Best Local Similarity 36.4%; Pred. No. 1.9e-17;

Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLPDQCTPNPCD-----RKGT-QACQDLM 48

Db 827 CINTVGSYTCQRNPLICARGYHASDDGAKCD-----VNSCETGVHRCGEGQVCHNLP 879

QY 49 GNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSPHCSCHGSFELS 103

Db 880 GSYRCDCKAGFQDAFGRC-IDVNECWSPGLCQHTCENTLGSYRSCNAGFLLAAG 938

QY 104 RTCQDIDECADSEACGEARCKNLPFGSYCLCDGFAFYSOQKACRDVDECLQGR---CEQ 160

Db 939 KHCEDVNEC-BAQRCSQ-ECANIYGSQCYCRQGYQLAEDGHTCTDIDECACGAGILCTF 996

QY 161 VCVNSPGSYTHCDGRGGLKLSQDMTDCEDILPC 194

Db 997 RCLNVPGSYQCACPQEGYTMNANGRSCKDVDEC 1029

RESULT 24

A54105

fibillin-2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C:Accession: A54105; S17063; S31101

R;Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, B.C.; Sanguinetti, C.; Bonadio, J.; Mecham, F.

J. Cell Biol. 124, 855-863, 1994

A:Title: Structure and expression of fibillin-2, a novel microfibrillar component preferentially expressed in bone

A:Reference number: A54105; MUID:94165150; PMID:8120105

A:Accession: A54105

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2918 <ZHA>

A:Cross-references: UNIPROT:P35556; GB:U03272

R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.; Nature 352, 330-334, 1991

A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different genes on chromosome 15

A:Reference number: S17062; MUID:91304567; PMID:1852206

A:Accession: S17063

A:Molecule type: mRNA

A:Residues: 752-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 1928 <LEE>

A:Cross-references: EMBL:X62009

R;Milewicz, D.M.

submitted to the EMBL Data Library, December 1992

A:Reference number: S31101

A:Accession: S31101

A:Molecule type: mRNA

A;Residues: 752-1407,'R',1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A;Cross-references: EMBL:X62009
C;Genetics:
A;Gene: GDB:FBN2
A;Cross-references: GDB:128122; OMIM:121050
A;Map position: 5q23-5q31
C;Superfamily: fibrillin; EGF homology
C;Keywords: extracellular protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-2918/Product: fibrillin-2 #status predicted <MAT>
F;1245-1280/Domain: EGF homology <EGF1>
F;1970-2013/Domain: EGF homology <EGF>
Query Match 25.6%; Score 331.5; DB 2; Length 2918;
Best Local Similarity 35.4%; Pred. No. 1e-16;
Matches 75; Conservative 32; Mismatches 76; Indels 29; Gaps 12;
QY 5 DCINKYGS-----PYTKNSGFATCVQNLDPDOCT--PNPCDRKGTQACQDLGMNFFCLC 55
Db 1339 ECENTKGSFICHQGLSVKVGKGTGCTD--VDECEIAGHNCMDHA--SCNIFGSPFKCSC 1394
QY 56 KAGH-GGRLCDKDVNECSQENGGL--QICHNKPFGSCHSGFELSSDGRTCQDIDEC 112
Db 1395 REGWIGNGIKCIDLDECSNGTHQCSINAQCWNTPGSYRCACSEGF--TGDGFTCSVDDEC 1452
QY 113 ADS-EAGGEARCKNLPQSGYSCLDDEGFAYSSQKACRDVDEC-LQGRG-EQVGVNPSGYS 169
Db 1453 AENINLCNGCQNLVPGAYRCECEMGFTPADSRSCQDIDECFQNICVSGTGNLPGMF 1512
QY 170 TCHCDGRGGLKLSQ-----DMDTCTDILPCV 195
Db 1513 HCICD--DGYELDRTGNGCTDIDECADPINC 1542
RESULT 25
A35626
transforming growth factor beta-1-binding protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
C;Accession: A35626
R;Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claessens
Cell 61, 1051-1061, 1990
A;Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1
A;Reference number: A35626; MUID:90275601; PMID:2350783
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1394 <KAN>
A;Cross-references: UNIPROT:P22064; GB:M34057; NID:g339547; PIDN:AAA61160.1; PID:g339548
C;Keywords: alternative splicing
F;750-791/Domain: EGF homology <EGF>
Query Match 25.5%; Score 330.5; DB 2; Length 1394;
Best Local Similarity 31.3%; Pred. No. 6.6e-17;
Matches 79; Conservative 33; Mismatches 77; Indels 63; Gaps 11;
QY 6 CINKYGS-----PYTKNSGF-----ATCVQNLDPQC--TPNPCDRKGTQACQDLGMNFFCLCK 56
Db 686 CVNPSGYSQYQVPCTE--GFRGWNQCLD--VDECLEPNCV---ANGDCSNLEGSYNCSCH 738
QY 57 AGNGRLCD-----KDVNECSQENGGLQICHNKPFGSCHSGFELSSDGRTCQDIDEC 112
Db 739 KGY-TRTPDHKCRDIDECQOQGLCNVNGQCNTGSGFRCTCGQYQLSAAKQDCEIDEC 797
QY 113 ADSEAGGEARCKNLPQSGYSCLDDEGFAYSSQKACRDVDECLOGR--CEQ--VCVNPSGYS 169
Db 798 QHRHLCAHQCRNTEGFSQCVQDQGYRASGLGDHCEIDNECLDEKSVQCGDCINTAGSY 857
QY 170 TC-----HCDGRGGLKLSQDMTDCED 190
Db 858 DCTCPDGFQLDNKTCCODINECEHPGLCGPQGECLNTEGFSFHCVCQCGFSISADGRTCED 917
QY 191 ILPCVFPVSAKS 202

Db 918 IDECVNNTVCDSS 929
RESULT 26
A57278
fibrillin-2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57278
R;Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A;Title: Developmental expression of fibrillin genes suggests heterogeneity of extracellular
A;Reference number: A57278; MUID:95263670; PMID:7744963
A;Accession: A57278
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2907 <ZHA>
A;Cross-references: UNIPROT:Q61555; GB:L39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
C;Superfamily: fibrillin; EGF homology
F;1239-1274/Domain: EGF homology <EGF1>
F;2488-2523/Domain: EGF homology <EGF>
Query Match 25.2%; Score 326.5; DB 2; Length 2907;
Best Local Similarity 31.7%; Pred. No. 2.4e-16;
Matches 80; Conservative 31; Mismatches 90; Indels 51; Gaps 10;
QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMNFFCLCKAG 58
Db 1167 CVNTEGFSQDCPLGHLSPSREDVCVDINECSLSNLC--RNG--KCVNMGTYQCCSNPG 1223
QY 59 WGG---RLCDKDVNECSQENGGLQICHNKPFGSCHSGFELSSDGRTCQDIDECADS 115
Db 1224 YQATPDROGCTDIDECIMNNGGCDTQCTNSGSEYSCSEGVALMPDGRSCADIDECENN 1283
QY 116 -EAGGEARCKNLPQSGYSCLDDEGFAYSSQKACRDVDE-----CLOGRCEQVCVNSPG 167
Db 1284 PDICDGGQCTNIPGEYRCCLCYDFWASMDMKTCTIDVNECDLNPNCIMFGECE-----NTKG 1339
QY 168 SYTCHCDGRGGLKLSQDMTDCEDILPC-----VPFS-----VAKSV 203
Db 1340 SFICHG--QLGYSYKVGKTTGCTDDECEIGAHCMDHASCNVNPGSFKSCREGWVGNGI 1397
QY 204 KSLYLGRMFSGT 215
Db 1398 KCIDLDECANGT 1409
RESULT 27
I38449
extracellular protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38449
R;Jeecka-Czernik, B.; Lumpkin, C.K.
Mol. Cell. Biol. 15, 120-128, 1995
A;Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts
A;Reference number: I38449; MUID:95097983; PMID:7799918
A;Accession: I38449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C;Genetics:
A;Gene: S1-5
Query Match 24.7%; Score 321; DB 2; Length 387;
Best Local Similarity 38.2%; Pred. No. 1.2e-16;
Matches 65; Conservative 30; Mismatches 65; Indels 10; Gaps 7;
QY 29 DQCTPNPCDRKGTQACQDLGMNFFCLCKAG--GGRLCDKDVNECSQENGGLQICHNKP 86
Db 69 DECTAGTHNCRADQVCINLRGSPACQCPGYQKRQGC--VDIDECTIP--PYHQRCVNTP 126

QY 87 GSFHCSHSGFELSSDGRTCQDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKA 146
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 127 GSFYCCQSPGFQLAANNYTCVDINECDASNQCAQ-QCYNILGSFICQCNQGYELSSDRLN 185
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 147 CRDVECLQGR--CEQVCNPSGYSYTHCDGRGGLKLSQDMTCEIDILPC 194
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 186 CEDIDECRTSSYLQYQCYNPEKFKSCMCP--QGYQVVRSR-TCQDINEC 232
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
RESULT 28
A55494
latent transforming growth factor-beta-binding protein - human
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55494
R:Moren, A.; Olofsson, A.; Stenman, G.; Sahlin, P.; Kanazaki, T.; Claesson-Welsh, L.; ten
J. Biol. Chem. 269, 32469-32478, 1994
A:Title: Identification and characterization of LTBP-2, a novel latent transforming grow
A:Reference number: A55494; MUID:95096101; PMID:7798248
A:Accession: A55494
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1820 <MOR>
A:Cross-references: UNIPROT:Q14767; GB:Z37976
C:Genetics:
A:Gene: GDB:LTBP2
A:Cross-references: GDB:568901
A:Map position: lippter-llqter
F:1222-1257/Domain: EGF homology <EGF>
F:1525-1565/Domain: EGF homology <EGF1>
Query Match 24.7%; Score 320.5; DB 2; Length 1820;
Best Local Similarity 27.0%; Pred. No. 4.5e-16;
Matches 81; Conservative 35; Mismatches 67; Indels 117; Gaps 13;
QY 7 INKYGSPYTKNSGFATCVONLPD-----QCTNPNCDRKGTOA 43
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 845 IDRCAGATNVCPGTCV-NLPDGYRCVSPGYQLHPSQAYCTDDNECLRDPQCGK--R 901
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 44 CQDLGNFFCLCKAGW-----GRL-----CD----- 65
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 902 CINRVGSYSCFCVPGYTLATSGATQBCDINECEQPGVCSGGQCTNTEGSHCECDQGYI 961
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 66 -----KDVNECSQ-----ENGSLQI----- 81
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 962 MVRKHQCQDINECRHFGTCDGRKVNPSGYTCLACEBGRGSGSCVDVNECLTPGVCA 1021
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 82 ---CHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGEARCKNLPGSYSLCDEG 137
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 1022 HGKCTNLGSGFRCSCEQGYEVTSDEKGCQDVDECASRASCPGLCLNTEGSPFACACENG 1081
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 138 FAYSSQEKACRDVDEC-LOGRCEQ-QVCNPSGYSYTC-HCDGRGGLKLSQDMTCEIDILPC 194
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 1082 YWNVEDGTACEDLDECAFPQGVCPGVCYTNTAGSFCKDCD--GGYRPSPLGSDCEDVDREC 1139
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
RESULT 29
JC5621
epidermal growth factor-like protein, T16 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: JC5621
R:Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, S.
Biochem. Biophys. Res. Commun. 237, 245-250, 1997
A:Title: Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-li
A:Reference number: JC5621; MUID:97415782; PMID:9268694
A:Accession: JC5621
A:Molecule type: mRNA
A:Residues: 1-493 <OZA>
A:Cross-references: UNIPROT:O35568; DDBJ:D89730; NID:92429082; PIDN:BAA22265.1; PID:d102
C:Comment: This protein plays a role in the regulation of cell growth by interacting wit
C:Keywords: glycoprotein

F:1-17/Domain: signal sequence #status predicted <SIG>
F:28-70,158-199,200-237,238-277,278-316,319-359/Region: epidermal growth factor-like rep
F:249/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 24.7%; Score 320; DB 2; Length 493;
Best Local Similarity 38.8%; Pred. No. 1.7e-16;
Matches 66; Conservative 30; Mismatches 64; Indels 10; Gaps 7;
QY 29 DOCTNPNCDRKGTOACODLMGNFFCLCKAGW--GGRLCDKDVNECSQENGGLQICHNKP 86
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 175 DECTSGTNCRLDQVCINLRGFTCHCLPGYKRGECQ-QVIDECSVP-PYCHQCVNTP 232
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 87 GSFHCSHSGFELSSDGRTCQDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKA 146
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 233 GSFYCCQSPGFQLAANNYTCVDINECDASNQCAQ-QCYNILGSFICQCNQGYELSSDRLN 291
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 147 CRDVECLQGR--CEQVCNPSGYSYTHCDGRGGLKLSQDMTCEIDILPC 194
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 292 CEDIDECRTSSYLQYQCYNPEKFKSCMCP--QGYQVVRSR-TCQDINEC 338
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
RESULT 30
A57293
latent transforming growth factor beta-binding protein 3 precursor - mouse
N:Alternate names: mitosis-inhibitory peptide
C:Species: Mus musculus (house mouse)
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A57293; A60487
R:Yin, W.; Smiley, E.; Germiller, J.; Mecham, R.P.; Florer, J.B.; Wenstrup, R.J.; Bonadic
J. Biol. Chem. 270, 10147-10160, 1995
A:Title: Isolation of a novel latent transforming growth factor-beta binding protein gen
A:Reference number: A57293; MUID:95247723; PMID:7730318
A:Accession: A57293
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1251 <YIN>
A:Cross-references: UNIPROT:Q61810; GB:L40459
R:Reichelt, K.L.; Paulsen, J.E.; Elgjo, K.
Virchows Arch. B Cell Pathol. 59, 137-142, 1990
A:Title: Isolation of a growth and mitosis inhibitory peptide from mouse liver.
A:Reference number: A60487
A:Accession: A60487
A:Molecule type: protein
A:Residues: 65-69 <REI>
C:Comment: The molecular source of this pentapeptide has not been shown but it correspon
C:Genetics:
A:Gene: lcbp-3
C:Keywords: liver; pyroglutamic acid
F:338-373/Domain: EGF homology <EGF>
F:65/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
Query Match 24.6%; Score 319.5; DB 2; Length 1251;
Best Local Similarity 30.5%; Pred. No. 3.9e-16;
Matches 72; Conservative 32; Mismatches 67; Indels 65; Gaps 12;
QY 17 NSGFAT-----CVQNLPDQCTPNPCDRKGTOACODLMGNFFCLCKAGW-----GGRLC 64
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 581 NAGYRSHQHYCVD--VNECEAEFCG-PKRGICNWTGSSYNCHCNRYRLHVGAGRSC 637
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 65 DKDVNECSQ-----ENGGLQI----- 81
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 638 -VDLNECAKPHLCGDGDFCINPPGHYKNCVPGYRLKASRPPICEDIDECRDPSTCPDGK 696
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 82 CHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGEARCKNLPGSYSLCDEGFAY 140
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 697 CENKPGSFKCIACQPGYR-SQGGAGCARDVNECSGTPCSPGWCEKLPGSYRCTCAQGIRT 755
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
QY 141 SSQEKACRDVDECLQGR-CEQ-QVCNPSGYSYTHCDGRGGLKLSQDMTCEIDILPC 194
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
Db 756 RTGRLLSCIDVDDCEAGKVCQDGICTNTGSGFQCC--LSGYHLSDRSRCEIDISC 809
| | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : |
RESULT 31

T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20336
A;Accession: T27283
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1620 <N1>
A;Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CA854471.1; CESP:Y64G10A.f
A;Experimental source: clone Y64G10A
C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7
Query Match 24.6%; Score 319.5; DB 2; Length 1620;
Best Local Similarity 37.3%; Pred. No. 4.8e-16;
Matches 66; Conservative 17; Mismatches 87; Indels 7; Gaps 4;
QY 23 CQVNLPOQCTPNPCDRKGTQACQDLGN-FPCLCKAGWGRLCDKDVNCSQENGGCLQI 81
DB 71 CLLRVQANCADLCHNGGTCVPSEHNDNEQVCEPVGFTAKQCYDANECHANNGGCEHE 130
QY 82 CHNKPFSFCHSGHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYS 141
DB 131 CVNTIGTYCRWPGFELSGDNTCSIDIECAVSNCGSDRCVNSPGFRCDPCSDLYLH 190
QY 142 SOEAKCRDVECL--QGRCEQVCVNSPGS--YTHCDGRGLKLSQMDTCEDILPC 194
DB 191 ADGRTCGVKTSCTDNGGCGEHCENDSNGEYRCR--RVGFKLSNKRSCQPVDPDC 245
RESULT 32
A38261
masking protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38261
R;Tsuiji, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 8835-8839, 1990
A;Title: Molecular cloning of the large subunit of transforming growth factor type beta
A;Reference number: A38261; MUID:91062373; PMID:224754
A;Accession: A38261
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1712 <TSU>
A;Cross-references: UNIPROT:Q00918; GB:M55431; NID:g207285; PIDN:AAA42235.1; PID:g207286
F;911-947/Domain: EGF homology <EGF>
Query Match 24.6%; Score 319.5; DB 2; Length 1712;
Best Local Similarity 31.3%; Pred. No. 5e-16;
Matches 79; Conservative 32; Mismatches 78; Indels 63; Gaps 12;
QY 6 CINKYGS----PYTKNSGF----ATCVQNLPDQC--TPNPCDRKGTQACQDLGNFFCLCK 56
DB 1005 CVNSPGSYQVCPTE--GFRGNGCQLD--VDECLQPKVCT--NGSCTNLEGSYMSCH 1057
QY 57 AGWG-----GRLCDKDVNCSQENGGCLQICHNKPFSFCHSGHSGFELSSDGRTCODIDEC 112
DB 1058 KGYSPTPDHRC--QDIDECQGNLCMNGQCKNTDGSFRCTCGQYQLSAAKQCEDIDEC 1116
QY 113 ADSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGR--CE-QVCVNSPGSY 169
DB 1117 EHRHLSHGCRNTEGSGFQCLCNQGYRASVLGDHCDINECLSDSSVCGQGDICNTAGSY 1176
QY 170 TCHC-----DGRG-----GLKLSQMDTCED 190
DB 1177 DCTCPDGLQNDNKGQDINECAQPGLCAPHGECLNTQGSFHCVEQGFISADGRCTED 1236
QY 191 ILPCVPFSVAKS 202

DB 1237 IDECVANTVCDSS 1248
RESULT 33
T46488
hypothetical protein DKFPZp434J065.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46488
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23035
A;Accession: T46488
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-741 <AAA>
A;Cross-references: UNIPROT:Q8ND86; EMBL:AL137638
A;Experimental source: adult testis; clone DKFPZp434J065
C;Genetics:
A;Note: DKFPZp434J065.1
Query Match 24.3%; Score 315.5; DB 2; Length 741;
Best Local Similarity 38.4%; Pred. No. 5.1e-16;
Matches 61; Conservative 21; Mismatches 64; Indels 13; Gaps 4;
QY 44 CQDLGMNFFCLCKAGWGRLCDKDVNE-----CSQENGGCLQICHNKPFSFCHSGHSGF 97
DB 38 CINIPGSYVCRCKQGY---ILNSDQTTCTRIQDLICAMEDHNCQELCVNPGSFVQCYSY 94
QY 98 ELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGR 157
DB 95 ALAEDGKRCVADVDCASENHGCEHCENADGSGYLQCHGEGFALNPDEKCTCTKIDYCASSN 154
QY 158 --CEQVCVNSPGSYTCHCDGRGLKLSQMDTCEDILPC 194
DB 155 HGCQHECVNTDDSYSHC--LKGFILNPDKTKTCTRRINYC 191
RESULT 34
A57172
probable hormone receptor EMR1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57172
R;Baud, V.; Chissole, S.L.; Viegas-Pequignot, E.; Diriong, S.; N'Guyen, V.C.; Roe, B.A.; I
Genomics 26, 334-344, 1995
A;Title: EMR1, an unusual member in the family of hormone receptors with seven transmembr
A;Reference number: A57172; MUID:95324926; PMID:7601460
A;Accession: A57172
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <BAU>
A;Cross-references: UNIPROT:Q14246; GB:X81479; NID:g784993; PIDN:CAAS7232.1; PID:g784994
C;Genetics:
A;Gene: GDB:EMR1
A;Cross-references: GDB:378349; OMIM:600493
A;Map position: 19p13.3-19p13.3
C;Keywords: transmembrane protein
F;136-170/Domain: EGF homology <EGF>
Query Match 24.1%; Score 312; DB 2; Length 886;
Best Local Similarity 30.8%; Pred. No. 1.1e-15;
Matches 82; Conservative 29; Mismatches 81; Indels 74; Gaps 15;
QY 1 PRYLDCINKYGSPTYNKSGFATCVQL-----PDQC--TPNPCDRKG 40
DB 42 PAYATCTN-----TVDSYCTCKQGLSSNGMHFPQVRCRKOIDECSPQPCG--P 93
QY 41 TOACQDLGNFFCLCKAGWG-----GRLCKDVNCSQENGGCLQICH 83
DB 94 NSSCKNLGRKSCSLDGFSSPTGNDWVFGKPGNFCTDINECLTSRVCPHEHSDCV---- 149

QY 84 NKPSPGSHCSHGFLSSDRTQDIDECADSEACGE-ARCKNLPGSYSLCDEGFAYSS 142
 DB 150 NSNGSYSCSCQGVF--ISRNSCEDVNECADPPACPEHATCNTTVNGSYCFNPGFESS 207
 QY 143 -----QEKACRDVDECIQGR-BOVCVNSPGSYTCHC-----DGRGLKLS----- 182
 DB 208 GHLSCQGLKASCEBIDECTE-MCPINSTCTNTPGSYFCTCHPGFADSPSQNLFTDQGVRC 266
 QY 183 QDMWTC-EDILPCVPFSAKSKSLY 207
 DB 267 RDIDECRQDPSTCGPNSICTNALGSY 292

RESULT 35
 T13954
 MEGF6 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13954
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; PMID:98360089; PMID:9693030
 A:Status: preliminary
 A:Accession: T13954
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 <NAK>
 A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:G3449293; PIDN:BA032462.1; PID:93
 A:Experimental source: strain Sprague-Dawley; brain
 C:Genetics:
 A:Gene: MEGF6

Query Match 23.9%; Score 310.5; DB 2; Length 1574;
 Best Local Similarity 34.5%; Pred. No. 2.2e-15;
 Matches 79; Conservative 23; Mismatches 76; Indels 51; Gaps 13;

QY 19 GFATCVQNLPDQCTPN---PCDRKGTQ-----ACQDLMGNFFCLCKAGW-- 59
 DB 267 GLAHC-----GCHPGYQLAARDKTEDVDICALGALQAQCLNLTQGSFKVCVCHAGYEL 320
 QY 60 --GGRLCDK----DVNECSQENGCGLOIC-HNKPSPGSHCSHGFLSSDRTQDIDSC 112
 DB 321 GADGRQCYRIEMEIVNSCEAGNGSGHGSHTSGPL-CTCPRGYELDEDQKTCIDIDDC 379
 QY 113 ADSEAGEARCKNLPGSYSLCDEGFAYSSQERKACRDVDECIQGR--CEQVCVNSPGSYT 170
 DB 380 ANSPCCQQA-CANTPGGYECSPAGYRLNTDGCCEDDVDEACSHGCGCEHHCSNLAGSFQ 438
 QY 171 CHCDGRGGLKLSQDMTCDILPCVPFSAKSKSLYLGPMFSGTPVIR 219
 DB 439 CFCE--AGYRLDEDRGCT-----SLEESVVDLD-GRL----PFVR 472

RESULT 36
 S78549
 notch3 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S78549; S71825
 R:Youtel, A.; Tournier-Lasserre, E.
 submitted to the EMBL Data Library, April 1997
 A:Reference number: S78549
 A:Accession: S78549
 A:Molecule type: mRNA
 A:Residues: 1-2321 <JOU1>
 A:Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:G2668591; PIDN:AA091371.1; PID:G266
 R:Youtel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowitc
 x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.
 Nature 383, 707-710, 1996
 A:Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
 A:Reference number: S71825; PMID:97032728; PMID:8878478
 A:Accession: S71825
 A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
 A:Residues: 67-113,138-194,268-333,'G',335-346,536-613,716-765,1240-1279,1815-1888 <JOU2>
 A:Cross-references: EMBL:U97669
 C:Genetics:
 A:Gene: notch3
 A:Map position: 19p13.1
 C:Description:
 A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: tandem repeat; transmembrane protein
 F:123-155/Domain: EGF homology <EGX1>
 F:162-194/Domain: EGF homology <EGF1>
 F:240-271/Domain: EGF homology <EGX2>
 F:318-349/Domain: EGF homology <EGF>
 F:473-504/Domain: EGF homology <EGX3>
 F:853-884/Domain: EGF homology <EGF3>
 F:928-959/Domain: EGF homology <EGX4>
 F:1838-1870/Domain: ankyrin repeat homology <AN1>
 F:1871-1903/Domain: ankyrin repeat homology <AN2>
 F:1905-1937/Domain: ankyrin repeat homology <AN3>
 F:1938-1970/Domain: ankyrin repeat homology <AN4>
 F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 23.1%; Score 299.5; DB 2; Length 2321;
 Best Local Similarity 33.5%; Pred. No. 1.9e-14;
 Matches 75; Conservative 29; Mismatches 87; Indels 33; Gaps 13;

QY 6 CLNKYGS-----PYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLMGNFFCLCKAG 58
 DB 408 CVNTQGSFLCQCGRYTG-----PRCETDV-NECLSGPCRNRQAT--CLDRIGQFTCLCMAG 460
 QY 59 WGRGLCDKDVNECSQE---NGGLQICHNKPSPGSHCSHGFLSSDRTQCO-DIDECAD 114
 DB 461 FGTGTYCEVDIDECQSSPCVNGG---VCKDRVNGFSCCTPSGF-----SGSTCQLDVDECA 513
 QY 115 SPACGEARCKNLPGSYSLCDEGFAYSSQERKAC-RDVDECIQGRCEQ-VCVNSPGSYTCH 172
 DB 514 TPCRNGAKCVDQPDGYECRCAEGF---EGTLCDRNVDDCSPPDCHGRCVDGIASFCA 569
 QY 173 C-DGRGGLKLSQDMTCDILPCVPFSAKSKSLYLGPMFSGT 215
 DB 570 CAPGYTGRCESQVDECRS-QPCRHGKGLDLVDKYLRCRPSGT 612

RESULT 37
 S45306
 notch3 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S45306
 R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
 Mech. Dev. 46, 123-136, 1994
 A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-
 A:Reference number: S45306; PMID:95001556; PMID:7918097
 A:Accession: S45306
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2318 <LAR>
 A:Cross-references: UNIPROT:Q61982; EMBL:X74760; NID:G483580; PIDN:CAA52776.1; PID:G48358
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F:163-195/Domain: EGF homology <EGF1>
 F:474-505/Domain: EGF homology <EGF>
 F:854-885/Domain: EGF homology <EGF2>
 F:1839-1871/Domain: ankyrin repeat homology <AN1>
 F:1872-1904/Domain: ankyrin repeat homology <AN2>
 F:1906-1938/Domain: ankyrin repeat homology <AN3>
 F:1939-1971/Domain: ankyrin repeat homology <AN4>
 F:1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 22.5%; Score 291.5; DB 2; Length 2318;
 Best Local Similarity 32.7%; Pred. No. 7.4e-14;
 Matches 73; Conservative 30; Mismatches 89; Indels 31; Gaps 12;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPQCTPNFCDRKGTQACODLMGNFFCLCKAG 58
 Db 409 CVNTQGSFLOCCGRGYTG----PRCETDV-NECLSGPCRQAT--CLDRIGQFTCIWAG 461
 QY 59 WGGRLCKDKNVCSQEQ---NGGCLQICHKPNSGFHCSHGFELSSDGRCTCO-DIDECAD 114
 Db 462 FTGYICEVDIDECOSSPCVNGG---VCKDRVNGFSCCTCPGPF-----SGSMCQLDVBECAS 514
 QY 115 SEACGEARCKNLPGSYCLCDEGFAYSQEKACRDVDECIQGRCEQ--VCVNSPGSYTCHC 173
 Db 515 TPCRNAGKCVDPQDGYECRAEGFEGTLCE---RNVDDCSPPDCHGRCVGDGIASFSCAC 571
 QY 174 -DCRGGGLKLSQDMTCEIDILPCVPFVSVAKSILYLGRMPSGT 215
 Db 572 APGYTGIRCSQVDECRS-QPCRYGKCLDLVDKYLRCPPGT 613
 RESULT 38
 T34513
 hypothetical protein ZK783.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T34513
 R;Pavello, A.; Vaudin, M.
 submitted to the EMBL Data Library, August 1994
 A;Description: The sequence of C. elegans cosmid ZK783.
 A;Reference number: 221536
 A;Accession: T34513
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3507 <FAV>
 A;Cross-references: UNIPROT:Q23587; EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783
 A;Experimental source: strain Bristol N2; clone ZK783
 C;Genetics:
 A;Gene: CESP:ZK783.1
 A;Map position: 3
 A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 3504/1
 Query Match 21.4%; Score 278; DB 2; Length 3507;
 Best Local Similarity 29.0%; Pred. No. 1e-12;
 Matches 79; Conservative 31; Mismatches 58; Indels 104; Gaps 18;
 QY 6 CINKYGSPTYK-NSGFATCVQNLDP--QCTP---NPKD-----RTCCDI 109
 Db 1510 CVNKPQGYSCENGF-----LGDGYCQVPTTKKPCDSTQSSKSHCSNMSCEVDVTD 1563
 QY 38 -----RKGTQACD-----LMGNFFCLCKAGW--GRLC 64
 Db 1564 GSVECKECMGYKSGKVCEDINECVAEKAPCSLNANCVNMNGTFCSCRQGYRGDGFMC 1623
 QY 65 DKDVNCSQENGGCLQICH-----NKPQSFHCSHGFELSSDG-----RTCCDI 109
 Db 1624 -TDINECDERHP-----CHPFAECTNLEGSFKCECHSGFE--GDGIYKCTNPLERSCEDV 1675
 QY 110 DE-C--ADSEACGEARCKNLPGSYCLCDEGFAYSQEKACRDVDECIQGR--CE----QV 161
 Db 1676 EKFCGRVDHVSCLSVRIYNGSLSSVCECPGFREKESNCVDIDEESRNCDPASAV 1735
 QY 162 CVNPSPGSYTCHC-----DGRGGLKLSQDMTCE 189
 Db 1736 CVNTEGSYRCEAGYEGEGG--VCTDIDEC 1765
 RESULT 39
 S16148
 gene serrate protein precursor - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
 C;Accession: S16148; S16878; A36666
 R;Thomas, U.; Speicher, S.A.; Knust, E.
 Development 111, 749-761, 1991
 A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a cd

A;Reference number: S16148; MUID:91347903; PMID:1840519
 A;Accession: S16148
 A;Molecule type: mRNA
 A;Residues: 1-1408 <THO1>
 A;Cross-references: UNIPROT:P18168; EMBL:X56811
 R;Thomas, U.
 submitted to the EMBL Data Library, November 1990
 A;Reference number: S16878
 A;Accession: S16878
 A;Molecule type: mRNA
 A;Residues: 1-1351,'T',1353-1408 <THO2>
 A;Cross-references: EMBL:X56811; NID:g8563; PID:g8564
 R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2188-2201, 1990
 A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential fo
 A;Reference number: A36666; MUID:91099666; PMID:2125287
 A;Accession: A36666
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-15,20-26,'A',28-1408 <FLB>
 A;Cross-references: GB:M35759; NID:g158605; PID:g158606
 C;Genetics:
 A;Gene: FlyBase:Ser
 A;Cross-references: FlyBase:FBgn0004197
 C;Keywords: glycoprotein; transmembrane protein
 F;1-84/Domain: signal sequence #status predicted <SIG>
 F;85-1408/Product: gene serrate protein #status predicted <MAT>
 F;85-1221/Domain: extracellular #status predicted <EXT>
 F;283-316/Domain: EGF homology <EG01>
 F;319-348/Domain: EGF homology <EG02>
 F;355-388/Domain: EGF homology <EG03>
 F;395-488/Domain: EGF homology #status atypical <EG04>
 F;495-526/Domain: EGF homology <EG05>
 F;533-608/Domain: EGF homology #status atypical <EG06>
 F;615-645/Domain: EGF homology <EG07>
 F;652-683/Domain: EGF homology <EG08>
 F;690-720/Domain: EGF homology <EG09>
 F;727-796/Domain: EGF homology #status atypical <EG10>
 F;803-834/Domain: EGF homology <EG11>
 F;841-876/Domain: EGF homology <EG12>
 F;883-914/Domain: EGF homology <EG13>
 F;921-952/Domain: EGF homology <EG14>
 F;997-1060/Region: cysteine-rich
 F;1222-1246/Domain: transmembrane #status predicted <TM1>
 F;1247-1408/Domain: intracellular #status predicted <INT>
 F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn)
 Query Match 21.2%; Score 275.5; DB 2; Length 1408;
 Best Local Similarity 27.3%; Pred. No. 7.4e-13;
 Matches 74; Conservative 25; Mismatches 75; Indels 97; Gaps 12;
 QY 5 DCINKYGSPTYKNSGFATCVQNLDPDCTPNPCDRKGTQACQDLMGNFFCLCKAGWGRLC 64
 Db 478 DCAAGWTGP-----TCEINI-DECAAGPCEHGT--CIDLIGFRCCEPPEWHGDVC 526
 QY 65 DKDVNCSQEN-----GGCLQI- 81
 Db 527 QVDVNECEAPHSGAGIAANALLTTTATAIGSNLSSTALLAALTSAAVASTSLAIGPCINAK 586
 QY 82 -CHNKPGSFHCSHSGF-----ELSSD-----GRTCC 107
 Db 587 ECRNQPQSFACICKEGMGVTCENLDCCVQCNRNGATCIDLYNDYRCACASGFTGRDCE 646
 QY 108 -DIDECADSEACGEARCKNLPGSYCLCDEGFAYSQEKACRDV--DECIQGRCEQVQCN 164
 Db 647 TDIDECATSPCRNGGECVDMVKFNCICPLGYSGSLCEEAENCTSPCLGEGH-----CLN 702
 QY 165 SPGSYTCCHC-DGRGGLKLSQDMTCEIDILPC 194
 Db 703 TPBGYCHCPDPRDAGRKHCQLRPLCSQ-PPC 732
 RESULT 40

A04043
notch protein homolog TAN-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
C:Accession: A40043
R:Billiken, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, R.
Cell 66, 649-661, 1991
A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal
A:Reference number: A40043; MUID:91347367; PMID:1931692
A:Accession: A40043
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2555 <ELL>
A:Cross-references: GB:M73980
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:261-292/Domain: EGF homology <EGX1>
F:494-525/Domain: EGF homology <EGF1>
F:987-1018/Domain: EGF homology <EGX2>
F:1149-1180/Domain: EGF homology <EGF>
F:1187-1218/Domain: EGF homology <EGF3>
F:1233-1264/Domain: EGF homology <EGX3>
F:1921-1959/Domain: ankyrin repeat homology <AN1>
F:1960-1992/Domain: ankyrin repeat homology <AN2>
F:1994-2026/Domain: ankyrin repeat homology <AN3>
F:2027-2059/Domain: ankyrin repeat homology <AN4>
F:2060-2092/Domain: ankyrin repeat homology <AN5>
Query Match 21.1%; Score 274; DB 2; Length 2555;
Best Local Similarity 30.7%; Pred. No. 1.5e-12;
Matches 69; Conservative 30; Mismatches 90; Indels 36; Gaps 11;
QY 6 CTNKYGSPTKNSGF-ATCVQNLP-----DOCTPNPCDRKGTQACODLMGNFPCLCK 56
DB 429 CINTLGS-----FSCQLQGYTPRCRCEIDVNECVSNPCQNDAT--CLDQIGEPQCMCM 479
QY 57 AGNGGRCLDKDVNECSQ----ENGGCLQICHNKPFGSHGSCFSLSDGRTCQDIDRC 112
DB 480 PGYEGVHCEVNTDECASSPLCHNGRCL----DKINEFQCEPTGF--TGHLCQDVDRSC 531
QY 113 ADSEAGEARCKNLPGSYCLDEGFAYSSQAEKADRDVECLQGRCEQ--VCVNSPGSYTC 171
DB 532 ASTPCKNGAKCLDGNPTNTCTVCTEGYTGHCVEV---DIDECDDPDPCHYGSKDGVATFTC 588
QY 172 HC-DGRGGLKLSQDMTDCEDILPCVPFVSAKSVKSLYLGRMFSGT 215
DB 589 LCRPGYTHHCHETNINECSS-QPCRURGTCQDPDPAIYLCFLKGT 632
RESULT 41
A24420
notch protein - fruit fly (Drosophila melanogaster)
N:Alternate names: neurogenic repetitive locus protein
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
R:Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A:Reference number: A24420; MUID:87064624; PMID:3097517
A:Accession: A24420
A:Molecule type: DNA
A:Residues: 1-2703 <KID>
A:Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PID:g157993
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539; PMID:3935325
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958,
A:Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R:Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
A:Reference number: S09358; MUID:89385974; PMID:2780284

A:Accession: S09358
A:Molecule type: DNA
A:Residues: 2505-2551, 'QOOQ', 2552-2576, 'E', 2578-2604 <TAU>
R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other c
A:Reference number: A05267; MUID:85099329; PMID:2981631
A:Accession: A05267
A:Molecule type: DNA
A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>
C:Genetics:
A:Gene: notch; opa
A:Cross-references: FlyBase:FBgn0004647
A:Map position: 8.96-9.36
A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C:Keywords: differentiation; tandem repeat; transmembrane protein
F:27-43/Domain: transmembrane #status predicted <TM1>
F:297-328/Domain: EGF homology <EGF1>
F:530-561/Domain: EGF homology <EGF1>
F:568-599/Domain: EGF homology <EGF>
F:988-1019/Domain: EGF homology <EGX2>
F:1064-1095/Domain: EGF homology <EGF3>
F:1187-1218/Domain: EGF homology <EGX3>
F:1746-1762/Domain: transmembrane #status predicted <TM2>
F:1950-1982/Domain: ankyrin repeat homology <AN1>
F:1983-2015/Domain: ankyrin repeat homology <AN2>
F:1988-2004/Domain: transmembrane #status predicted <TM3>
F:2017-2049/Domain: ankyrin repeat homology <AN3>
F:2050-2082/Domain: ankyrin repeat homology <AN4>
F:2083-2115/Domain: ankyrin repeat homology <AN5>
F:2538-2568/Region: glutamine-rich
F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
Query Match 21.0%; Score 272; DB 1; Length 2703;
Best Local Similarity 28.7%; Pred. No. 2.3e-12;
Matches 74; Conservative 25; Mismatches 71; Indels 88; Gaps 14;
QY 19 GFA--TCVQNLPDQCTPNPCDRKGTQACODLMGNFPCLCKAGWGRLCDKVNECSQ--- 73
DB 208 GFTGDTCSYDI-EECQSNPKYGGT--CVNTHGYSQCMCPGTGTGRDCTDKYKPCSPSC 264
QY 74 ENGGCLQICHNKPFGSHGSCFSE-----LSSDGRTC----- 106
DB 265 QNGG---ICRNSGLSVECKPKGFKGKCEQNYDDCLGHLCONGTCTDIDISDYTCRCPP 321
QY 107 -----ODIDECA--DSEAC-GEARCKNLPGSYCLCDEGFA---YSSQEKACRDV-- 150
DB 322 NFGTRFCDDVDECAQRDPVCQNGATCTNTHGSYSYCICVNGWAGLDCSNNTDDCKQAAC 381
QY 151 -----DECLQGRC--EQVCVNSP--GSYTCHC-DGR 176
DB 382 FYGATCIDGVGSFYCQCTKGKTLGLCHLDDACTSNPCHADALCDTSPNGSYACSCATGY 441
QY 177 GGLKLSQDMTDCEDILPC 194
DB 442 KGVDCSEIDEDCDQGSPC 459
RESULT 42
A56136
jagged protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
R:Kindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A:Title: Jagged: a mammalian ligand that activates Notch1.
A:Reference number: A56136; MUID:95211842; PMID:7697721
A:Accession: A56136
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1220 <LIN>

A:Cross-references: GB:L38483

F:379-410/Domain: EGF homology <EGF1>
F:492-523/Domain: EGF homology <EGF>
F:634-665/Domain: EGF homology <EGF2>

Query Match 20.9%; Score 271.5; DB 2; Length 1220;
Best Local Similarity 33.5%; Pred. No. 1.3e-12;
Matches 68; Conservative 25; Mismatches 83; Indels 27; Gaps 11;

Qy 6 CINKYGSPTKNSGF-----ATCVNLPDQCTPNPCDRKGTQACODLGMNFFCLC 55
Db CHNR-GSKETSSGCECECPGWTGPTCTSTNI-DDCSNNCSHGTT--CQDLVNGFKVC 401

Qy 56 KAGHGRLDKDVNECSQENGGLQICHNPGSFCHSGFELSSDGRTCQ-DIDECAD 114
Db PPQWTGRTQCLDANECAKPCVNARSCKNLIASYCDLFGWM-----GQNCININDCL- 456

Qy 115 SEACGEARCKNLPGSYCLDCEGAYSSQEKACRVDDECLQRCQ--VCVNSPGSYTCH 172
Db 457 GQONDASCRDLVNGYRCICPPGVAGDHCE---RDIDECASNPLCGHGHCNEINRFQCL 513

Qy 173 C-DGRGGLKLSQMDMTCTEDILPC 194
Db 514 CPTGFSNLCQLDIDYCEP-NPC 535

RESULT 43

A49175
N:Alternate names: Notch homolog
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: A49175; PH1570; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of tissues
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:9287989; PIDN:CAA48340.1; PID:g2879
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Superfamily: Notch protein; ankyrin repeat homolog; EGF homology
F:143-174/Domain: EGF homology <EGX1>
F:143-174/Domain: EGF homology <EGX1>
F:482-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF>
F:674-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGF3>
F:836-867/Domain: EGF homology <EGX3>

Query Match 20.9%; Score 270.5; DB 2; Length 1203;
Best Local Similarity 28.9%; Pred. No. 1.5e-12;
Matches 79; Conservative 23; Mismatches 66; Indels 105; Gaps 15;

Qy 4 LDCINKYG---SPYTKNSGFATCVNLP-DOCTPNPCDRKGTQACODLGM------ 49
Db 343 VGINRYSCVSP-----GFTGRCNIDIDECASNPC-RKATCINDVNGFRICPEGPH 396

Qy 50 -----NFFCLCKAGMGRLCKDVNECSQ---ENGGLQ 80
Db 397 HPSCYSQVNECLSNPCIHGNTGGLSGYKCLDAGWGVNCEVDKNECLSNPCQNGG--- 453

Qy 81 ICHNPGSFCHSGFELSSDGRTCQ-DIDECADSEACE----- 120
Db 454 TCNNLVNGYRCKTKGFK-----GYNCQVNIDECASNPLNQGTCTFDVSGYTCHCMLPYT 509

Qy 121 -----ARCKNLPG--SYSLCDEGFAYSSQEKACR-DVDECLQRC 158
Db 510 GKNCQTVLAPCSPNCPENAAVKEAPNFESFSLCAPGW-----QGRCTVDVDECISKPC 565

Qy 159 --EQVCVNSPGSYTCHC-DGRGGLKLSQMDTC 188
Db 566 MNGVGVCHTQGSYVCECPGPGFGMGDCEDINDC 598

RESULT 44

T30201
Notch homolog protein - sea squirt (Halocynthia roretzi)
C:Species: Halocynthia roretzi
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2002
C:Accession: T30201
R:Hori, S.; Saichoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A:Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the central nervous system
A:Reference number: Z20775
A:Accession: T30201
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2352 <HOR>
A:Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1
C:Genetics:
A:Gene: Notch
C:Superfamily: notch protein; ankyrin repeat homolog; EGF homology

Query Match 20.9%; Score 270.5; DB 2; Length 2352;
Best Local Similarity 29.4%; Pred. No. 2.6e-12;
Matches 67; Conservative 25; Mismatches 69; Indels 67; Gaps 12;

Qy 6 CINKYGSPTKNSGFATCVNLPDQCTPNPCDRKGTQACODLGMNFFCLCKAGMGRLCD 65
Db 367 CVAGYSGP-----RCETNI-NECEPNCRNDAT--CLDMIGNFNCVCMPTGTGLICD 415

Qy 66 KDVNECSQE---NGGCLQICHNPGSFCHSGFELSSDGRTC-QIDECADSEACEA 121
Db 416 EDIDECESNFCANGG---TCIDENVATYTCALGF-----TGDDCSQNIDECSTPCWNKA 468

Qy 122 RCNLPGSYSCLCDEGFA-----YSSQEKACR----- 148
Db 469 TCIDKANAYECECAPGYTGVHCEINDDCVINPCHYGS---CRDGVNTFYCDLLGYEG 524

Qy 149 -----DVDECLQRCQ--VCVNSPGSYTCHC-DGRGGLKLSQMDTC 188
Db 525 TKQDTNNECASPENCGTCTDEIGYTYCTCTPTGTSGSSCEINPDDC 572

RESULT 45

S42612
transmembrane protein precursor - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S42612
R:Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A:Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern of expression
A:Reference number: S42612; MUID:94128602; PMID:8297791
A:Accession: S42612
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2437 <BIE>
A:Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g43386
C:Superfamily: notch protein; ankyrin repeat homolog; EGF homology
F:755-786/Domain: EGF homology <EGF1>
F:1023-1054/Domain: EGF homology <EGF2>
F:1185-1216/Domain: EGF homology <EGF2>
F:1915-1947/Domain: ankyrin repeat homolog <AN1>
F:1948-1980/Domain: ankyrin repeat homolog <AN2>
F:1982-2014/Domain: ankyrin repeat homolog <AN3>
F:2015-2047/Domain: ankyrin repeat homolog <AN4>
F:2048-2080/Domain: ankyrin repeat homolog <AN5>

Query Match 20.8%; Score 270; DB 2; Length 2437;
Best Local Similarity 30.4%; Pred. No. 2.9e-12;

QY 23 CVON-----LPDQCTPNPCDRKGTQACODL-MGNFFCLCKAGWGRLCDKDVNECSQ 73
Db 597 CVONQICLPENKVCNQATQCQNGG--ECVDLPNGDYECKTRGWTGTCGNDVDDBCTL 654
QY 74 E-----NGGCLIQICHNKPFGSCHGSEFELSSDGRTC-QDIDECADSEACGEARCKNLP 127
Db 655 HPKICGNG-----ICKNEKGSYKVCYCTPGF-----TGVHCDSDVDCLSFPPCLNGATCHNKI 706
QY 128 GSYSCLCDEGPAYSSQKACR-DVDECLQGRCE--QVCVNSPGSYTCHC-DGRGLKLSQ 183
Db 707 NAYECVCPQGY-----EGENCEVDIDECGNSPCNSGSTCIDRINNFTCNCPGMRGRICDI 762
QY 184 DMDTCEIDILPCV 195
Db 763 DIDDCVGD-PCL 773

RESULT 49
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into
A;Reference number: Z20966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 20.4%; Score 264; DB 2; Length 2531;
Best Local Similarity 29.9%; Pred. No. 8.3e-12;
Matches 64; Conservative 38; Mismatches 78; Indels 34; Gaps 14;

QY 5 DCINKYSPYTKNSGFATCVQNLDPQCT---PNPCDRKGTQACODLMGNFFCLCKAGWG 61
Db 421 DCATGY-----QGF-NCSEDI-DECSLMSDSICQSGGT--CQFDPGWSCLCSSGFTG 469
QY 62 RLCDKDVNECSQE---NGGCLQICHNKPFGSCHGSEFELSSDGRTCQ-DIDECADSEA 117
Db 470 SRCETDIDECDDDPYNGG---TCLNKRGGYACICLAGF---TGTLCETDINECSSNPC 522
QY 118 CGEARCKNLPGSYCLDEGPAYSSQKACR-DVDECLQGRCEQ--VCVNSPGSYTCHCD 174
Db 523 LNGASCFDITGRFECACLAGTGT---CQVNIIDCQSSPCENGSGTICIDGVNQFTCLCE 578
QY 175 -GRGGLKLSQDMDTCEIDILPCVPFSAKSVKSLY 207
Db 579 TGYEGHRCMDSDECAS-RPCWNGVCEDLIGFY 611

RESULT 50
T08618
intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayser, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A;Reference number: Z16459; MUID:98148073; PMID:9478979
A;Accession: T08618
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <MOE>
A;Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3834379
C;Genetics:
A;Gene: CUBILIN
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;133-164/Domain: EGF homology <EGF1>
F;436-467/Domain: EGF homology <EGF>

Query Match 20.3%; Score 263.5; DB 2; Length 3623;
Best Local Similarity 31.9%; Pred. No. 1.2e-11;
Matches 82; Conservative 33; Mismatches 79; Indels 63; Gaps 20;

QY 5 DCINKYSPYTKNSGFATCVQNLDPD---OCTP-----NPDCKGTQ-----ACQ 45
Db 170 ECVYSGTPFGCQSG-STCVNTVGSFRCDCTPTTYGPQCAKYNDCEQSKQLCKHGICE 228
QY 46 DL-----MGNFFCLCKAGW-----GGRLCDKDVNECSQENGGLQ---ICHNKPSPHFC-S 92
Db 229 DLQRVHHGQPNFHCICDAGWTPPNNGISCTEDKDECSLQSPCSEHAQCFTQGSFYCGA 288
QY 93 CHSGFELSSDGRTCQDIDEC-ADSEACGEA---RCNLPQSYSC-LCDEGFAYSSQKAC 147
Db 289 CPKGMQ--GNGYECODINECEINNGGCSQAPLVPLNTPGSFSCGNCPCAGF--SGDGRVC 344
QY 148 RDVDECL--QGRG--EQVCVNSP--GSY--TCHC-----DGRGLKLSQDMDTCE 190
Db 345 TPVDICSIHNGGCHPEATCSCSSPVLGSFLPVCTCPGTYGNGYSGNCGVRLS---NICS 401
QY 191 ILPCVPFSAKSVKSLY 207
Db 402 -HPCVNGQCIETVSSYP 417

Search completed: July 7, 2005, 09:38:46
Job time : 67.1154 secs

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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:06:22 ; Search time 119.736 Seconds
(without alignments)
141.522 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PRYLDCINKGSPYTKNSGF.....LGRMFGTPVIRLRFKRLQP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1297	100.0	678	1	US-08-282-141-2
2	1297	100.0	678	1	US-08-435-434-2
3	1297	100.0	678	1	US-08-435-436-2
4	1297	100.0	678	2	US-08-438-863-2
5	1297	100.0	678	2	US-08-438-864-2
6	1297	100.0	678	3	US-08-438-862-2
7	1297	100.0	678	3	US-08-402-253-2
8	1297	100.0	678	3	US-08-443-866B-2
9	1289	99.4	678	3	US-08-628-747-2
10	1113	85.8	673	1	US-08-282-141-3
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13	1113	85.8	673	2	US-08-438-863-1
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18	1113	85.8	673	3	US-08-443-866B-1
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20	601.5	46.4	635	1	US-07-985-691-2
21	601.5	46.4	635	1	US-08-436-804-2
22	601.5	46.4	635	1	US-08-267-387-2
23	601.5	46.4	676	1	US-08-282-141-4
24	601.5	46.4	676	1	US-08-435-434-3
25	601.5	46.4	676	1	US-08-435-436-3
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27	601.5	46.4	676	2	US-08-438-864-3

28	601.5	46.4	676	3	US-08-438-862-3	Sequence 3, Appli
29	601.5	46.4	676	3	US-08-628-747-3	Sequence 3, Appli
30	601.5	46.4	676	3	US-08-402-253-3	Sequence 3, Appli
31	601.5	46.4	676	3	US-08-443-866B-3	Sequence 3, Appli
32	596.5	46.0	675	6	5258288-1	Patent No. 5258288
33	596.5	46.0	675	6	5258288-1	Patent No. 5258288
34	586.5	45.2	652	6	5258288-4	Patent No. 5258288
35	586.5	45.2	652	6	5258288-4	Patent No. 5258288
36	353.5	27.3	997	4	US-09-747-371-3	Sequence 3, Appli
37	348.5	26.9	1935	4	US-09-949-016-10403	Sequence 10403, A
38	348.5	26.9	2871	4	US-09-538-092-1076	Sequence 1076, Ap
39	345	26.6	999	4	US-09-747-371-2	Sequence 2, Appli
40	339	26.1	575	4	US-09-949-016-11264	Sequence 11264, A
41	339	26.1	575	4	US-09-949-016-11265	Sequence 11265, A
42	339	26.1	575	4	US-09-949-016-11266	Sequence 11266, A
43	339	26.1	575	4	US-09-949-016-11267	Sequence 11267, A
44	339	26.1	575	4	US-09-949-016-11267	Sequence 11267, A
45	339	26.1	575	4	US-09-949-016-11365	Sequence 11365, A
46	339	26.1	575	4	US-09-949-016-11366	Sequence 11366, A
47	339	26.1	575	4	US-09-949-016-11367	Sequence 11367, A
48	339	26.1	575	4	US-09-949-016-11368	Sequence 11368, A
49	339	26.1	575	4	US-09-949-016-11369	Sequence 11369, A
50	339	26.1	575	4	US-09-949-016-11370	Sequence 11370, A
51	339	26.1	575	4	US-09-949-016-11371	Sequence 11371, A
52	330.5	25.5	956	4	US-09-949-016-11372	Sequence 11372, A
53	330.5	25.5	1394	4	US-09-949-016-8254	Sequence 8254, Ap
54	330.5	25.5	1394	6	US-09-949-016-5971	Sequence 5971, Ap
55	330.5	25.5	1394	6	5177197-30	Patent No. 5177197
56	328.5	25.3	1253	3	US-08-479-722B-4	Sequence 4, Appli
57	328.5	25.3	1253	4	US-09-592-685-4	Sequence 4, Appli
58	327	25.2	448	4	US-09-409-096-4	Sequence 4, Appli
59	323	24.9	335	4	US-09-312-283C-186	Sequence 186, App
60	323	24.9	448	2	US-08-884-072-1	Sequence 1, Appli
61	323	24.9	448	3	US-09-212-168-1	Sequence 1, Appli
62	323	24.9	504	4	US-09-949-016-7403	Sequence 7403, Ap
63	322	24.8	956	4	US-09-949-016-6215	Sequence 6215, Ap
64	321	24.7	325	4	US-09-949-016-11467	Sequence 11467, A
65	321	24.7	325	4	US-09-949-016-11468	Sequence 11468, A
66	321	24.7	352	4	US-09-949-016-8273	Sequence 8273, Ap
67	321	24.7	352	4	US-09-949-016-8274	Sequence 8274, Ap
68	321	24.7	387	2	US-08-884-072-5	Sequence 5, Appli
69	321	24.7	387	2	US-08-833-963C-9	Sequence 9, Appli
70	321	24.7	387	3	US-08-980-514-3	Sequence 3, Appli
71	321	24.7	387	3	US-09-212-168-5	Sequence 5, Appli
72	321	24.7	387	4	US-09-409-096-2	Sequence 2, Appli
73	321	24.7	493	4	US-09-322-357-1	Sequence 1, Appli
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77	319.5	24.6	1656	4	US-09-949-016-7247	Sequence 7247, Ap
78	319.5	24.6	1821	4	US-09-949-016-5938	Sequence 5938, Ap
79	318	24.5	337	3	US-09-188-930-186	Sequence 186, App
80	318	24.5	638	2	US-08-897-443-1	Sequence 1, Appli
81	318	24.5	915	4	US-09-307-794A-34	Sequence 34, Appl
82	318	24.5	915	4	US-09-305-125A-34	Sequence 34, Appl
83	318	24.5	915	4	US-09-302-775A-34	Sequence 34, Appl
84	318	24.5	915	4	US-09-306-700-34	Sequence 34, Appl
85	318	24.5	915	4	US-09-303-603A-34	Sequence 34, Appl
86	318	24.5	915	4	US-09-304-920A-34	Sequence 34, Appl
87	318	24.5	915	4	US-09-309-064-34	Sequence 34, Appl
88	318	24.5	915	4	US-09-305-381A-34	Sequence 34, Appl
89	318	24.5	915	4	US-09-906-618-34	Sequence 34, Appl
90	318	24.5	915	4	US-09-949-016-11519	Sequence 11519, A
91	318	24.5	963	4	US-09-949-016-11520	Sequence 11520, A
92	314.5	24.2	443	2	US-08-833-963C-2	Sequence 2, Appli
93	314.5	24.2	443	3	US-08-980-514-1	Sequence 1, Appli
94	314.5	24.2	486	3	US-09-949-016-7792	Sequence 7792, Ap
95	312	24.1	886	3	US-09-110-116-3	Sequence 3, Appli
96	312	24.1	886	4	US-09-631-603-14	Sequence 14, Appl
97	308.5	23.8	1833	3	US-08-479-722B-2	Sequence 2, Appli
98	308.5	23.8	1833	4	US-09-592-685-2	Sequence 2, Appli
99	308.5	23.8	1833	5	PCT-US95-02251-18	Sequence 18, Appl
100	304	23.4	439	4	US-09-409-096-6	Sequence 6, Appli

101	299.5	23.1	2321	4	US-09-230-652-2	Sequence 2, Appli	174	249	19.2	456	1	US-08-307-444A-3	Sequence 3, Appli
102	289	22.3	956	2	US-08-897-443-3	Sequence 3, Appli	175	249	19.2	456	1	US-08-307-444A-4	Sequence 4, Appli
103	279.5	21.5	274	3	US-09-188-930-336	Sequence 336, App	176	249	19.2	456	1	US-08-587-389-3	Sequence 3, Appli
104	279.5	21.5	274	4	US-08-312-283C-336	Sequence 336, App	177	249	19.2	456	1	US-08-587-389-4	Sequence 4, Appli
105	275.5	21.2	1404	2	US-08-400-159-2	Sequence 2, Appli	178	249	19.2	475	1	US-08-307-444A-1	Sequence 1, Appli
106	275.5	21.2	1404	3	US-08-611-729A-2	Sequence 2, Appli	179	249	19.2	475	1	US-08-307-444A-2	Sequence 2, Appli
107	275.5	21.2	1404	4	US-09-195-524-2	Sequence 2, Appli	180	249	19.2	475	1	US-08-587-389-1	Sequence 1, Appli
108	274.5	21.2	481	4	US-09-914-259-36	Sequence 36, Appl	181	249	19.2	475	1	US-08-587-389-2	Sequence 2, Appli
109	273	21.0	1193	2	US-08-400-159-10	Sequence 10, Appl	182	249	19.2	476	1	US-08-014-723-1	Sequence 1, Appli
110	273	21.0	1193	3	US-08-611-729A-10	Sequence 10, Appl	183	249	19.2	476	1	US-08-014-723-2	Sequence 2, Appli
111	273	21.0	1193	4	US-09-195-524-10	Sequence 10, Appl	184	249	19.2	476	1	US-08-014-723-18	Sequence 18, Appl
112	271.5	20.9	1219	3	US-08-882-046-5	Sequence 5, Appli	185	249	19.2	476	1	US-08-110-011A-1	Sequence 1, Appli
113	271.5	20.9	1219	4	US-09-566-047-5	Sequence 5, Appli	186	249	19.2	476	1	US-08-110-011A-2	Sequence 2, Appli
114	269	20.7	652	2	US-08-751-305-2	Sequence 2, Appli	187	249	19.2	476	1	US-08-110-011A-18	Sequence 18, Appl
115	269	20.7	2703	1	US-08-185-432-19	Sequence 19, Appl	188	249	19.2	494	1	US-08-014-723-14	Sequence 14, Appl
116	269	20.7	2703	4	US-08-899-232-4	Sequence 4, Appli	189	249	19.2	494	1	US-08-014-723-16	Sequence 16, Appl
117	269	20.7	2703	4	US-09-121-457-4	Sequence 4, Appli	190	249	19.2	494	1	US-08-014-723-14	Sequence 14, Appl
118	268	20.7	452	4	US-09-914-259-34	Sequence 34, Appl	191	249	19.2	494	1	US-08-110-011A-16	Sequence 16, Appl
119	267.5	20.6	2556	1	US-08-185-432-17	Sequence 17, Appl	192	249	19.2	497	1	US-08-312-870-3	Sequence 3, Appli
120	267.5	20.6	2556	4	US-08-899-232-2	Sequence 2, Appli	193	249	19.2	497	4	US-09-331-793-4	Sequence 4, Appli
121	267.5	20.6	2556	4	US-09-121-457-2	Sequence 2, Appli	194	249	19.2	498	2	US-08-733-564-2	Sequence 2, Appli
122	266	20.5	1964	3	US-09-467-997-1	Sequence 1, Appli	195	249	19.2	516	4	US-09-509-994-1	Sequence 1, Appli
123	265.5	20.5	1010	3	US-08-882-046-7	Sequence 7, Appli	196	249	19.2	516	4	US-09-509-994-2	Sequence 2, Appli
124	265.5	20.5	1010	4	US-09-566-047-7	Sequence 7, Appli	197	249	19.2	575	1	US-08-261-206A-59	Sequence 59, Appl
125	265.5	20.5	1036	3	US-09-068-740A-6	Sequence 6, Appli	198	249	19.2	575	1	US-08-312-870-1	Sequence 1, Appli
126	265.5	20.5	1067	4	US-09-579-536C-18	Sequence 18, Appl	199	249	19.2	575	1	US-08-170-290A-54	Sequence 54, Appl
127	265.5	20.5	1187	3	US-09-068-740A-7	Sequence 7, Appli	200	249	19.2	575	4	US-09-880-484D-2	Sequence 2, Appli
128	265.5	20.5	1208	4	US-09-199-865-1	Sequence 1, Appli	201	249	19.2	575	6	US-10-438-648-2	Sequence 2, Appli
129	265.5	20.5	1208	4	US-10-213-329-1	Sequence 1, Appli	202	249	19.2	575	6	5466688-6	Patent No. 5466688
130	265.5	20.5	1218	2	US-08-400-159-6	Sequence 6, Appli	203	249	19.2	575	6	5466688-6	Patent No. 5466688
131	265.5	20.5	1218	3	US-08-611-729A-6	Sequence 6, Appli	204	247	19.0	572	6	5256770-7	Patent No. 5256770
132	265.5	20.5	1218	3	US-08-882-046-2	Sequence 2, Appli	205	247	19.0	572	6	5256770-7	Patent No. 5256770
133	265.5	20.5	1218	3	US-09-214-278-7	Sequence 7, Appli	206	244.5	18.9	720	3	US-08-872-855-4	Sequence 4, Appli
134	265.5	20.5	1218	4	US-09-068-740A-11	Sequence 11, Appl	207	243.5	18.8	725	1	US-08-312-870-7	Sequence 7, Appli
135	265.5	20.5	1218	4	US-09-855-722-7	Sequence 7, Appli	208	243.5	18.8	722	3	US-08-981-392-12	Sequence 12, Appl
136	265.5	20.5	1218	4	US-09-566-047-2	Sequence 2, Appli	209	243.5	18.8	722	3	US-09-908-322-12	Sequence 12, Appl
137	265.5	20.5	1218	4	US-09-917-254-85	Sequence 85, Appl	210	242.5	18.7	713	3	US-08-872-855-5	Sequence 5, Appli
138	265.5	20.5	1218	4	US-09-195-524-6	Sequence 6, Appli	211	242	18.7	1055	3	US-09-214-278-2	Sequence 2, Appli
139	265.5	20.5	1218	4	US-09-579-536C-1	Sequence 1, Appli	212	242	18.7	1055	3	US-09-855-722-2	Sequence 2, Appli
140	265.5	20.5	1218	4	US-09-949-016-5902	Sequence 5902, Ap	213	242	18.7	1065	2	US-08-400-159-8	Sequence 8, Appli
141	265.5	20.5	1254	4	US-09-949-016-10297	Sequence 10297, A	214	242	18.7	1212	3	US-09-214-278-3	Sequence 3, Appli
142	263.5	20.3	2523	1	US-08-185-432-18	Sequence 18, Appl	215	242	18.7	1212	3	US-09-855-722-3	Sequence 3, Appli
143	263.5	20.3	2523	4	US-08-899-232-3	Sequence 3, Appli	216	242	18.7	1238	3	US-09-214-278-5	Sequence 5, Appli
144	263.5	20.3	2523	4	US-09-121-457-3	Sequence 3, Appli	217	242	18.7	1238	4	US-09-855-722-5	Sequence 5, Appli
145	263.5	20.3	2556	1	US-08-083-590A-20	Sequence 20, Appl	218	242	18.7	1257	3	US-08-611-729A-8	Sequence 8, Appli
146	263.5	20.3	2556	3	US-08-532-384-20	Sequence 20, Appl	219	242	18.7	1257	4	US-09-195-524-8	Sequence 8, Appli
147	262.5	20.2	575	4	US-09-482-273-159	Sequence 159, App	220	238.5	18.4	172	4	US-09-706-722A-8	Sequence 8, Appli
148	262.5	20.2	638	4	US-09-482-273-245	Sequence 245, App	221	238.5	18.4	835	3	US-09-284-819-6	Sequence 6, Appli
149	262	20.2	3623	4	US-09-341-461-2	Sequence 2, Appli	222	238.5	18.4	835	4	US-09-262-537-12	Sequence 12, Appl
150	261.5	20.2	2471	1	US-08-185-432-16	Sequence 16, Appl	223	238.5	18.4	835	4	US-09-631-603-9	Sequence 9, Appli
151	261.5	20.2	2471	1	US-08-083-590A-19	Sequence 19, Appl	224	238	18.4	1148	3	US-08-883-046-4	Sequence 4, Appli
152	261.5	20.2	2471	3	US-08-532-384-19	Sequence 19, Appl	225	238	18.4	1148	4	US-09-566-047-4	Sequence 4, Appli
153	261.5	20.2	2471	4	US-08-899-232-1	Sequence 1, Appli	226	236.5	18.2	321	4	US-09-270-767-3762	Sequence 3762, A
154	261.5	20.2	2471	4	US-09-121-457-1	Sequence 1, Appli	227	236.5	18.2	321	4	US-09-270-767-48979	Sequence 48979, A
155	261	20.1	486	4	US-09-914-259-35	Sequence 35, Appl	228	234.5	18.1	1139	3	US-08-537-210A-4	Sequence 4, Appli
156	261	20.1	486	4	US-09-976-594-278	Sequence 278, App	229	234.5	18.1	1139	3	US-09-113-825-4	Sequence 4, Appli
157	261	20.1	486	4	US-09-949-016-6216	Sequence 6216, Ap	230	234	18.0	1064	1	US-08-537-210A-3	Sequence 3, Appli
158	261	20.1	507	4	US-09-949-016-9878	Sequence 9878, Ap	231	234	18.0	1064	1	US-09-113-825-3	Sequence 3, Appli
159	255	19.7	509	4	US-09-307-794A-315	Sequence 315, App	232	233.5	18.0	1074	2	US-08-470-058-2	Sequence 2, Appli
160	255	19.7	509	4	US-09-305-125A-315	Sequence 315, App	233	233.5	18.0	1074	3	US-09-037-188-2	Sequence 2, Appli
161	255	19.7	509	4	US-09-302-775A-315	Sequence 315, App	234	233.5	18.0	1074	3	US-09-285-310-2	Sequence 2, Appli
162	255	19.7	509	4	US-09-306-700-315	Sequence 315, App	235	233	17.8	284	4	US-09-312-283C-389	Sequence 389, App
163	255	19.7	509	4	US-09-303-603A-315	Sequence 315, App	236	231.5	17.8	353	4	US-09-482-273-243	Sequence 243, App
164	255	19.7	509	4	US-09-304-920A-315	Sequence 315, App	237	231.5	17.8	823	4	US-09-949-016-6852	Sequence 6852, Ap
165	255	19.7	509	4	US-09-309-064-315	Sequence 315, App	238	231	17.8	1068	1	US-08-537-210A-2	Sequence 2, Appli
166	255	19.7	509	4	US-09-305-381A-315	Sequence 315, App	239	229.5	17.7	1068	3	US-09-113-825-2	Sequence 2, Appli
167	255	19.7	509	4	US-09-306-618-315	Sequence 315, App	240	229.5	17.7	520	3	US-09-068-740A-3	Sequence 3, Appli
168	253.5	19.5	3571	4	US-09-911-842A-2	Sequence 2, Appli	241	229.5	17.7	702	3	US-09-068-740A-4	Sequence 4, Appli
169	253	19.5	3594	4	US-09-911-842A-4	Sequence 4, Appli	242	229.5	17.7	723	3	US-09-068-740A-9	Sequence 9, Appli
170	250	19.3	1246	4	US-09-319-497-85	Sequence 85, Appl	243	229.5	17.7	723	4	US-09-423-753-27	Sequence 27, Appl
171	250	19.3	1247	4	US-09-361-403-14	Sequence 14, Appl	244	229.5	17.7	723	4	US-09-641-612-6	Sequence 6, Appli
172	249	19.2	446	1	US-08-307-444A-5	Sequence 5, Appli	245	229.5	17.7	846	4	US-09-949-016-10381	Sequence 10381, A
173	249	19.2	446	1	US-08-587-389-5	Sequence 5, Appli	246	228.5	17.6	729	3	US-08-872-855-8	Sequence 8, Appli

247	228	17.6	816	2	US-08-820-170A-37	Sequence 37, Appl	320	203.5	15.7	750	4	US-09-270-767-42975	Sequence 42975, A
248	228	17.6	816	3	US-09-055-699-37	Sequence 37, Appl	321	201	15.5	105	4	US-09-621-976-5035	Sequence 5035, Ap
249	228	17.6	816	3	US-09-273-565-37	Sequence 37, Appl	322	201	15.5	4544	1	US-08-469-486-52	Sequence 52, Appl
250	228	17.6	816	3	US-09-565-538-37	Sequence 37, Appl	323	201	15.5	4544	2	US-08-469-486-52	Sequence 52, Appl
251	228	17.6	816	3	US-09-661-468-37	Sequence 37, Appl	324	201	15.4	584	4	US-09-949-016-10340	Sequence 10340, A
252	228	17.6	816	4	US-09-976-165-37	Sequence 37, Appl	325	200	15.4	584	4	US-09-949-016-10341	Sequence 10341, A
253	228	17.6	1248	3	US-08-802-046-6	Sequence 6, Appl	326	199	15.3	1523	3	US-09-182-024A-2	Sequence 2, Appl
254	228	17.6	1248	4	US-09-566-047-6	Sequence 6, Appl	327	198.5	15.3	545	3	US-10-067-422-11	Sequence 11, Appl
255	227.5	17.5	860	1	US-08-092-817-4	Sequence 4, Appl	328	198.5	15.3	737	4	US-09-866-028-15	Sequence 15, Appl
256	227.5	17.5	860	3	US-08-485-128-4	Sequence 4, Appl	329	198.5	15.3	737	4	US-09-944-457-15	Sequence 15, Appl
257	227.5	17.5	860	4	US-09-804-778A-8	Sequence 8, Appl	330	198	15.3	578	3	US-08-981-392-13	Sequence 13, Appl
258	227.5	17.5	860	4	US-09-824-637-4	Sequence 4, Appl	331	198	15.3	578	3	US-09-908-322-13	Sequence 13, Appl
259	227.5	17.5	1410	2	US-08-470-058-4	Sequence 4, Appl	332	195	15.0	846	1	US-08-149-103-4	Sequence 4, Appl
260	227.5	17.5	1410	3	US-09-037-188-4	Sequence 4, Appl	333	195	15.0	846	1	US-08-451-883-4	Sequence 4, Appl
261	227.5	17.5	1410	3	US-09-285-310-4	Sequence 4, Appl	334	195	15.0	4654	3	US-08-476-515A-84	Sequence 84, Appl
262	227	17.5	721	3	US-08-872-855-7	Sequence 7, Appl	335	195	15.0	4655	3	US-08-652-877-86	Sequence 86, Appl
263	227	17.5	721	3	US-08-981-392-5	Sequence 5, Appl	336	195	15.0	4655	3	US-08-652-877-86	Sequence 86, Appl
264	227	17.5	721	4	US-09-908-322-5	Sequence 5, Appl	337	195	15.0	4655	3	US-08-652-877-88	Sequence 88, Appl
265	223	17.2	642	3	US-08-872-855-10	Sequence 10, Appl	338	195	15.0	4655	3	US-08-652-877-90	Sequence 90, Appl
266	222.5	17.2	502	3	US-09-363-316B-18	Sequence 18, Appl	339	191.5	14.8	735	3	US-09-191-647-9	Sequence 9, Appl
267	222.5	17.2	502	4	US-10-136-227A-18	Sequence 18, Appl	340	191.5	14.8	735	3	US-09-540-245A-9	Sequence 9, Appl
268	222.5	17.2	502	4	US-09-981-649A-18	Sequence 18, Appl	341	191.5	14.8	735	3	US-09-540-153-9	Sequence 9, Appl
269	222.5	17.2	537	3	US-09-249-697A-4	Sequence 4, Appl	342	190	14.6	846	1	US-08-149-103-3	Sequence 3, Appl
270	222.5	17.2	537	3	US-09-363-316B-4	Sequence 4, Appl	343	190	14.6	846	1	US-08-451-883-3	Sequence 3, Appl
271	222.5	17.2	537	4	US-10-136-227A-4	Sequence 4, Appl	344	190	14.6	904	4	US-09-949-016-9528	Sequence 9528, Ap
272	222.5	17.2	537	4	US-09-981-649A-4	Sequence 4, Appl	345	189.5	14.6	353	4	US-09-907-794A-2	Sequence 2, Appl
273	222.5	17.2	553	3	US-09-249-697A-6	Sequence 6, Appl	346	189.5	14.6	353	4	US-09-905-125A-2	Sequence 2, Appl
274	222.5	17.2	553	3	US-09-363-316B-6	Sequence 6, Appl	347	189.5	14.6	353	4	US-09-902-775A-2	Sequence 2, Appl
275	222.5	17.2	553	3	US-09-363-316B-6	Sequence 6, Appl	348	189.5	14.6	353	4	US-09-906-700-2	Sequence 2, Appl
276	222.5	17.2	553	3	US-09-363-316B-24	Sequence 24, Appl	349	189.5	14.6	353	4	US-09-903-603A-2	Sequence 2, Appl
277	222.5	17.2	553	4	US-10-136-227A-6	Sequence 6, Appl	350	189.5	14.6	353	4	US-09-904-920A-2	Sequence 2, Appl
278	222.5	17.2	553	4	US-09-981-649A-6	Sequence 24, Appl	351	189.5	14.6	353	4	US-09-909-064-2	Sequence 2, Appl
279	222.5	17.2	553	4	US-09-981-649A-6	Sequence 6, Appl	352	189.5	14.6	353	4	US-09-905-381A-2	Sequence 2, Appl
280	222.5	17.2	553	4	US-10-136-227A-30	Sequence 30, Appl	353	189.5	14.6	353	4	US-09-906-618-2	Sequence 2, Appl
281	222.5	17.2	554	4	US-10-136-227A-30	Sequence 30, Appl	354	186.5	14.4	383	1	US-08-597-545-2	Sequence 2, Appl
282	222.5	17.2	554	4	US-09-981-649A-30	Sequence 30, Appl	355	186.5	14.4	383	1	US-08-457-135-2	Sequence 2, Appl
283	222.5	17.2	554	4	US-09-981-649A-30	Sequence 30, Appl	356	186.5	14.4	726	6	5208144-37	Patent No. 5208144
284	222.5	17.2	554	4	US-09-981-649A-32	Sequence 32, Appl	357	186.5	14.4	726	6	5208144-37	Patent No. 5208144
285	222.5	17.2	559	4	US-10-136-227A-28	Sequence 28, Appl	358	186.5	14.3	726	6	5208144-37	Patent No. 5208144
286	222.5	17.2	559	4	US-09-981-649A-28	Sequence 28, Appl	359	185.5	14.3	595	4	US-09-641-612-5	Sequence 5, Appl
287	222.5	17.2	594	4	US-09-949-016-8175	Sequence 8175, Ap	360	184	14.2	437	1	US-08-487-037-2	Sequence 2, Appl
288	222	17.1	728	3	US-08-981-392-2	Sequence 2, Appl	361	184	14.2	437	1	US-08-487-037-3	Sequence 3, Appl
289	222	17.1	728	4	US-09-908-322-2	Sequence 2, Appl	362	184	14.2	873	3	US-08-393-734-2	Sequence 2, Appl
290	218.5	16.8	1015	1	US-08-537-210A-1	Sequence 1, Appl	363	184	14.2	873	3	US-08-894-489-2	Sequence 2, Appl
291	218.5	16.8	1015	3	US-09-113-825-1	Sequence 1, Appl	364	182.5	14.1	500	4	US-09-423-753-2	Sequence 2, Appl
292	217.5	16.8	148	4	US-09-270-767-31657	Sequence 31657, A	365	182.5	14.1	500	4	US-09-423-753-3	Sequence 3, Appl
293	217	16.7	757	4	US-09-949-016-6963	Sequence 6963, Ap	366	182.5	14.1	685	3	US-08-872-855-2	Sequence 2, Appl
294	217	16.7	758	4	US-09-949-016-8087	Sequence 8087, Ap	367	182.5	14.1	685	3	US-09-423-753-25	Sequence 25, Appl
295	216.5	16.7	717	3	US-08-872-855-9	Sequence 9, Appl	368	182.5	14.1	685	4	US-09-641-612-7	Sequence 7, Appl
296	214.5	16.5	1529	4	US-09-312-283C-396	Sequence 396, App	369	182	14.0	2362	4	US-09-949-016-8985	Sequence 8985, Ap
297	214	16.5	830	3	US-08-872-855-11	Sequence 11, Appl	370	180.5	13.9	583	4	US-09-641-612-2	Sequence 2, Appl
298	214	16.5	833	1	US-08-264-534-6	Sequence 6, Appl	371	179.5	13.8	385	1	US-08-597-545-1	Sequence 1, Appl
299	214	16.5	833	1	US-08-083-590A-2	Sequence 2, Appl	372	179.5	13.8	385	1	US-08-457-135-1	Sequence 1, Appl
300	214	16.5	833	1	US-08-455-500-6	Sequence 6, Appl	373	179.5	13.8	385	4	US-09-142-027A-10	Sequence 10, Appl
301	214	16.5	833	2	US-08-346-126-6	Sequence 6, Appl	374	179.5	13.8	448	5	PCT-US92-10068-1	Sequence 1, Appl
302	214	16.5	833	2	US-08-346-126-6	Sequence 6, Appl	375	179.5	13.8	448	4	US-09-367-777-44	Sequence 44, Appl
303	214	16.5	833	3	US-08-532-384-2	Sequence 2, Appl	376	179.5	13.8	488	4	US-09-367-791A-27	Sequence 27, Appl
304	214	16.5	833	3	US-08-893-828-6	Sequence 6, Appl	377	179.5	13.8	496	4	US-09-949-016-9524	Sequence 9524, Ap
305	212.5	16.4	492	3	US-09-724-864-39	Sequence 39, Appl	378	177.5	13.7	448	1	US-08-295-411-3	Sequence 3, Appl
306	211.5	16.3	810	2	US-08-820-170A-34	Sequence 34, Appl	379	177.5	13.7	448	2	US-08-855-471-3	Sequence 3, Appl
307	211.5	16.3	810	3	US-09-055-699-34	Sequence 34, Appl	380	177.5	13.7	448	5	PCT-US92-10242-3	Sequence 3, Appl
308	211.5	16.3	810	3	US-09-273-565-34	Sequence 34, Appl	381	174.5	13.5	788	1	US-08-572-225-1	Sequence 1, Appl
309	211.5	16.3	810	3	US-09-565-538-34	Sequence 34, Appl	382	174.5	13.5	986	4	US-09-285-385C-19	Sequence 19, Appl
310	211.5	16.3	810	3	US-09-661-468-34	Sequence 34, Appl	383	174.5	13.5	986	4	US-09-949-016-6690	Sequence 6690, Ap
311	211.5	16.3	810	4	US-09-976-165-34	Sequence 34, Appl	384	174.5	13.5	1012	4	US-09-285-385C-4	Sequence 4, Appl
312	211.5	16.3	1525	3	US-09-131-647-2	Sequence 2, Appl	385	174.5	13.5	1480	3	US-09-191-647-7	Sequence 7, Appl
313	211.5	16.3	1525	3	US-09-540-245A-2	Sequence 2, Appl	386	174.5	13.5	1480	3	US-09-540-245A-7	Sequence 7, Appl
314	211.5	16.3	1525	3	US-09-540-153-2	Sequence 2, Appl	387	174.5	13.5	1480	3	US-09-540-153-7	Sequence 7, Appl
315	211	16.3	832	3	US-08-981-392-6	Sequence 6, Appl	388	174.5	13.5	1480	3	PCT-US91-09055-5	Sequence 5, Appl
316	211	16.3	832	4	US-09-908-322-6	Sequence 6, Appl	389	174.5	13.5	1480	5	PCT-US91-09055-5	Sequence 2, Appl
317	210.5	16.2	716	4	US-09-312-283C-183	Sequence 183, App	390	172.5	13.3	488	1	US-08-487-037-1	Sequence 1, Appl
318	210.5	16.2	771	3	US-09-188-930-183	Sequence 183, App	391	172	13.3	164	3	US-09-449-697A-9	Sequence 9, Appl
319	203.5	15.7	614	4	US-09-949-016-8536	Sequence 8536, Ap	392	172	13.3	164	3	US-09-363-316B-9	Sequence 9, Appl

393	172	13.3	164	4	US-10-136-227A-9	Sequence 9, Appl1	466	164	12.6	460	6	5270178-15	Patent No. 5270178
394	172	13.3	164	4	US-09-981-649A-9	Sequence 9, Appl1	467	164	12.6	460	6	5270178-16	Patent No. 5270178
395	170.5	13.1	139	1	US-08-330-978-2	Sequence 2, Appl1	468	164	12.6	461	4	US-10-182-263-2	Sequence 2, Appl1
396	170.5	13.1	139	1	US-08-474-042-2	Sequence 2, Appl1	469	164	12.6	461	4	US-09-054-272-32	Sequence 32, Appl1
397	170.5	13.1	139	1	US-08-484-558-2	Sequence 2, Appl1	470	164	12.6	461	4	US-09-949-016-5921	Sequence 5921, Ap
398	170.5	13.1	139	1	US-08-774-592-2	Sequence 2, Appl1	471	164	12.6	461	6	525537-2	Patent No. 525537
399	169.5	13.1	157	3	US-08-981-392-68	Sequence 68, Appl1	472	164	12.6	461	6	5270178-2	Patent No. 5270178
400	169.5	13.1	157	3	US-08-981-392-68	Sequence 68, Appl1	473	164	12.6	461	6	5270178-17	Patent No. 5270178
401	169.5	13.1	157	4	US-09-307-794A-109	Sequence 109, App	474	164	12.6	461	6	5270178-18	Patent No. 5270178
402	169.5	13.1	420	4	US-09-305-125A-109	Sequence 109, App	475	164	12.6	461	6	5460953-3	Patent No. 5460953
403	169.5	13.1	420	4	US-09-302-775A-109	Sequence 109, App	476	164	12.6	461	6	525537-2	Patent No. 525537
404	169.5	13.1	420	4	US-09-306-700-109	Sequence 109, App	477	164	12.6	461	6	5270178-2	Patent No. 5270178
405	169.5	13.1	420	4	US-09-303-603A-109	Sequence 109, App	478	164	12.6	461	6	5270178-17	Patent No. 5270178
406	169.5	13.1	420	4	US-09-304-920A-109	Sequence 109, App	479	164	12.6	461	6	5270178-18	Patent No. 5270178
407	169.5	13.1	420	4	US-09-309-064-109	Sequence 109, App	480	164	12.6	461	6	5460953-3	Patent No. 5460953
408	169.5	13.1	420	4	US-09-305-381A-109	Sequence 109, App	481	164	12.6	485	4	US-09-949-016-10882	Sequence 10882, A
409	169.5	13.1	420	4	US-09-306-618-109	Sequence 109, App	482	162.5	12.5	591	3	US-08-991-408-4	Sequence 4, Appl1
410	168.5	13.0	242	4	US-09-312-283C-393	Sequence 393, App	483	162.5	12.5	591	3	US-09-432-473-4	Sequence 4, Appl1
411	168.5	13.0	487	1	US-08-469-486-53	Sequence 53, Appl1	484	162.5	12.5	1013	2	US-08-866-650-5	Sequence 5, Appl1
412	168.5	13.0	487	1	US-08-469-658-53	Sequence 53, Appl1	485	162.5	12.5	1013	2	US-09-021-287-5	Sequence 5, Appl1
413	168.5	13.0	482	1	US-08-469-486-2	Sequence 2, Appl1	486	162.5	12.5	1013	3	US-08-991-408-2	Sequence 2, Appl1
414	168.5	13.0	422	2	US-08-469-658-2	Sequence 2, Appl1	487	162.5	12.5	1013	3	US-09-240-473-5	Sequence 5, Appl1
415	168.5	13.0	1013	2	US-08-866-650-3	Sequence 3, Appl1	488	162.5	12.5	1013	3	US-09-432-473-2	Sequence 2, Appl1
416	168.5	13.0	1013	3	US-09-021-287-3	Sequence 3, Appl1	489	162.5	12.5	1013	4	US-09-285-385C-20	Sequence 20, Appl1
417	168.5	13.0	1013	3	US-09-240-473-3	Sequence 3, Appl1	490	160	12.3	884	6	5208144-8	Patent No. 5208144
418	167.5	12.9	157	3	US-08-872-855-6	Sequence 6, Appl1	491	160	12.3	884	6	5208144-8	Patent No. 5208144
419	165	12.7	136	3	US-08-981-392-35	Sequence 35, Appl1	492	160	12.3	2200	4	US-09-796-575-2	Sequence 2, Appl1
420	165	12.7	136	4	US-09-308-322-35	Sequence 35, Appl1	493	159.5	12.3	961	4	US-09-657-472-4	Sequence 4, Appl1
421	165	12.7	406	1	US-08-295-411-5	Sequence 5, Appl1	494	159.5	12.3	961	5	PCT-US93-11725-4	Sequence 4, Appl1
422	165	12.7	406	2	US-08-955-471-5	Sequence 5, Appl1	495	158.5	12.2	970	4	US-09-949-016-10131	Sequence 24, Appl1
423	165	12.7	406	4	US-09-782-587B-1	Sequence 1, Appl1	496	158	12.2	406	1	US-08-293-778-24	Sequence 4, Appl1
424	165	12.7	406	4	US-09-782-587B-3	Sequence 3, Appl1	497	157.5	12.1	986	3	US-08-872-757-4	Sequence 4, Appl1
425	165	12.7	406	5	PCT-US92-10243-5	Sequence 5, Appl1	498	157.5	12.1	986	4	US-09-850-048A-4	Sequence 4, Appl1
426	165	12.7	444	1	US-08-475-845-2	Sequence 2, Appl1	499	157.5	12.1	1810	4	US-08-793-273C-4	Sequence 4, Appl1
427	165	12.7	444	2	US-08-327-690-2	Sequence 2, Appl1	500	157.5	12.1	1810	5	PCT-US95-11684-4	Sequence 4, Appl1
428	165	12.7	444	2	US-08-660-289-2	Sequence 2, Appl1	501	157	12.1	356	4	US-09-054-272-18	Sequence 18, Appl1
429	165	12.7	444	2	US-08-537-807-2	Sequence 2, Appl1	502	157	12.1	943	3	US-08-476-515A-12	Sequence 12, Appl1
430	165	12.7	444	2	US-08-871-003-2	Sequence 2, Appl1	503	157	12.1	944	3	US-08-652-877-12	Sequence 12, Appl1
431	165	12.7	444	3	US-08-464-233-2	Sequence 2, Appl1	504	157	12.1	1170	1	US-08-313-288B-20	Sequence 20, Appl1
432	165	12.7	444	3	US-09-189-607-2	Sequence 2, Appl1	505	157	12.1	1170	4	US-09-657-472-2	Sequence 2, Appl1
433	165	12.7	444	3	US-09-378-907-2	Sequence 2, Appl1	506	155.5	12.0	2015	4	US-09-285-385C-2	Sequence 2, Appl1
434	165	12.7	444	3	PCT-US94-05779-2	Sequence 2, Appl1	507	155.5	12.0	2199	4	US-08-793-273C-2	Sequence 2, Appl1
435	165	12.7	461	4	US-09-949-016-8839	Sequence 8839, Ap	508	155.5	12.0	2199	5	PCT-US95-11684-2	Sequence 2, Appl1
436	165	12.7	466	1	US-07-982-202A-4	Sequence 4, Appl1	509	154.5	11.9	777	4	US-09-270-767-44409	Sequence 44409, A
437	165	12.7	466	1	US-08-021-615A-4	Sequence 4, Appl1	510	152	11.7	233	4	US-09-216-393B-110	Sequence 110, App
438	165	12.7	466	1	US-08-321-777-4	Sequence 14, Appl1	511	152	11.7	3635	4	US-09-845-583A-2	Sequence 2, Appl1
439	165	12.7	466	3	US-09-009-217-14	Sequence 14, Appl1	512	150	11.6	415	1	US-08-073-531B-1	Sequence 1, Appl1
440	165	12.7	466	3	US-09-009-656-14	Sequence 14, Appl1	513	150	11.6	415	1	US-08-295-411-2	Sequence 2, Appl1
441	165	12.7	466	5	PCT-US93-04493-4	Sequence 4, Appl1	514	150	11.6	415	2	US-08-955-471-2	Sequence 2, Appl1
442	165	12.7	483	4	US-09-949-016-9523	Sequence 9523, Ap	515	150	11.6	415	2	US-08-766-288-1	Sequence 1, Appl1
443	164.5	12.7	239	4	US-09-270-767-33770	Sequence 33770, A	516	150	11.6	415	4	US-09-118-748-2	Sequence 2, Appl1
444	164.5	12.7	239	4	US-09-270-767-48987	Sequence 48987, A	517	150	11.6	415	5	PCT-US92-10242-2	Sequence 2, Appl1
445	164	12.6	409	3	US-09-065-872-2	Sequence 2, Appl1	518	150	11.6	461	3	US-08-742-877-2	Sequence 2, Appl1
446	164	12.6	409	4	US-09-667-570A-2	Sequence 2, Appl1	519	150	11.6	461	3	US-09-053-871A-21	Sequence 21, Appl1
447	164	12.6	410	3	US-09-065-872-1	Sequence 1, Appl1	520	150	11.6	461	4	US-10-133-907-5	Sequence 5, Appl1
448	164	12.6	410	4	US-09-667-570A-1	Sequence 1, Appl1	521	150	11.6	461	6	5521070-2	Patent No. 5521070
449	164	12.6	419	1	US-08-395-411-1	Sequence 1, Appl1	522	150	11.6	461	6	5521070-2	Patent No. 5521070
450	164	12.6	419	2	US-08-955-471-1	Sequence 1, Appl1	523	150	11.6	480	4	US-09-949-016-11123	Sequence 11123, A
451	164	12.6	419	4	US-09-667-570A-3	Sequence 3, Appl1	524	149	11.5	956	4	US-09-949-016-11332	Sequence 11332, A
452	164	12.6	419	4	US-10-182-263-1	Sequence 1, Appl1	525	146.5	11.3	192	3	US-08-981-392-65	Sequence 65, Appl1
453	164	12.6	419	4	US-10-182-263-3	Sequence 3, Appl1	526	146.5	11.3	192	4	US-09-908-322-65	Sequence 65, Appl1
454	164	12.6	419	4	US-10-182-263-4	Sequence 4, Appl1	527	146.5	11.3	276	3	US-08-981-392-43	Sequence 43, Appl1
455	164	12.6	419	4	US-10-182-263-5	Sequence 5, Appl1	528	146.5	11.3	276	4	US-09-908-322-43	Sequence 43, Appl1
456	164	12.6	419	4	US-10-182-263-6	Sequence 6, Appl1	529	146.5	11.3	549	1	US-08-325-071-61	Sequence 61, Appl1
457	164	12.6	419	5	PCT-US92-10242-1	Sequence 1, Appl1	530	146.5	11.3	549	3	US-08-461-004A-61	Sequence 61, Appl1
458	164	12.6	460	2	US-08-756-506-2	Sequence 2, Appl1	531	146.5	11.3	650	1	US-08-325-071-63	Sequence 63, Appl1
459	164	12.6	460	2	US-08-756-506-4	Sequence 4, Appl1	532	146.5	11.3	650	3	US-08-461-004A-63	Sequence 63, Appl1
460	164	12.6	460	6	5270178-13	Patent No. 5270178	533	145.5	11.2	299	3	US-09-188-930-332	Sequence 332, App
461	164	12.6	460	6	5270178-14	Patent No. 5270178	534	145.5	11.2	299	4	US-09-312-283C-192	Sequence 192, App
462	164	12.6	460	6	5270178-15	Patent No. 5270178	535	145.5	11.2	299	4	US-09-312-283C-332	Sequence 332, App
463	164	12.6	460	6	5270178-16	Patent No. 5270178	536	144	11.1	235	4	US-09-902-540-15031	Sequence 15031, A
464	164	12.6	460	6	5270178-13	Patent No. 5270178	537	143.5	11.1	620	1	US-08-325-071-65	Sequence 65, Appl1
465	164	12.6	460	6	5270178-14	Patent No. 5270178	538	143.5	11.1	620	3	US-08-461-004A-65	Sequence 65, Appl1

539	143.5	11.1	650	1	US-08-325-071-56	Sequence 56, Appl	612	133.5	10.3	1481	2	US-08-599-654-40	Sequence 40, Appl
540	143.5	11.1	650	3	US-08-461-004A-56	Sequence 56, Appl	613	133.5	10.3	1481	3	US-08-944-868A-40	Sequence 40, Appl
541	143.5	11.1	688	1	US-08-325-071-57	Sequence 57, Appl	614	133.5	10.3	1481	3	US-08-944-868A-40	Sequence 40, Appl
542	143.5	11.1	688	3	US-08-461-004A-57	Sequence 57, Appl	615	133.5	10.3	1481	3	US-08-944-868A-40	Sequence 40, Appl
543	143.5	11.1	3647	4	US-09-949-016-10932	Sequence 10932, A	616	133.5	10.3	1587	4	US-09-845-583A-10	Sequence 10, Appl
544	143	11.0	491	3	US-08-030-335-2	Sequence 2, Appl	617	133.5	10.3	1587	4	US-09-561-709B-3	Sequence 3, Appl
545	143	11.0	748	2	US-08-920-234-2	Sequence 2, Appl	618	132	10.2	229	3	US-09-188-930-192	Sequence 192, Appl
546	143	11.0	748	2	US-08-937-931-4	Sequence 4, Appl	619	132	10.2	1138	1	US-08-323-474-8	Sequence 8, Appl
547	143	11.0	748	3	US-08-285-502-4	Sequence 4, Appl	620	132	10.2	1138	2	US-08-469-537A-98	Sequence 98, Appl
548	143	11.0	748	3	US-09-030-335-9	Sequence 9, Appl	621	132	10.2	1138	2	US-08-320-240A-5	Sequence 5, Appl
549	143	11.0	748	3	US-09-709-126-4	Sequence 4, Appl	622	132	10.2	1150	4	US-09-949-016-7769	Sequence 7769, Ap
550	143	11.0	748	3	US-08-871-385A-4	Sequence 4, Appl	623	132	10.2	1451	4	US-09-060-299-25	Sequence 25, Appl
551	143	11.0	761	3	US-09-949-016-10631	Sequence 10631, A	624	132	10.2	1451	4	US-09-402-923A-25	Sequence 25, Appl
552	143	11.0	799	3	US-08-030-335-4	Sequence 4, Appl	625	132	10.2	1584	4	US-09-060-299-39	Sequence 39, Appl
553	142.5	11.0	278	3	US-09-724-864-52	Sequence 52, Appl	626	132	10.2	1584	4	US-09-402-923A-39	Sequence 39, Appl
554	141	10.9	1358	1	US-08-404-665-4	Sequence 4, Appl	627	132	10.2	1591	4	US-09-060-299-4	Sequence 4, Appl
555	141	10.9	1358	1	US-08-404-671-4	Sequence 4, Appl	628	132	10.2	1591	4	US-09-060-299-43	Sequence 43, Appl
556	141	10.9	1358	1	US-08-404-781-4	Sequence 4, Appl	629	132	10.2	1591	4	US-09-402-923A-4	Sequence 4, Appl
557	140.5	10.8	650	1	US-08-325-071-59	Sequence 59, Appl	630	132	10.2	1591	4	US-09-402-923A-43	Sequence 43, Appl
558	140.5	10.8	650	3	US-08-461-004A-59	Sequence 59, Appl	631	132	10.2	1615	4	US-09-060-299-3	Sequence 3, Appl
559	139.5	10.8	44	6	5177197-48	Patent No. 5177197	632	132	10.2	1615	4	US-09-402-923A-3	Sequence 3, Appl
560	139.5	10.8	44	6	5177197-48	Patent No. 5177197	633	132	10.2	1639	4	US-09-060-299-29	Sequence 29, Appl
561	139	10.7	77	1	US-08-264-534-1	Sequence 1, Appl	634	132	10.2	1639	4	US-09-402-923A-29	Sequence 29, Appl
562	139	10.7	77	1	US-08-083-590A-14	Sequence 14, Appl	635	131.5	10.1	765	4	US-09-949-016-10117	Sequence 10117, A
563	139	10.7	77	1	US-08-465-500-1	Sequence 1, Appl	636	131	10.1	704	4	US-09-590-656-2	Sequence 2, Appl
564	139	10.7	77	2	US-08-346-126-1	Sequence 1, Appl	637	131	10.1	704	4	US-09-733-764-2	Sequence 2, Appl
565	139	10.7	77	2	US-08-346-126-1	Sequence 1, Appl	638	131	10.1	718	1	US-08-444-792-4	Sequence 4, Appl
566	139	10.7	77	3	US-08-532-384-14	Sequence 14, Appl	639	131	10.1	718	1	US-08-445-042-4	Sequence 4, Appl
567	139	10.7	77	3	US-08-893-828-1	Sequence 1, Appl	640	131	10.1	784	4	US-09-949-016-9467	Sequence 9467, Ap
568	139	10.7	100	3	US-09-249-973A-3	Sequence 3, Appl	641	131	10.1	788	2	US-07-728-215-32	Sequence 32, Appl
569	139	10.7	100	3	US-09-363-316B-3	Sequence 3, Appl	642	131	10.1	788	3	US-08-938-085A-32	Sequence 32, Appl
570	139	10.7	100	4	US-10-136-227A-3	Sequence 3, Appl	643	131	10.1	788	3	US-09-409-648-3	Sequence 3, Appl
571	139	10.7	100	4	US-09-981-649A-3	Sequence 3, Appl	644	131	10.1	788	3	US-09-409-648-4	Sequence 4, Appl
572	138	10.6	2254	4	US-09-949-016-9270	Sequence 9270, Ap	645	131	10.1	788	4	US-10-072-844-32	Sequence 32, Appl
573	137.5	10.6	889	5	PCT-US93-11725-2	Sequence 2, Appl	646	131	10.1	788	4	US-10-072-844-32	Sequence 32, Appl
574	137	10.6	221	2	US-08-480-229C-29	Sequence 29, Appl	647	131	10.1	788	4	US-10-072-841A-32	Sequence 32, Appl
575	137	10.6	221	2	US-08-659-235C-29	Sequence 29, Appl	648	131	10.1	788	4	US-09-054-272-8	Sequence 8, Appl
576	137	10.6	480	2	US-08-480-229C-10	Sequence 10, Appl	649	131	10.1	788	4	US-09-054-272-44	Sequence 44, Appl
577	137	10.6	480	2	US-08-659-235C-10	Sequence 10, Appl	650	131	10.1	788	4	US-10-219-631A-32	Sequence 32, Appl
578	137	10.6	730	3	US-08-872-757-2	Sequence 2, Appl	651	131	10.1	788	4	US-09-949-016-5901	Sequence 5901, Ap
579	137	10.6	730	4	US-09-850-048A-2	Sequence 2, Appl	652	131	10.1	977	4	US-09-590-656-1	Sequence 1, Appl
580	136.5	10.5	243	3	US-09-191-647-14	Sequence 14, Appl	653	131	10.1	977	4	US-09-733-764-1	Sequence 1, Appl
581	136.5	10.5	243	3	US-09-540-245A-14	Sequence 14, Appl	654	131	10.1	1124	1	US-08-323-474-2	Sequence 2, Appl
582	136.5	10.5	243	3	US-09-540-153-14	Sequence 14, Appl	655	131	10.1	1124	1	US-09-949-016-5946	Sequence 5946, Ap
583	136.5	10.5	650	1	US-08-325-071-67	Sequence 67, Appl	656	131	10.1	1124	5	PCT-US93-06093-2	Sequence 2, Appl
584	136.5	10.5	650	3	US-08-461-004A-67	Sequence 67, Appl	657	131	10.1	1157	4	US-09-949-016-9568	Sequence 9568, Ap
585	136.5	10.5	1799	4	US-09-845-583A-6	Sequence 6, Appl	658	131	10.1	1615	4	US-09-544-398B-3	Sequence 3, Appl
586	136	10.5	749	2	US-08-937-931-8	Sequence 8, Appl	659	131	10.1	1615	4	US-09-544-398B-4	Sequence 4, Appl
587	136	10.5	749	3	US-09-285-502-8	Sequence 8, Appl	660	131	10.1	1615	4	US-09-543-771B-3	Sequence 3, Appl
588	136	10.5	749	3	US-09-709-126-8	Sequence 8, Appl	661	131	10.1	1615	4	US-09-543-771B-4	Sequence 4, Appl
589	136	10.5	749	3	US-09-871-385A-8	Sequence 8, Appl	662	130.5	10.1	690	4	US-09-907-794A-49	Sequence 49, Appl
590	136	10.5	1171	1	US-08-445-135-1	Sequence 1, Appl	663	130.5	10.1	690	4	US-09-905-125A-49	Sequence 49, Appl
591	136	10.5	1854	4	US-09-949-016-11625	Sequence 11625, A	664	130.5	10.1	690	4	US-09-902-775A-49	Sequence 49, Appl
592	135.5	10.4	1798	4	US-09-845-583A-8	Sequence 8, Appl	665	130.5	10.1	690	4	US-09-906-700-49	Sequence 49, Appl
593	135.5	10.4	1798	4	US-09-561-709B-11	Sequence 11, Appl	666	130.5	10.1	690	4	US-09-903-603A-49	Sequence 49, Appl
594	135.5	10.4	1798	4	US-09-917-254-87	Sequence 87, Appl	667	130.5	10.1	690	4	US-09-904-920A-49	Sequence 49, Appl
595	135	10.4	448	4	US-09-949-016-10130	Sequence 10130, A	668	130.5	10.1	690	4	US-09-909-064-49	Sequence 49, Appl
596	135	10.4	513	2	US-08-480-229C-14	Sequence 14, Appl	669	130.5	10.1	690	4	US-09-905-381A-49	Sequence 49, Appl
597	135	10.4	513	2	US-08-659-235C-14	Sequence 14, Appl	670	130.5	10.1	690	4	US-09-906-618-49	Sequence 49, Appl
598	134	10.3	78	1	US-08-264-534-2	Sequence 2, Appl	671	130	10.0	717	4	US-09-949-016-11182	Sequence 11182, A
599	134	10.3	78	1	US-08-083-590A-15	Sequence 15, Appl	672	129.5	10.0	114	2	US-08-733-564-1	Sequence 1, Appl
600	134	10.3	78	1	US-08-465-500-2	Sequence 2, Appl	673	129.5	10.0	115	1	US-08-312-870-9	Sequence 9, Appl
601	134	10.3	78	2	US-08-346-126-2	Sequence 2, Appl	674	129	9.9	1725	4	US-09-562-702A-20	Sequence 20, Appl
602	134	10.3	78	2	US-08-346-126-2	Sequence 2, Appl	675	129	9.9	1725	4	US-09-561-818A-20	Sequence 20, Appl
603	134	10.3	78	3	US-08-532-384-15	Sequence 15, Appl	676	129	9.9	1786	4	US-09-562-702A-18	Sequence 18, Appl
604	134	10.3	78	3	US-08-893-828-2	Sequence 2, Appl	677	129	9.9	1786	4	US-09-561-818A-18	Sequence 18, Appl
605	134	10.3	1586	4	US-09-060-299-44	Sequence 44, Appl	678	128	9.9	699	1	US-09-949-016-6138	Sequence 6138, Ap
606	134	10.3	1586	4	US-09-402-923A-44	Sequence 44, Appl	679	127.5	9.8	356	1	US-08-228-162-2	Sequence 2, Appl
607	134	10.3	1614	4	US-09-060-299-42	Sequence 42, Appl	680	127.5	9.8	721	4	US-09-949-016-11031	Sequence 11031, A
608	134	10.3	1614	4	US-09-402-923A-42	Sequence 42, Appl	681	127.5	9.8	799	1	US-08-054-077C-2	Sequence 2, Appl
609	134	10.3	3084	4	US-09-562-702A-12	Sequence 12, Appl	682	127.5	9.8	1576	4	US-09-562-702A-24	Sequence 24, Appl
610	134	10.3	3106	4	US-09-562-702A-10	Sequence 10, Appl	683	127.5	9.8	1576	4	US-09-561-818A-24	Sequence 24, Appl
611	133.5	10.3	1481	2	US-08-616-844-40	Sequence 40, Appl	684	127.5	9.8	1584	4	US-09-562-702A-28	Sequence 28, Appl

685	127.5	9.8	1609	4	US-09-562-702A-22	Sequence 22, Appl	758	119	9.2	496	4	US-09-949-016-11306	Sequence 11306, A
686	127.5	9.8	1609	4	US-09-561-818A-22	Sequence 22, Appl	759	119	9.2	496	5	PCT-US94-00253-1	Sequence 1, Appli
687	127.5	9.8	1609	4	US-09-538-092-900	Sequence 900, App	760	119	9.2	583	4	US-09-902-540-10714	Sequence 10714, A
688	127.5	9.8	1617	4	US-09-562-702A-26	Sequence 26, Appl	761	119	9.2	830	6	5378464-2	Patent No. 5378464
689	127.5	9.8	1213	4	US-09-949-016-7517	Sequence 7517, Ap	762	119	9.2	830	6	5378464-2	Patent No. 5378464
690	127.5	9.8	3070	4	US-09-961-403-7	Sequence 7, Appli	763	119	9.2	849	4	US-09-949-016-10271	Sequence 10271, A
691	127.5	9.8	3089	4	US-09-562-702A-8	Sequence 8, Appli	764	119	9.2	902	4	US-09-644-600-10	Sequence 10, Appl
692	127.5	9.8	3089	4	US-09-562-702A-4	Sequence 4, Appli	765	119	9.2	902	4	US-09-654-600A-10	Sequence 10, Appl
693	127.5	9.8	3110	4	US-09-562-702A-2	Sequence 2, Appli	766	119	9.2	1572	4	US-09-562-702A-32	Sequence 32, Appl
694	127.5	9.8	3110	4	US-09-562-702A-6	Sequence 6, Appli	767	119	9.2	1572	4	US-09-561-818A-28	Sequence 28, Appl
695	127.5	9.8	3110	4	US-09-561-709B-7	Sequence 7, Appli	768	119	9.2	1605	4	US-09-562-702A-30	Sequence 30, Appl
696	127.5	9.8	3110	4	US-09-917-254-86	Sequence 86, Appl	769	119	9.2	1605	4	US-09-561-818A-26	Sequence 26, Appl
697	127.5	9.8	3110	4	US-09-949-016-5937	Sequence 5937, Ap	770	118.5	9.1	410	6	5177197-1	Patent No. 5177197
698	127.5	9.8	3111	2	US-08-460-309-4	Sequence 4, Appli	771	118.5	9.1	410	6	5177197-1	Patent No. 5177197
699	127.5	9.8	3111	2	US-08-125-077-4	Sequence 4, Appli	772	118.5	9.1	495	4	US-10-006-011A-4	Sequence 4, Appli
700	126.5	9.8	281	3	US-08-652-877-7	Sequence 7, Appli	773	118.5	9.1	705	4	US-10-006-011A-3	Sequence 3, Appli
701	126.5	9.8	281	3	US-08-476-515A-7	Sequence 7, Appli	774	118.5	9.1	769	1	US-08-454-455-6	Sequence 6, Appli
702	126.5	9.8	610	1	US-08-365-470-3	Sequence 3, Appli	775	118.5	9.1	831	4	US-09-949-016-10169	Sequence 10169, A
703	126.5	9.8	610	3	US-09-209-668-19	Sequence 19, Appl	776	118.5	9.1	1113	4	US-09-959-392-4	Sequence 4, Appli
704	126.5	9.8	610	3	US-09-209-490A-89	Sequence 89, Appl	777	118.5	9.1	1172	1	US-08-313-288B-19	Sequence 19, Appl
705	126.5	9.8	610	4	US-09-949-016-5942	Sequence 5942, Ap	778	118.5	9.1	1172	1	US-09-949-016-6333	Sequence 6333, Ap
706	126.5	9.8	610	6	5217870-2	Sequence 5942, Ap	779	118.5	9.1	4391	4	US-10-006-011A-2	Sequence 2, Appli
707	126.5	9.8	610	6	5217870-2	Patent No. 5217870	780	118	9.1	577	2	US-07-728-215-29	Sequence 29, Appl
708	126.5	9.8	647	4	US-09-949-016-10272	Sequence 10272, A	781	118	9.1	577	3	US-08-938-085A-29	Sequence 29, Appl
709	126	9.7	41	4	US-09-341-461-16	Sequence 16, Appl	782	118	9.1	577	4	US-10-072-84A-29	Sequence 29, Appl
710	126	9.7	155	4	US-09-270-767-32193	Sequence 32193, A	783	118	9.1	577	4	US-10-072-838-29	Sequence 29, Appl
711	126	9.7	715	4	US-10-101-464A-924	Sequence 924, App	784	118	9.1	577	4	US-10-072-841A-29	Sequence 29, Appl
712	126	9.7	1135	2	US-08-469-537A-97	Sequence 97, Appl	785	118	9.1	577	4	US-10-219-631A-29	Sequence 29, Appl
713	125.5	9.7	2409	6	5180808-2	Sequence 97, Appl	786	118	9.1	830	5	PCT-US91-05059-2	Sequence 2, Appli
714	125.5	9.7	2409	6	5180808-2	Patent No. 5180808	787	118	9.1	933	2	US-08-313-200-1	Sequence 1, Appli
715	125	9.6	1765	4	US-09-562-702A-16	Sequence 16, Appl	788	118	9.1	933	4	US-09-251-039-2	Sequence 1, Appli
716	125	9.6	1765	4	US-09-561-818A-16	Sequence 16, Appl	789	118	9.1	933	5	PCT-US93-03837-1	Sequence 1, Appli
717	125	9.6	1786	4	US-09-562-702A-14	Sequence 14, Appl	790	118	9.1	1172	4	US-09-560-385A-32	Sequence 32, Appl
718	125	9.6	1786	4	US-09-561-818A-14	Sequence 14, Appl	791	118	9.1	1193	4	US-09-560-385A-30	Sequence 30, Appl
719	125	9.6	1786	4	US-09-561-709B-9	Sequence 9, Appli	792	118	9.1	1257	1	US-08-340-428B-49	Sequence 49, Appl
720	125	9.6	1786	4	US-09-538-092-869	Sequence 869, App	793	117.5	9.1	42	4	US-09-341-461-14	Sequence 14, Appl
721	124.5	9.6	179	4	US-09-148-545-177	Sequence 177, App	794	117.5	9.1	1073	4	US-09-949-016-9771	Sequence 9771, Ap
722	124.5	9.6	265	2	US-08-937-931-6	Sequence 6, Appli	795	117.5	9.1	1342	4	US-09-561-709B-13	Sequence 13, Appl
723	124.5	9.6	265	3	US-09-385-502-6	Sequence 6, Appli	796	117	9.0	933	4	US-09-949-016-5953	Sequence 5953, Ap
724	124.5	9.6	265	3	US-09-709-126-6	Sequence 6, Appli	797	117	9.0	933	4	US-09-949-016-7322	Sequence 7322, Ap
725	124.5	9.6	265	3	US-09-871-385A-6	Sequence 6, Appli	798	117	9.0	1621	4	US-09-949-016-8450	Sequence 8450, Ap
726	124.5	9.6	1761	4	US-09-561-709B-1	Sequence 1, Appli	799	116.5	9.0	42	6	5177197-41	Patent No. 5177197
727	123.5	9.5	197	4	US-09-370-838-206	Sequence 206, App	800	116.5	9.0	42	6	5177197-41	Patent No. 5177197
728	123.5	9.5	197	4	US-09-854-133-206	Sequence 206, App	801	116.5	9.0	131	2	US-08-650-598-3	Sequence 3, Appli
729	123.5	9.5	652	3	US-09-110-116-1	Sequence 1, Appli	802	116.5	9.0	1101	4	US-09-561-709B-5	Sequence 5, Appli
730	123.5	9.5	652	3	US-08-356-322-2	Sequence 2, Appli	803	116	8.9	794	4	US-09-949-016-10746	Sequence 10746, A
731	123	9.5	991	4	US-09-949-016-7768	Sequence 7768, Ap	804	116	8.9	1118	1	US-07-934-393B-2	Sequence 2, Appli
732	123	9.5	1551	4	US-09-949-016-6785	Sequence 6785, Ap	805	116	8.9	1118	1	US-08-278-089A-2	Sequence 2, Appli
733	122.5	9.4	441	4	US-09-949-016-10792	Sequence 10792, A	806	116	8.9	1118	2	US-08-838-957A-2	Sequence 2, Appli
734	122.5	9.4	560	4	US-09-949-016-6458	Sequence 6458, Ap	807	116	8.9	1122	1	US-08-278-089A-6	Sequence 6, Appli
735	122.5	9.4	560	4	US-09-912-559-3	Sequence 3, Appli	808	116	8.9	1122	2	US-08-838-957A-6	Sequence 6, Appli
736	122.5	9.4	560	4	US-09-312-559-4	Sequence 4, Appli	809	114.5	8.8	96	4	US-09-270-767-32102	Sequence 32102, A
737	122	9.4	1106	4	US-09-949-016-9626	Sequence 9626, Ap	810	114.5	8.8	830	1	US-08-110-158-4	Sequence 4, Appli
738	121	9.3	234	4	US-09-502-540-15175	Sequence 15175, A	811	114	8.8	788	2	US-07-728-215-27	Sequence 27, Appl
739	121	9.3	1101	2	US-08-469-537A-96	Sequence 96, Appl	812	114	8.8	788	3	US-08-938-085A-27	Sequence 27, Appl
740	120.5	9.3	1104	2	US-08-327-832-5	Sequence 5, Appli	813	114	8.8	788	4	US-10-072-84A-27	Sequence 27, Appl
741	120.5	9.3	1104	2	US-08-828-584-5	Sequence 5, Appli	814	114	8.8	788	4	US-10-072-838-27	Sequence 27, Appl
742	120	9.3	788	1	US-08-454-455-4	Sequence 4, Appli	815	114	8.8	788	4	US-10-072-841A-27	Sequence 27, Appl
743	120	9.3	1111	3	US-08-317-450B-15	Sequence 15, Appl	816	114	8.8	788	4	US-10-219-631A-27	Sequence 27, Appl
744	120	9.3	1111	3	US-08-800-593-15	Sequence 15, Appl	817	114	8.8	1345	4	US-09-949-016-8313	Sequence 8313, Ap
745	120	9.3	1172	4	US-09-560-385A-28	Sequence 28, Appl	818	114	8.8	2214	1	US-08-727-034-7	Sequence 7, Appli
746	120	9.3	1193	1	US-08-317-450B-13	Sequence 13, Appl	819	114	8.8	2214	4	US-09-919-039-40	Sequence 40, Appl
747	120	9.3	1193	3	US-08-800-593-13	Sequence 13, Appl	820	114	8.8	2476	2	US-08-276-967-2	Sequence 2, Appli
748	120	9.3	1193	4	US-09-560-385A-26	Sequence 26, Appl	821	113.5	8.8	194	3	US-09-188-930-335	Sequence 335, App
749	119.5	9.2	439	4	US-09-949-016-9260	Sequence 9260, Ap	822	113.5	8.8	194	4	US-09-312-285C-335	Sequence 335, App
750	119	9.2	41	4	US-09-341-461-15	Sequence 15, Appl	823	113.5	8.8	240	4	US-10-006-011A-5	Sequence 5, Appli
751	119	9.2	314	2	US-08-460-309-19	Sequence 19, Appl	824	113.5	8.8	709	4	US-09-874-923-121	Sequence 121, App
752	119	9.2	314	2	US-08-125-077-19	Sequence 19, Appl	825	113	8.7	302	4	US-09-270-767-33326	Sequence 33326, A
753	119	9.2	496	1	US-08-462-128-37	Sequence 37, Appl	826	113	8.7	302	4	US-09-270-767-48543	Sequence 48543, A
754	119	9.2	496	1	US-08-463-180-37	Sequence 37, Appl	827	113	8.7	798	2	US-07-728-215-30	Sequence 30, Appl
755	119	9.2	496	2	US-08-001-078A-1	Sequence 1, Appli	828	113	8.7	798	3	US-08-938-085A-30	Sequence 30, Appl
756	119	9.2	496	2	US-08-897-443-4	Sequence 4, Appli	829	113	8.7	798	4	US-10-072-844-30	Sequence 30, Appl
757	119	9.2	496	2	US-08-463-218-1	Sequence 1, Appli	830	113	8.7	798	4	US-10-072-838-30	Sequence 30, Appl

831	113	8.7	798	4	US-10-072-841A-30	Sequence 30, Appl	904	108.5	8.4	589	2	US-08-429-998-6	Sequence 6, Appl
832	113	8.7	798	4	US-10-219-631A-30	Sequence 30, Appl	905	108.5	8.4	589	2	US-08-431-333-6	Sequence 6, Appl
833	113	8.7	798	4	US-09-949-016-6193	Sequence 6193, Ap	906	108.5	8.4	589	2	US-08-991-862-2	Sequence 2, Appl
834	113	8.7	846	3	US-07-728-215-33	Sequence 33, Appl	907	108.5	8.4	589	4	US-09-813-156-2	Sequence 2, Appl
835	113	8.7	846	3	US-08-938-085A-33	Sequence 33, Appl	908	108.5	8.4	589	4	US-09-456-886-2	Sequence 2, Appl
836	113	8.7	846	4	US-10-072-844-33	Sequence 33, Appl	909	108.5	8.4	589	4	US-09-824-647-2	Sequence 2, Appl
837	113	8.7	846	4	US-10-072-838-33	Sequence 33, Appl	910	108.5	8.4	589	5	PCT-US91-02321-6	Sequence 6, Appl
838	113	8.7	846	4	US-10-072-841A-33	Sequence 33, Appl	911	108.5	8.4	686	4	US-09-949-016-11203	Sequence 11203, A
839	113	8.7	846	4	US-10-219-631A-33	Sequence 33, Appl	912	108.5	8.4	696	3	US-09-351-414-2	Sequence 4, Appl
840	113	8.7	1042	4	US-09-959-392-2	Sequence 2, Appl	913	108.5	8.4	832	4	US-09-634-252A-4	Sequence 4, Appl
841	112.5	8.7	266	4	US-09-686-583B-31	Sequence 31, Appl	914	108.5	8.4	1153	4	US-09-560-385A-16	Sequence 16, Appl
842	112.5	8.7	285	4	US-09-686-583B-26	Sequence 26, Appl	915	108.5	8.4	1170	4	US-09-561-709B-12	Sequence 12, Appl
843	112.5	8.7	799	2	US-08-525-940-23	Sequence 23, Appl	916	108.5	8.4	1170	4	US-09-560-385A-14	Sequence 14, Appl
844	112.5	8.7	799	2	US-08-976-838-23	Sequence 23, Appl	917	108.5	8.4	5179	4	US-09-538-092-1258	Sequence 1258, Ap
845	112.5	8.7	881	2	US-08-525-940-21	Sequence 21, Appl	918	107.5	8.3	1198	4	US-09-902-540-15333	Sequence 15333, A
846	112.5	8.7	881	2	US-08-976-838-21	Sequence 21, Appl	919	107.5	8.3	415	3	US-08-795-430-11	Sequence 11, Appl
847	112.5	8.7	915	2	US-08-525-940-18	Sequence 18, Appl	920	107.5	8.3	415	3	US-09-355-700-11	Sequence 11, Appl
848	112.5	8.7	915	2	US-08-976-838-18	Sequence 18, Appl	921	107.5	8.3	415	4	US-08-601-132-41	Sequence 41, Appl
849	112.5	8.7	915	3	US-09-214-555B-2	Sequence 2, Appl	922	107.5	8.3	415	4	US-08-671-573B-41	Sequence 41, Appl
850	112.5	8.7	915	3	US-09-214-555B-7	Sequence 7, Appl	923	107.5	8.3	415	4	US-09-631-092B-41	Sequence 41, Appl
851	112.5	8.7	2213	1	US-08-727-034-3	Sequence 3, Appl	924	107.5	8.3	415	4	US-09-534-376A-11	Sequence 11, Appl
852	112	8.6	855	2	US-09-027-337-2	Sequence 2, Appl	925	107.5	8.3	574	6	5378464-3	Patent No. 5378464
853	112	8.6	855	4	US-09-644-600-2	Sequence 2, Appl	926	107.5	8.3	574	6	5378464-3	Patent No. 5378464
854	112	8.6	855	4	US-09-654-600A-2	Sequence 2, Appl	927	107.5	8.3	1235	4	US-09-949-016-8455	Sequence 8455, Ap
855	112	8.6	1171	4	US-09-560-385A-36	Sequence 36, Appl	928	107.5	8.3	1235	4	US-09-949-016-8456	Sequence 8456, Ap
856	112	8.6	1192	4	US-09-560-385A-34	Sequence 34, Appl	929	107.5	8.3	2169	4	US-09-949-016-6930	Sequence 6930, Ap
857	111.5	8.6	42	2	US-08-751-305-7	Sequence 7, Appl	930	107.5	8.3	5405	3	US-08-718-388-9	Sequence 9, Appl
858	111.5	8.6	320	3	US-09-183-861-22	Sequence 22, Appl	931	107	8.2	45	1	US-08-278-089A-25	Sequence 25, Appl
859	111.5	8.6	320	3	US-09-183-861-55	Sequence 55, Appl	932	107	8.2	79	4	US-10-006-011A-7	Sequence 7, Appl
860	111.5	8.6	320	3	US-09-022-765-22	Sequence 22, Appl	933	107	8.2	160	3	US-09-191-647-5	Sequence 5, Appl
861	111.5	8.6	320	3	US-09-022-765-55	Sequence 55, Appl	934	107	8.2	160	3	US-09-540-245A-5	Sequence 5, Appl
862	111.5	8.6	320	4	US-09-551-974A-22	Sequence 22, Appl	935	107	8.2	160	3	US-09-540-153-5	Sequence 5, Appl
863	111.5	8.6	320	4	US-09-551-974A-55	Sequence 55, Appl	936	107	8.2	217	1	US-07-697-275-2	Sequence 2, Appl
864	111.5	8.6	320	4	US-09-565-501A-22	Sequence 22, Appl	937	107	8.2	217	4	US-08-400-421-2	Sequence 2, Appl
865	111.5	8.6	320	4	US-09-565-501A-55	Sequence 55, Appl	938	107	8.2	462	4	US-09-026-001A-16	Sequence 16, Appl
866	111.5	8.6	320	4	US-09-639-206A-22	Sequence 22, Appl	939	107	8.2	592	2	US-09-026-001A-14	Sequence 14, Appl
867	111.5	8.6	320	4	US-09-639-206A-55	Sequence 55, Appl	940	107	8.2	769	2	US-08-789-078-1	Sequence 1, Appl
868	111.5	8.6	320	4	US-09-874-923-22	Sequence 22, Appl	941	107	8.2	769	2	US-08-752-633-1	Sequence 1, Appl
869	111.5	8.6	320	4	US-09-874-923-55	Sequence 55, Appl	942	107	8.2	769	2	US-08-476-062A-45	Sequence 45, Appl
870	111.5	8.6	320	4	US-08-798-841-22	Sequence 22, Appl	943	107	8.2	769	2	US-07-728-215-31	Sequence 31, Appl
871	110.5	8.5	44	4	US-09-341-461-10	Sequence 10, Appl	944	107	8.2	769	3	US-08-938-085A-31	Sequence 31, Appl
872	110.5	8.5	265	4	US-09-270-767-43427	Sequence 43427, A	945	107	8.2	769	4	US-10-072-844-31	Sequence 31, Appl
873	110.5	8.5	379	4	US-09-907-794A-4	Sequence 4, Appl	946	107	8.2	769	4	US-10-072-838-31	Sequence 31, Appl
874	110.5	8.5	379	4	US-09-905-125A-4	Sequence 4, Appl	947	107	8.2	769	4	US-10-072-841A-31	Sequence 31, Appl
875	110.5	8.5	379	4	US-09-902-775A-4	Sequence 4, Appl	948	107	8.2	769	4	US-10-219-631A-31	Sequence 31, Appl
876	110.5	8.5	379	4	US-09-906-700-4	Sequence 4, Appl	949	107	8.2	769	5	PCT-US95-04886-1	Sequence 1, Appl
877	110.5	8.5	379	4	US-09-903-603A-4	Sequence 4, Appl	950	107	8.2	769	5	PCT-US96-01314-45	Sequence 45, Appl
878	110.5	8.5	379	4	US-09-904-920A-4	Sequence 4, Appl	951	107	8.2	1940	2	US-08-644-271-30	Sequence 30, Appl
879	110.5	8.5	379	4	US-09-909-064-4	Sequence 4, Appl	952	107	8.2	1940	2	US-09-077-955-34	Sequence 34, Appl
880	110.5	8.5	379	4	US-09-905-381A-4	Sequence 4, Appl	953	106.5	8.2	42	6	5177197-33	Patent No. 5177197
881	110.5	8.5	379	4	US-09-906-618-4	Sequence 4, Appl	954	106.5	8.2	42	6	5177197-33	Patent No. 5177197
882	110	8.5	41	6	5177197-37	Patent No. 5177197	955	106.5	8.2	154	3	US-09-191-647-10	Sequence 10, Appl
883	110	8.5	41	6	5177197-37	Patent No. 5177197	956	106.5	8.2	154	3	US-09-540-245A-10	Sequence 10, Appl
884	110	8.5	166	4	US-09-489-847-148	Sequence 148, App	957	106.5	8.2	154	3	US-09-540-153-10	Sequence 10, Appl
885	110	8.5	167	4	US-09-489-847-230	Sequence 230, App	958	106.5	8.2	219	1	US-08-152-019A-31	Sequence 31, Appl
886	110	8.5	321	4	US-09-270-767-45035	Sequence 45035, A	959	106.5	8.2	219	2	US-08-460-309-18	Sequence 18, Appl
887	110	8.5	589	1	US-07-668-648-2	Sequence 2, Appl	960	106.5	8.2	219	2	US-08-125-077-18	Sequence 18, Appl
888	110	8.5	589	2	US-08-429-998-2	Sequence 2, Appl	961	106.5	8.2	722	4	US-09-617-145-2	Sequence 2, Appl
889	110	8.5	589	2	US-08-431-333-2	Sequence 2, Appl	962	106.5	8.2	722	4	US-09-949-016-6418	Sequence 6418, Ap
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891	110	8.5	691	4	US-09-949-016-7775	Sequence 7775, Ap	964	106.5	8.2	1167	4	US-09-560-385A-20	Sequence 20, Appl
892	109.5	8.4	484	2	US-08-252-493C-9	Sequence 9, Appl	965	106.5	8.2	1172	4	US-09-919-172-16	Sequence 16, Appl
893	109.5	8.4	484	3	US-09-276-197-9	Sequence 9, Appl	966	106.5	8.2	1174	4	US-09-560-385A-22	Sequence 22, Appl
894	109.5	8.4	676	3	US-08-630-172-10	Sequence 10, Appl	967	106.5	8.2	1186	4	US-09-560-385A-18	Sequence 18, Appl
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897	109.5	8.4	1292	3	US-08-569-214-5	Sequence 5, Appl	970	106.5	8.2	1291	3	US-08-937-236-2	Sequence 2, Appl
898	109.5	8.4	1292	3	US-08-569-214-6	Sequence 6, Appl	971	106.5	8.2	1295	3	US-08-569-214-2	Sequence 2, Appl
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900	108.5	8.4	45	2	US-08-838-957A-24	Sequence 24, Appl	973	106	8.2	1049	4	US-09-949-016-11522	Sequence 11522, A
901	108.5	8.4	288	2	US-08-525-940-15	Sequence 15, Appl	974	105.5	8.1	37	4	US-09-060-299-10	Sequence 10, Appl
902	108.5	8.4	288	2	US-08-976-838-15	Sequence 15, Appl	975	105.5	8.1	37	4	US-09-402-923A-10	Sequence 10, Appl
903	108.5	8.4	589	1	US-07-668-648-6	Sequence 6, Appl	976	105.5	8.1	39	4	US-09-060-299-16	Sequence 16, Appl

977 105.5 8.1 39 4 US-09-402-923A-16 Sequence 16, Appl
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 980 105 8.1 161 4 US-10-293-622-4 Sequence 4, Appl
 981 105 8.1 345 4 US-10-293-622-2 Sequence 2, Appl
 982 105 8.1 469 4 US-09-902-540-16788 Sequence 16788, A
 983 105 8.1 2813 3 US-08-896-449A-2 Sequence 2, Appl
 984 105 8.1 2813 3 US-09-132-652-2 Sequence 2, Appl
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 986 105 8.1 2813 4 US-09-662-478C-2 Sequence 2, Appl
 987 104.5 8.1 241 2 US-08-460-309-17 Sequence 17, Appl
 988 104.5 8.1 241 2 US-08-125-077-17 Sequence 17, Appl
 989 104.5 8.1 288 1 US-08-368-852-15 Sequence 15, Appl
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 992 104.5 8.1 3075 2 US-08-125-077-5 Sequence 5, Appl
 993 104 8.0 178 4 US-09-706-722A-7 Sequence 7, Appl
 994 104 8.0 455 4 US-09-866-028-50 Sequence 50, Appl
 995 104 8.0 455 4 US-09-944-457-50 Sequence 50, Appl
 996 104 8.0 908 5 PCT-US95-03747-3 Sequence 3, Appl
 997 104 8.0 1694 4 US-09-560-385A-12 Sequence 12, Appl
 998 104 8.0 1725 4 US-09-560-385A-10 Sequence 10, Appl
 999 103.5 8.0 115 4 US-08-270-767-42013 Sequence 42013, A
 1000 103.5 8.0 165 4 US-09-706-722A-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
 US-08-282-141-2
 ; Sequence 2, Application US/08282141
 ; Patent No. 5538861
 ; GENERAL INFORMATION:
 ; APPLICANT: Schneider, Claudio
 ; APPLICANT: Varnum, Brian
 ; APPLICANT: Avanzi, Giancarlo
 ; APPLICANT: Brancolini, Claudio
 ; APPLICANT: Manfioletti, Guidalberto
 ; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/282,141
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 678 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-282-141-2

Query Match 100.0%; Score 1297; DB 1; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.3e-103;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 90 PRYLDCKVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 149

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 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCBQVCVNSPGSYTCHCDGRGGJLK 269
 QY 181 LSQDMTCDIILPCVPFVSVAKSVKSLYLGRMFSGTGVIRLRFKRLQP 227
 DB 270 LSQDMTCDIILPCVPFVSVAKSVKSLYLGRMFSGTGVIRLRFKRLQP 316
 RESULT 2
 US-08-435-434-2
 ; Sequence 2, Application US/08435434
 ; Patent No. 5714385
 ; GENERAL INFORMATION:
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Li, Ronghao
 ; APPLICANT: Chen, Jian
 ; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,434
 ; FILING DATE: 10-MAY-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 00,000
 ; REFERENCE/DOCKET NUMBER: 946-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 678 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-435-434-2
 Query Match 100.0%; Score 1297; DB 1; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.3e-103;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 90 PRYLDCKVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 149
 QY 61 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 120
 DB 150 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 209
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RESULT 3

US-08-435-436-2
; Sequence 2, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,436
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-436-2

Query Match 100.0%; Score 1297; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 90 PRYLDCKVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 149
QY 61 GRLCDKDVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 120
Db 150 GRLCDKDVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 209
QY 121 ARCKNLPGSYCLDEGFAYSSQEKACRDVDECLQRCQVCSVNSPGSYTCHCDGRGGLK 180
Db 210 ARCKNLPGSYCLDEGFAYSSQEKACRDVDECLQRCQVCSVNSPGSYTCHCDGRGGLK 269
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Db 270 LSQDMTCECILPCVPFSAKSVKSLYLGRMFSGTPIRLRFRKLP 316

RESULT 4

US-08-438-863-2

; Sequence 2, Application US/08438863
; Patent No. 5849585
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Ronghao Li
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,863
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-863-2
Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRYLDCKVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 120
Db 90 PRYLDCKVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 149
QY 61 GRLCDKDVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 120
Db 150 GRLCDKDVNECSQENGGLQICHNKGSPHCSHGFELSSDGRTCQDIDECADSEACGE 209
QY 121 ARCKNLPGSYCLDEGFAYSSQEKACRDVDECLQRCQVCSVNSPGSYTCHCDGRGGLK 180
Db 210 ARCKNLPGSYCLDEGFAYSSQEKACRDVDECLQRCQVCSVNSPGSYTCHCDGRGGLK 269
QY 181 LSQDMTCECILPCVPFSAKSVKSLYLGRMFSGTPIRLRFRKLP 227
Db 270 LSQDMTCECILPCVPFSAKSVKSLYLGRMFSGTPIRLRFRKLP 316
RESULT 5
US-08-438-864-2
; Sequence 2, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.

APPLICANT: Li, Ronghao
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,864
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402253
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 929P1-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-864-2

Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRYLDCKNGYSPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLNMGNFCLCKAGWG 60
Db 90 PRYLDCKNGYSPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLNMGNFCLCKAGWG 149
Qy 61 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 150 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 209
Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
Db 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 269
Qy 181 LSQDMTCDILPCVPFVSVAKSLSYLGFMFSGTPVIRLRFKRLQP 227
Db 270 LSQDMTCDILPCVPFVSVAKSLSYLGFMFSGTPVIRLRFKRLQP 316

RESULT 6
US-08-438-862-2
Sequence 2, Application US/08438862
Patent No. 6033660
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-2

Query Match 100.0%; Score 1297; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRYLDCKNGYSPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLNMGNFCLCKAGWG 60
Db 90 PRYLDCKNGYSPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLNMGNFCLCKAGWG 149
Qy 61 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 150 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGE 209
Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
Db 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 269
Qy 181 LSQDMTCDILPCVPFVSVAKSLSYLGFMFSGTPVIRLRFKRLQP 227
Db 270 LSQDMTCDILPCVPFVSVAKSLSYLGFMFSGTPVIRLRFKRLQP 316

RESULT 7
US-08-402-253-2
Sequence 2, Application US/08402253
Patent No. 6211142
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Hammonds, R. Glenn
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-402-253-2
;
; Query Match 100.0%; Score 1297; DB 3; Length 678;
; Best Local Similarity 100.0%; Pred. No. 2.3e-103;
; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 PRYLDCKVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 120
; DB 90 PRYLDCKVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 149
;
; QY 61 GRLCDKDVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 120
; DB 150 GRLCDKDVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 209
;
; QY 121 ARCKNLPFSYCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 180
; DB 210 ARCKNLPFSYCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 269
;
; QY 181 LSQDMTCEIDILPCVPFSAKSVKSLYLGRMFGSTPVIRLRFKRLQ 227
; DB 270 LSQDMTCEIDILPCVPFSAKSVKSLYLGRMFGSTPVIRLRFKRLQ 316
;
; RESULT 8
; US-08-443-866B-2
; Sequence 2, Application US/08443866B
; Patent No. 6255068
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
; FILING DATE: 31-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
;
; US-08-443-866B-2
;
; Query Match 100.0%; Score 1297; DB 3; Length 678;
; Best Local Similarity 100.0%; Pred. No. 2.3e-103;
; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 PRYLDCKVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 120
; DB 90 PRYLDCKVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 149
;
; QY 61 GRLCDKDVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 120
; DB 150 GRLCDKDVNECSQENGCLQICHNKPFSFCHSCGHSFELSSDGRGTCODIDECADSEACGE 209
;
; QY 121 ARCKNLPFSYCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 180
; DB 210 ARCKNLPFSYCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 269
;
; QY 181 LSQDMTCEIDILPCVPFSAKSVKSLYLGRMFGSTPVIRLRFKRLQ 227
; DB 270 LSQDMTCEIDILPCVPFSAKSVKSLYLGRMFGSTPVIRLRFKRLQ 316
;
; RESULT 9
; US-08-628-747-2
; Sequence 2, Application US/08628747
; Patent No. 6169070
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: One DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,747
; FILING DATE: 17-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/402,253
; FILING DATE: 10-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,861
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
```

```

; REFERENCE/DOCKET NUMBER: P929P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-225-1994
; TELEFAX: 650-952-9881
; TELEX: 910-371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-628-747-2

Query Match          99.4%; Score 1289; DB 3; Length 678;
Best Local Similarity 99.6%; Pred. No. 1.1e-102;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRYLDICINKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDICINKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQENGCGCLOICRNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGE 209

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 269

QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 270 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 316

RESULT 10
US-08-282-141-3
; Sequence 3, Application US/08282141
; Patent No. 553861
; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manfioletti, Guidalberto
; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-282-141-3

Query Match          85.8%; Score 1113; DB 1; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDICINKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDKFACVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGE 120
DB 87 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGE 266

RESULT 11
US-08-435-434-1
; Sequence 1, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-1

Query Match          85.8%; Score 1113; DB 1; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDICINKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDKFACVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGE 120
DB 87 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHSGFELSSDGRTCQDIDECADSEACGE 266
```



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; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929p1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-864-1

```

```

Query Match 85.8%; Score 1113; DB 2; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGCLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 60
Db 87 PRYQECMRKYGPRPEKNPDPFAKCVQNLDPDQCTNPDCRKGTHICQDLGMGNFFCVCIDGNG 146

QY 61 GRLCDKDVNECSQENGCLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQENGCLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 206

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 266

QY 181 LSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQ 313

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RESULT 15
US-08-438-862-1
; Sequence 1, Application US/08438862
; Patent No. 6033660
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS

```

```

; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,862
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-862-1

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGCLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 60
Db 87 PRYQECMRKYGPRPEKNPDPFAKCVQNLDPDQCTNPDCRKGTHICQDLGMGNFFCVCIDGNG 146

QY 61 GRLCDKDVNECSQENGCLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQENGCLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 206

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 266

QY 181 LSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQ 313

RESULT 16
US-08-628-747-1
; Sequence 1, Application US/08628747
; Patent No. 6169070
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: One DNA Way
; CITY: South San Francisco

```

```
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-402-253-1

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKINRGSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECWKYGRPEEKPDFAKCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146

Qy 61 GRLCDKDVNECSQNGGLQICHNKGPSFCHSGFELSSDGTCDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQNGGCSQVCHNKGPSFQACHSGFSLASDGTCDIDECTDSDTCDG 206

Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCHNKGPSYTCDCDGRGLK 180
Db 207 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCHNKGPSYTCDCDGRGLK 266

Qy 181 LSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQP 227
Db 267 LSPDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQP 313

RESULT 17
US-08-402-253-1
; Sequence 1, Application US/08402253
; Patent No. 6211142
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B

; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-402-253-1

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKINRGSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECWKYGRPEEKPDFAKCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146

Qy 61 GRLCDKDVNECSQNGGLQICHNKGPSFCHSGFELSSDGTCDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQNGGCSQVCHNKGPSFQACHSGFSLASDGTCDIDECTDSDTCDG 206

Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCHNKGPSYTCDCDGRGLK 180
Db 207 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCHNKGPSYTCDCDGRGLK 266

Qy 181 LSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQP 227
Db 267 LSPDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFKRLQP 313

RESULT 18
US-08-443-866B-1
; Sequence 1, Application US/08443866B
; Patent No. 6255068
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
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/
/ FILING DATE: 31-May-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/402253
/ FILING DATE: 10-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: P0929D1
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 673 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
/ US-08-443-866B-1
/
Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCINKYSPYTKNSGFATCVQNLPDQCTNPDCRKGTOACQDLMGNFFCLCKAGWG 60
DB 87 PRYQECWRKYGREPEKNPDPFAKCVQNLPDQCTNPDCRKGTHICQDLMGNFFCVCTDGGW 146
QY 61 GRLCDKDVNECSGNGCLOICHNKPFGSHCSGFSLSDDRTQDIDECADSSACGE 120
DB 147 GRLCDKDVNECVQNGGCSQVCHNKPFGSFOACHSGFSLSADGQTCQDIDECTDSDTCGD 206
QY 121 ARCKNLPGSYSLCDGSGFAYSSOEKACRDVDECLQRCRQVCVNSPGSYTCHCDGRGGGLK 180
DB 207 ARCKNLPGSYSLCDGSGYTYSSKEKTCQDQVDECCQDRCEQTCVNSPGSYTCHCDGRGGGLK 266
QY 181 LSDMDTCEIDILCVFPFSAKSVKSLYLGRMFGSTPVIRLRFKRLQ 227
DB 267 LSDMDTCEIDILCVFPFSAKSVKSLYLGRMFGSTPVIRLRFKRLQ 313

RESULT 19
US-07-907-190-1
/ Sequence 1, Application US/07907190
/ Patent No. 5321123
/ GENERAL INFORMATION:
/ APPLICANT: Griffin, John H.
/ APPLICANT: Fernandez, Jose A.
/ TITLE OF INVENTION: PROTEIN S POLYPEPTIDES AND ANTI-PEPTIDE
/ TITLE OF INVENTION: ANTIBODIES THAT INHIBIT PROTEIN S BINDING TO C4b BINDING
/ TITLE OF INVENTION: PROTEIN, DIAGNOSTIC SYSTEMS AND THERAPEUTIC METHODS
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: The Scripps Research Institute, Office of
/ ADDRESSEE: Patent Counsel
/ STREET: 10666 No. 5321123th Torrey Pines Road, Mail Drop TPC8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/907,190
/ FILING DATE: 19920701
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/724,746
/ FILING DATE: 02-JUL-1991
/ ATTORNEY/AGENT INFORMATION:
```

```
/
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR1119P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 635 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/
/ US-07-907-190-1
/
Query Match 46.4%; Score 601.5; DB 1; Length 635;
Best Local Similarity 43.4%; Pred. No. 9.5e-44;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLDCINKY-----GSPYTKNS--GFATCVQNLPDQCTNPDCRKGTOACQDLMGNFF 52
DB 42 PKYLVLCLRSFOTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 101
QY 53 CLCKAGWGRLCDKDVNEC---SQNGGCLQICHNKPFGSHCSGFSLSDDRTQDIDECADSSACGE 109
DB 102 CTCKPQWQGEKCFDINECKDPSSNNGGCSQICDNTPGSYHCSCKNGFYMLSNKKDKCDV 161
QY 110 DSCA-DSEACGEARCKNLPGSYSLCDGSGFAYSSOEKACRDVDECLQRCRQVCVNSPGS 168
DB 162 DSCSLKPSICGTAVCKNIPDGFECPCPEGYRNLKSKCEDIDECSENWCAQLCVNYPFG 221
QY 169 YTCHCDGRGLKSLQDMDTCEIDILCVFPFSAKSVKSLYLGRMFGSTPVIRLRFK 223
DB 222 YTCYCDGKGGFKLAQDKSCVSVVCLPLNLTQKVELLYLAEQFAGV-VLYLKF 275

RESULT 20
US-07-985-691-2
/ Sequence 2, Application US/07985691
/ Patent No. 5405946
/ GENERAL INFORMATION:
/ APPLICANT: Griffin, John H
/ APPLICANT: Bouma, Bonno N
/ APPLICANT: Bertina, Rogier
/ TITLE OF INVENTION: RECOMBINANT PROTEIN S VARIANTS DEFICIENT
/ TITLE OF INVENTION: IN C4BP BINDING ACTIVITY, COMPOSITIONS AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: The Scripps Research Institute, Office of
/ ADDRESSEE: Patent Counsel
/ STREET: 10666 No. 5405946th Torrey Pines Road, TPC 8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/985,691
/ FILING DATE: 19921202
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSR0042P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
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; LENGTH: 635 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-985-691-2

Query Match 46.4%; Score 601.5; DB 1; Length 635;
Best Local Similarity 43.4%; Pred. No. 9.5e-44;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

Qy 1 PRLVLCINIKY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGTQACODLMGNFF 52
Db 42 PKYLVCLRSFQTGLFTAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 101
Qy 53 CLCKAGWGRCLDKDVNEC---SOENGGLQICHNKPGSFHCSCHSGFELSSDGRTCQDI 109
Db 102 CTCKPQWQEKCEPDINECKDPNSINGGCSQICDNTPGSYHCSCKNGFVMSLNKKDCKOV 161
Qy 110 DECA-DSEACGEARCKNLPGSYCLCDGEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 162 DECSLKPSICGTAVCKNIPGDCECEPEGYRYNLKSKSCEDIDECSENMCQAQLCVNYPGG 221
Qy 169 YTCHCDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFSGTPVIRLRPK 223
Db 222 YTCYCDGKGFKLQADQKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKER 275

RESULT 21
US-08-436-804-2
; Sequence 2, Application US/08436804
; Patent No. 5656484
; GENERAL INFORMATION:
; APPLICANT: BOUMA, Bonno N.
; APPLICANT: BERTINA, Rogier M.
; TITLE OF INVENTION: PROTEIN S DELETION VARIANTS DEFICIENT IN
; TITLE OF INVENTION: C4BP BINDING ACTIVITY, BUT HAVING APC COFACTOR ACTIVITY,
; TITLE OF INVENTION: COMPOSITIONS AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; STREET: Second Floor, 745 South 23rd Street.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,804
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 201 906.0
; FILING DATE: 30-JUN-1994
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: B038633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: protein
US-08-436-804-2

Query Match 46.4%; Score 601.5; DB 1; Length 635;
Best Local Similarity 43.4%; Pred. No. 9.5e-44;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

Qy 1 PRLVLCINIKY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGTQACODLMGNFF 52
Db 42 PKYLVCLRSFQTGLFTAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 101
Qy 53 CLCKAGWGRCLDKDVNEC---SOENGGLQICHNKPGSFHCSCHSGFELSSDGRTCQDI 109
Db 102 CTCKPQWQEKCEPDINECKDPNSINGGCSQICDNTPGSYHCSCKNGFVMSLNKKDCKOV 161
Qy 110 DECA-DSEACGEARCKNLPGSYCLCDGEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 162 DECSLKPSICGTAVCKNIPGDCECEPEGYRYNLKSKSCEDIDECSENMCQAQLCVNYPGG 221
Qy 169 YTCHCDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFSGTPVIRLRPK 223
Db 222 YTCYCDGKGFKLQADQKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKER 275

RESULT 22
US-08-267-387-2
; Sequence 2, Application US/08267387
; Patent No. 5663142
; GENERAL INFORMATION:
; APPLICANT: BOUMA, Bonno N.
; APPLICANT: BERTINA, Rogier M.
; TITLE OF INVENTION: PROTEIN S DELETION VARIANTS DEFICIENT IN
; TITLE OF INVENTION: C4BP BINDING ACTIVITY, BUT HAVING APC COFACTOR ACTIVITY,
; TITLE OF INVENTION: COMPOSITIONS AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; STREET: Second Floor, 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,387
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 201 906.0
; FILING DATE: 30-JUN-1994
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: B038633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-267-387-2

Query Match 46.4%; Score 601.5; DB 1; Length 635;
Best Local Similarity 43.4%; Pred. No. 9.5e-44;

```

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Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKINXY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGKGTQACQDLGNFF 52
Db 42 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLFCNEDGYMSCKDGKASFT 101
QY 53 CLCKAGGRLCDKDVNEC---SQENGGCLQICHNKPFGSHCSHGFSLSGRTCDI 109
Db 102 CTCCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCSCKNGFVMSLNKKDCKDV 161
QY 110 DECA-DSEACGEARCKNLPGSYCLCDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 162 DECSLKPSICGTAACKNIPGDFCECEPEGYRYNLKSKSCEDIDECSENMAQLCVNYPGG 221
QY 169 YTHCDGRGGLKLSQDMTCEIDLPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
Db 222 YTCYCDGKGFKLQADQKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 275

RESULT 23
US-08-282-141-4
; Sequence 4, Application US/08282141
; Patent No. 5538861
; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manfioletti, Gudaiberto
; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-282-141-4

Query Match 46.4%; Score 601.5; DB 1; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKINXY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGKGTQACQDLGNFF 52
Db 83 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLFCNEDGYMSCKDGKASFT 142
QY 53 CLCKAGGRLCDKDVNEC---SQENGGCLQICHNKPFGSHCSHGFSLSGRTCDI 109
Db 143 CTCCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCSCKNGFVMSLNKKDCKDV 202
QY 110 DECA-DSEACGEARCKNLPGSYCLCDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAACKNIPGDFCECEPEGYRYNLKSKSCEDIDECSENMAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMTCEIDLPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
QY 222 YTCYCDGKGFKLQADQKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 275
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Db 263 YTCYCDGKGFKLQADQKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 24
US-08-435-434-3
; Sequence 3, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-3

Query Match 46.4%; Score 601.5; DB 1; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKINXY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGKGTQACQDLGNFF 52
Db 83 PKYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLFCNEDGYMSCKDGKASFT 142
QY 53 CLCKAGGRLCDKDVNEC---SQENGGCLQICHNKPFGSHCSHGFSLSGRTCDI 109
Db 143 CTCCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCSCKNGFVMSLNKKDCKDV 202
QY 110 DECA-DSEACGEARCKNLPGSYCLCDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAACKNIPGDFCECEPEGYRYNLKSKSCEDIDECSENMAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMTCEIDLPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
Db 263 YTCYCDGKGFKLQADQKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 25
US-08-435-436-3
; Sequence 3, Application US/08435436
; Patent No. 5721139
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/438,864
/ FILING DATE: 10-MAY-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/402253
/ FILING DATE: 10-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wendy M. Lee
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 929P1-1
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 676 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-438-864-3

Query Match 46.4%; Score 601.5; DB 2; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLDCINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPGRSFHCSHGFSLSDDGRTCDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNSNGGCSQICDNTPGSYHCSCKNGFVMLSNKKDKDV 202
QY 110 DECA-DSEACGEARKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIIPGDFECPCPEGYRNLSKSCEDIDECSENCAQLCVNYPGG 262
QY 169 YTCHCDGRGLKLSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 263 YTCYCDGKGGFKLAQDKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 28
US-08-438-862-3
/ Sequence 3, Application US/08438862
/ Patent No. 6033660
/ GENERAL INFORMATION:
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Li, Ronghao
/ APPLICANT: Chen, Jian
/ TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/438,862
/ FILING DATE: 10-MAY-1995
/
```

```
/
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 946-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 676 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-438-862-3

Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLDCINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPGRSFHCSHGFSLSDDGRTCDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNSNGGCSQICDNTPGSYHCSCKNGFVMLSNKKDKDV 202
QY 110 DECA-DSEACGEARKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIIPGDFECPCPEGYRNLSKSCEDIDECSENCAQLCVNYPGG 262
QY 169 YTCHCDGRGLKLSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 263 YTCYCDGKGGFKLAQDKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 29
US-08-628-747-3
/ Sequence 3, Application US/08628747
/ Patent No. 6169070
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Jian
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Hammonds, R. Glenn
/ APPLICANT: Mark, Melanie
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Li, Ronghao
/ TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: One DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/628,747
/ FILING DATE: 17-APR-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/402,253
/ FILING DATE: 10-MAR-1995
/
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```
; APPLICATION NUMBER: US 08/438,861
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P929P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-225-1994
; TELEFAX: 650-952-9881
; TELEX: 910-371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-628-747-3

Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

Qy 1 PRYLDCKIN-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACODLMGNFF 52
Db 83 PKYLVLRSFQTGLFTAAQSTNAYDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
Qy 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPFGSHCSHGFSLSGRTSQDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCCKNGFVMSLNKKDCKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECIQGRCEQVCVNSPGS 168
Db 203 DECSLKPSCGTAACKNIPGDCECEPEGYRYNLKSKSCEDIDECSENMCQALCVNYPGG 262
Qy 169 YTHCDGRGLKLSQDMTCEIDLPCVPPSVAKSVLKSLYLRGMSFGTPTVIRLRFK 223
Db 263 YTCYCDGKGFKLQADQKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 30
US-08-402-253-3
; Sequence 3, Application US/08402253
; Patent No. 6211142
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000

Qy 1 PRYLDCKIN-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACODLMGNFF 52
Db 83 PKYLVLRSFQTGLFTAAQSTNAYDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
Qy 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPFGSHCSHGFSLSGRTSQDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCCKNGFVMSLNKKDCKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECIQGRCEQVCVNSPGS 168
Db 203 DECSLKPSCGTAACKNIPGDCECEPEGYRYNLKSKSCEDIDECSENMCQALCVNYPGG 262
Qy 169 YTHCDGRGLKLSQDMTCEIDLPCVPPSVAKSVLKSLYLRGMSFGTPTVIRLRFK 223
Db 263 YTCYCDGKGFKLQADQKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 31
US-08-443-866B-3
; Sequence 3, Application US/08443866B
; Patent No. 6255088
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
; FILING DATE: 31-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0929D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-443-866B-3

Query Match      46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLVLCINIKYSPYTKNSGAT-----GFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
Db 83 PRLVLCIRSFQGLFTAAARQSTNAYPDLRSVCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
QY 53 CLCKAGWGRGLCDKDVNECSQE---SQENGGLQICHNKPFSFHCSHGFSFELSSDGRTCQDI 109
Db 143 CTCKPGWQGEKCFDINECKDPVNINGGCSQICDNTPGSVHCCKNGFVMLSNNKDKDV 202
QY 110 DECA-DSEACGEARCNLPKGSYCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECVLKPSICGTAVCKNIPGDFECBCEGGRYRNLSKSCDIDECSENWCAQLCVNYPGG 262
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 263 YTCYCDGKKGFKLAQDKQKCEVSVVCLPLDLTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 32
5258288-1
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO:1:
; LENGTH: 675
5258288-1

Query Match      46.0%; Score 596.5; DB 6; Length 675;
Best Local Similarity 43.0%; Pred. No. 2.7e-43;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

QY 1 PRLVLCINIKYSPYTKNSGAT-----GFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
Db 83 PRLVLCIRSFQGLFTAAARQSTNAYPDLRSVCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
QY 53 CLCKAGWGRGLCDKDVNECSQE---SQENGGLQICHNKPFSFHCSHGFSFELSSDGRTCQDI 109
Db 143 CTCKPGWQGEKCFDINECKDPVNINGGCSQICDNTPGSVHCCKNGFVMLSNNKDKDV 202
QY 110 DECA-DSEACGEARCNLPKGSYCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECVLKPSICGTAVCKNIPGDFECBCEGGRYRNLSKSCDIDECSENWCAQLCVNYPGG 262
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 263 YTCYCDGKKGFKLAQDKQKCEVSVVCLPLDLTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 33
5258288-1
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO:1:
; LENGTH: 675
5258288-1

Query Match      45.2%; Score 586.5; DB 6; Length 652;
Best Local Similarity 42.6%; Pred. No. 1.9e-42;
Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

QY 1 PRLVLCINIKYSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
Db 57 PRLVLCIRSFQGLFTAAARQSTNAYPDLRSVCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 116
QY 53 CLCKAGWGRGLCDKDVNECSQE---SQENGGLQICHNKPFSFHCSHGFSFELSSDGRTCQDI 109
Db 117 CTCKPGWQGEKCFDINECKDPVNINGGCSQICDNTPGSVHCCKNGFVMLSNNKDKDV 176
QY 110 DECA-DSEACGEARCNLPKGSYCLDEGFAYSSQKACRDVDECLQGRCEQVCVNSPGS 168
Db 177 DECVLKPSICGTAVCKNIPGDFECBCEGGRYRNLSKSCDIDECSENWCAQLCVNYPGG 236
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 237 HTCYCDGKKGFKLAQDKQKCEVSVVCLPLDLTKYELLYLAEQFAGV-VLYLKFR 290

RESULT 35
5258288-4
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO:4:
; LENGTH: 652
5258288-4
```


APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11266
LENGTH: 575
TYPE: PRT
ORGANISM: Human
US-09-949-016-11266

Query Match 26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKYSPYTKNSGPATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB 299 CINTGSG-----YTCQKNVPCGRGYHLNBEGRTRCVDVDECAPPAEFCG-KG-HRCV 348

QY 46 DLMGNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSGSELS 100
DB 349 NSPGSFRCCKTGYFDGISRMC-VDVNECQRYPGRLCGHKCENTGLSYLSCSVGFRLS 407

QY 101 SDGRTCCQDIDECADSEACGEARCKNLPGSYCLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB 408 VDGSRCEIDNECSSSPCSQE--CANVGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY 158 --CEQVCVNSPGSYTCHDGRGGLKLSQDMTDCEDILPCV 195
DB 466 HICSYRCINIPGSFQSCPS-SGYRLAPNRCQDIDECV 504

RESULT 43
US-09-949-016-11267
Sequence 11267, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11267
LENGTH: 575
TYPE: PRT
ORGANISM: Human
US-09-949-016-11267

Query Match 26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKYSPYTKNSGPATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB 299 CINTGSG-----YTCQKNVPCGRGYHLNBEGRTRCVDVDECAPPAEFCG-KG-HRCV 348

QY 46 DLMGNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSGSELS 100
DB 349 NSPGSFRCCKTGYFDGISRMC-VDVNECQRYPGRLCGHKCENTGLSYLSCSVGFRLS 407

QY 101 SDGRTCCQDIDECADSEACGEARCKNLPGSYCLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB 408 VDGSRCEIDNECSSSPCSQE--CANVGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY 158 --CEQVCVNSPGSYTCHDGRGGLKLSQDMTDCEDILPCV 195
DB 466 HICSYRCINIPGSFQSCPS-SGYRLAPNRCQDIDECV 504

RESULT 44
US-09-949-016-11365
Sequence 11365, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11365
LENGTH: 657
TYPE: PRT
ORGANISM: Human
US-09-949-016-11365

Query Match 26.1%; Score 339; DB 4; Length 657;
Best Local Similarity 37.3%; Pred. No. 3.2e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKYSPYTKNSGPATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB 299 CINTGSG-----YTCQKNVPCGRGYHLNBEGRTRCVDVDECAPPAEFCG-KG-HRCV 348

QY 46 DLMGNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSGSELS 100
DB 349 NSPGSFRCCKTGYFDGISRMC-VDVNECQRYPGRLCGHKCENTGLSYLSCSVGFRLS 407

QY 101 SDGRTCCQDIDECADSEACGEARCKNLPGSYCLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB 408 VDGSRCEIDNECSSSPCSQE--CANVGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY 158 --CEQVCVNSPGSYTCHDGRGGLKLSQDMTDCEDILPCV 195
DB 466 HICSYRCINIPGSFQSCPS-SGYRLAPNRCQDIDECV 504

RESULT 45
US-09-949-016-11366
Sequence 11366, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

```

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11366
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11366

Query Match          26.1%; Score 339; DB 4; Length 657;
Best Local Similarity 37.3%; Pred. No. 3.2e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKYGSPTYKNSGFATCVQNLP-----DOCTP--NPCDRKGTQACQ 45
    |||||
DB 299 CINTEGS-----YTCQKNVPNCGRGYHLNEEGTRCVDVDECAAPPAPCG-KG-HRCV 348

QY 46 DLMGNFCLCKAGW---GRLCDKDVNCSOBNGG-CLQICHNKPGSFHCSHGFFLS 100
    |||||
DB 349 NSPFSRCECKTGYFDGTSRMC-VDVNECQRYPGRLCGHKCENTILGSLCSCSVGFRLS 407

QY 101 SDGRTQDIDECADSEACGEARKNLPGSYSCLCDEGFAYSSQE-KACRDVDECLQGR-- 157
    |||||
DB 408 VDRGSCEDINECSSPSCOE--CANYGSGYQCYCRRGYQLSDVDGVTCTEDIDECALPTGG 465

QY 158 --CEQVCVNSPGSYTCHDGRGLKLSQDMTCDILPCV 195
    |||||
DB 466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

RESULT 46
US-09-949-016-11367
; Sequence 11367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11367
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11367

Query Match          26.1%; Score 339; DB 4; Length 657;
Best Local Similarity 37.3%; Pred. No. 3.2e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKYGSPTYKNSGFATCVQNLP-----DOCTP--NPCDRKGTQACQ 45
    |||||
DB 299 CINTEGS-----YTCQKNVPNCGRGYHLNEEGTRCVDVDECAAPPAPCG-KG-HRCV 348

QY 46 DLMGNFCLCKAGW---GRLCDKDVNCSOBNGG-CLQICHNKPGSFHCSHGFFLS 100
    |||||
DB 349 NSPFSRCECKTGYFDGTSRMC-VDVNECQRYPGRLCGHKCENTILGSLCSCSVGFRLS 407

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RESULT 47
US-09-949-016-11368
; Sequence 11368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11368
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11368

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Best Local Similarity 37.3%; Pred. No. 3.2e-21;
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RESULT 48
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; Sequence 11369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; TYPE: PRT
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Search completed: July 7, 2005, 09:41:26
Job time : 126.836 secs
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; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11370

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Query Match      26.1%; Score 339; DB 4; Length 677;
Best Local Similarity 37.3%; Pred. No. 3.3e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

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QY 101 SDGRTCODIDECADSEACGEARCKNLPSSYCLCDEGFAYSSOE--KACRDVDECLQGR-- 157
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Search completed: July 7, 2005, 09:41:26
Job time : 126.836 secs
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RESULT 50

US-09-949-016-11371

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258	319	24.6	448	14	US-10-187-745-408	Sequence 408, App	331	319	24.6	448	14	US-10-184-626-408	Sequence 408, App
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271	319	24.6	448	14	US-10-180-999-408	Sequence 408, App	344	319	24.6	448	14	US-10-066-193-15	Sequence 15, Appl
272	319	24.6	448	14	US-10-183-013-408	Sequence 408, App	345	319	24.6	448	14	US-10-176-484-408	Sequence 408, App
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283	319	24.6	448	14	US-10-184-640-408	Sequence 408, App	356	319	24.6	448	14	US-10-184-615-408	Sequence 408, App
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377	319	24.6	448	14	US-10-197-708-408	Sequence 408, App	450	319	24.6	448	14	US-10-187-738-408	Sequence 408, App
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547	319	24.6	448	14	US-10-205-896-408	Sequence 408, App	620	319	24.6	448	14	US-10-184-624-408	Sequence 408, App
548	319	24.6	448	14	US-10-205-898-408	Sequence 408, App	621	319	24.6	448	14	US-10-184-657-408	Sequence 408, App
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563	319	24.6	448	14	US-10-207-916-408	Sequence 408, App	636	319	24.6	448	14	US-10-187-739-408	Sequence 408, App
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571	319	24.6	448	14	US-10-208-023-408	Sequence 408, App	644	319	24.6	448	14	US-10-196-747-408	Sequence 408, App
572	319	24.6	448	14	US-10-208-026-408	Sequence 408, App	645	319	24.6	448	14	US-10-173-689-408	Sequence 408, App
573	319	24.6	448	14	US-10-208-029-408	Sequence 408, App	646	319	24.6	448	14	US-10-173-690-408	Sequence 408, App
574	319	24.6	448	14	US-10-208-030-408	Sequence 408, App	647	319	24.6	448	14	US-10-173-691-408	Sequence 408, App
575	319	24.6	448	14	US-10-232-232-408	Sequence 408, App	648	319	24.6	448	14	US-10-173-694-408	Sequence 408, App
576	319	24.6	448	14	US-10-195-898-408	Sequence 408, App	649	319	24.6	448	14	US-10-173-698-408	Sequence 408, App
577	319	24.6	448	14	US-10-196-759-408	Sequence 408, App	650	319	24.6	448	14	US-10-173-699-408	Sequence 408, App
578	319	24.6	448	14	US-10-193-693-408	Sequence 408, App	651	319	24.6	448	14	US-10-173-707-408	Sequence 408, App
579	319	24.6	448	14	US-10-174-578-408	Sequence 408, App	652	319	24.6	448	14	US-10-174-569-408	Sequence 408, App
580	319	24.6	448	14	US-10-175-741-408	Sequence 408, App	653	319	24.6	448	14	US-10-174-583-408	Sequence 408, App
581	319	24.6	448	14	US-10-175-750-408	Sequence 408, App	654	319	24.6	448	14	US-10-174-587-408	Sequence 408, App
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669	319	24.6	448	14	US-10-176-920-408	Sequence 408, App	742	318	24.5	915	10	US-09-907-794-34	Sequence 34, App
670	319	24.6	448	14	US-10-176-922-408	Sequence 408, App	743	318	24.5	915	10	US-09-903-943-34	Sequence 34, App
671	319	24.6	448	14	US-10-176-924-408	Sequence 408, App	744	318	24.5	915	10	US-09-904-462-34	Sequence 34, App
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713	319	24.6	448	17	US-10-491-997-2	Sequence 2, Appl	786	318	24.5	915	11	US-09-908-576-34	Sequence 34, App
714	318.5	24.6	1145	15	US-10-309-290-12	Sequence 12, Appl	787	318	24.5	915	14	US-10-028-072-294	Sequence 294, App
715	318	24.5	811	15	US-10-363-616-394	Sequence 394, App	788	318	24.5	915	14	US-10-140-808-294	Sequence 294, App
716	318	24.5	830	15	US-10-363-616-393	Sequence 393, App	789	318	24.5	915	14	US-10-121-049-294	Sequence 294, App
717	318	24.5	915	9	US-09-909-320-34	Sequence 34, Appl	790	318	24.5	915	14	US-10-121-049-294	Sequence 294, App
718	318	24.5	915	9	US-09-909-088B-34	Sequence 34, Appl	791	318	24.5	915	14	US-10-140-470-294	Sequence 294, App
719	318	24.5	915	9	US-09-905-291A-34	Sequence 34, Appl	792	318	24.5	915	14	US-10-175-746-294	Sequence 294, App
720	318	24.5	915	9	US-09-902-853-34	Sequence 34, Appl	793	318	24.5	915	14	US-10-176-918-294	Sequence 294, App
721	318	24.5	915	9	US-09-907-824-34	Sequence 34, Appl	794	318	24.5	915	14	US-10-176-921-294	Sequence 294, App
722	318	24.5	915	9	US-09-907-841-34	Sequence 34, Appl	795	318	24.5	915	14	US-10-137-865-294	Sequence 294, App
723	318	24.5	915	10	US-09-904-011-34	Sequence 34, Appl	796	318	24.5	915	14	US-10-140-474-294	Sequence 294, App
724	318	24.5	915	10	US-09-903-640-34	Sequence 34, Appl	797	318	24.5	915	14	US-10-142-431-294	Sequence 294, App
725	318	24.5	915	10	US-09-908-093-34	Sequence 34, Appl	798	318	24.5	915	14	US-10-143-114-294	Sequence 294, App
726	318	24.5	915	10	US-09-906-742-34	Sequence 34, Appl	799	318	24.5	915	14	US-10-142-419-294	Sequence 294, App
727	318	24.5	915	10	US-09-908-838-34	Sequence 34, Appl	800	318	24.5	915	14	US-10-123-862-294	Sequence 294, App
728	318	24.5	915	10	US-09-907-613-34	Sequence 34, Appl	801	318	24.5	915	14	US-10-142-423-294	Sequence 294, App
729	318	24.5	915	10	US-09-907-942-34	Sequence 34, Appl	802	318	24.5	915	14	US-10-121-050-294	Sequence 294, App
730	318	24.5	915	10	US-09-904-859-34	Sequence 34, Appl	803	318	24.5	915	14	US-10-141-755-294	Sequence 294, App
731	318	24.5	915	10	US-09-909-204-34	Sequence 34, Appl	804	318	24.5	915	14	US-10-143-032-294	Sequence 294, App
732	318	24.5	915	10	US-09-904-820-34	Sequence 34, Appl	805	318	24.5	915	14	US-10-123-108-294	Sequence 294, App
733	318	24.5	915	10	US-09-904-786-34	Sequence 34, Appl	806	318	24.5	915	14	US-10-123-236-294	Sequence 294, App
734	318	24.5	915	10	US-09-906-646-34	Sequence 34, Appl	807	318	24.5	915	14	US-10-123-261-294	Sequence 294, App
735	318	24.5	915	10	US-09-906-700-34	Sequence 34, Appl	808	318	24.5	915	14	US-10-140-921-294	Sequence 294, App
736	318	24.5	915	10	US-09-903-786-34	Sequence 34, Appl	809	318	24.5	915	14	US-10-140-928-294	Sequence 294, App
737	318	24.5	915	10	US-09-902-903-34	Sequence 34, Appl	810	318	24.5	915	14	US-10-121-045-294	Sequence 294, App
738	318	24.5	915	10	US-09-903-749A-34	Sequence 34, Appl	811	318	24.5	915	14	US-10-123-292-294	Sequence 294, App
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740	318	24.5	915	10	US-09-904-956-34	Sequence 34, Appl	813	318	24.5	915	14	US-10-124-819-294	Sequence 294, App
741	318	24.5	915	10	US-09-902-736-34	Sequence 34, Appl	814	318	24.5	915	14	US-10-124-822-294	Sequence 294, App

815	318	24.5	915	14	US-10-140-925-294	Sequence 294, App	888	318	24.5	915	14	US-10-123-905-294	Sequence 294, App
816	318	24.5	915	14	US-10-160-498-294	Sequence 294, App	889	318	24.5	915	14	US-10-123-907-294	Sequence 294, App
817	318	24.5	915	14	US-10-124-824-294	Sequence 294, App	890	318	24.5	915	14	US-10-124-815-294	Sequence 294, App
818	318	24.5	915	14	US-10-127-825A-294	Sequence 294, App	891	318	24.5	915	14	US-10-125-921A-294	Sequence 294, App
819	318	24.5	915	14	US-10-127-829A-294	Sequence 294, App	892	318	24.5	915	14	US-10-125-928A-294	Sequence 294, App
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821	318	24.5	915	14	US-10-127-839A-294	Sequence 294, App	894	318	24.5	915	14	US-10-127-822A-294	Sequence 294, App
822	318	24.5	915	14	US-10-127-901A-294	Sequence 294, App	895	318	24.5	915	14	US-10-127-824A-294	Sequence 294, App
823	318	24.5	915	14	US-10-128-693A-294	Sequence 294, App	896	318	24.5	915	14	US-10-127-826A-294	Sequence 294, App
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826	318	24.5	915	14	US-10-131-823A-294	Sequence 294, App	899	318	24.5	915	14	US-10-127-830A-294	Sequence 294, App
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829	318	24.5	915	14	US-10-131-837A-294	Sequence 294, App	902	318	24.5	915	14	US-10-127-834A-294	Sequence 294, App
830	318	24.5	915	14	US-10-137-872A-294	Sequence 294, App	903	318	24.5	915	14	US-10-127-836A-294	Sequence 294, App
831	318	24.5	915	14	US-10-147-500-294	Sequence 294, App	904	318	24.5	915	14	US-10-127-841A-294	Sequence 294, App
832	318	24.5	915	14	US-10-147-502-294	Sequence 294, App	905	318	24.5	915	14	US-10-127-844A-294	Sequence 294, App
833	318	24.5	915	14	US-10-147-515-294	Sequence 294, App	906	318	24.5	915	14	US-10-128-687A-294	Sequence 294, App
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835	318	24.5	915	14	US-10-147-526-294	Sequence 294, App	908	318	24.5	915	14	US-10-128-689A-294	Sequence 294, App
836	318	24.5	915	14	US-10-147-527-294	Sequence 294, App	909	318	24.5	915	14	US-10-128-694A-294	Sequence 294, App
837	318	24.5	915	14	US-10-121-041-294	Sequence 294, App	910	318	24.5	915	14	US-10-131-825A-294	Sequence 294, App
838	318	24.5	915	14	US-10-121-043-294	Sequence 294, App	911	318	24.5	915	14	US-10-130-417-294	Sequence 294, App
839	318	24.5	915	14	US-10-121-047-294	Sequence 294, App	912	318	24.5	915	14	US-10-131-815A-294	Sequence 294, App
840	318	24.5	915	14	US-10-123-215-294	Sequence 294, App	913	318	24.5	915	14	US-10-131-817A-294	Sequence 294, App
841	318	24.5	915	14	US-10-123-902-294	Sequence 294, App	914	318	24.5	915	14	US-10-131-821A-294	Sequence 294, App
842	318	24.5	915	14	US-10-123-908-294	Sequence 294, App	915	318	24.5	915	14	US-10-131-822A-294	Sequence 294, App
843	318	24.5	915	14	US-10-123-909-294	Sequence 294, App	916	318	24.5	915	14	US-10-131-828A-294	Sequence 294, App
844	318	24.5	915	14	US-10-123-910-294	Sequence 294, App	917	318	24.5	915	14	US-10-131-835A-294	Sequence 294, App
845	318	24.5	915	14	US-10-124-813-294	Sequence 294, App	918	318	24.5	915	14	US-10-137-864A-294	Sequence 294, App
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847	318	24.5	915	14	US-10-125-922-294	Sequence 294, App	920	318	24.5	915	14	US-10-147-523-294	Sequence 294, App
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872	318	24.5	915	14	US-10-131-829A-294	Sequence 294, App	945	318	24.5	915	14	US-10-145-628-294	Sequence 294, App
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876	318	24.5	915	14	US-10-147-508-294	Sequence 294, App	949	318	24.5	915	14	US-10-145-826-294	Sequence 294, App
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880	318	24.5	915	14	US-10-121-040-294	Sequence 294, App	953	318	24.5	915	14	US-10-146-724-294	Sequence 294, App
881	318	24.5	915	14	US-10-121-056-294	Sequence 294, App	954	318	24.5	915	14	US-10-146-725-294	Sequence 294, App
882	318	24.5	915	14	US-10-121-061-294	Sequence 294, App	955	318	24.5	915	14	US-10-146-795-294	Sequence 294, App
883	318	24.5	915	14	US-10-123-235-294	Sequence 294, App	956	318	24.5	915	14	US-10-147-495-294	Sequence 294, App
884	318	24.5	915	14	US-10-124-818-294	Sequence 294, App	957	318	24.5	915	14	US-10-147-501-294	Sequence 294, App
885	318	24.5	915	14	US-10-137-868-294	Sequence 294, App	958	318	24.5	915	14	US-10-147-504-294	Sequence 294, App
886	318	24.5	915	14	US-10-147-482-294	Sequence 294, App	959	318	24.5	915	14	US-10-147-506-294	Sequence 294, App
887	318	24.5	915	14	US-10-158-792-294	Sequence 294, App	960	318	24.5	915	14	US-10-147-509-294	Sequence 294, App

; CURRENT APPLICATION NUMBER: US/10/671,054
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/413157
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-1

Query Match 100.0%; Score 1297; DB 16; Length 686;
Best Local Similarity 100.0%; Pred. No. 2.7e-99;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRYLDCKINKYSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDCKINKYSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY 61 GRLCDKDVNECSQNGGCLQICHNKPFSFHCSCHSFGFELSSDGRTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQNGGCLQICHNKPFSFHCSCHSFGFELSSDGRTCQDIDECADSEACGE 209
QY 121 ARCKNLPGSYSCLEDGFAYSOQKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
DB 210 ARCKNLPGSYSCLEDGFAYSOQKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 269
QY 181 LSQDMTDCEDILPCVPFVSVAKSLSYLGFMFSGTVPVIRLRFKRLQ 227
DB 270 LSQDMTDCEDILPCVPFVSVAKSLSYLGFMFSGTVPVIRLRFKRLQ 316

RESULT 4

US-10-223-085-48
; Sequence 48, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657

; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673.
; TYPE: PRT
; ORGANISM: Murine
US-10-223-085-48

Query Match 85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKINKYSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYLDCKINKYSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146
QY 61 GRLCDKDVNECSQNGGCLQICHNKPFSFHCSCHSFGFELSSDGRTCQDIDECADSEACGE 120
DB 147 GRLCDKDVNECSQNGGCLQICHNKPFSFHCSCHSFGFELSSDGRTCQDIDECADSEACGE 206
QY 121 ARCKNLPGSYSCLEDGFAYSOQKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
DB 207 ARCKNLPGSYSCLEDGFAYSOQKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 266
QY 181 LSQDMTDCEDILPCVPFVSVAKSLSYLGFMFSGTVPVIRLRFKRLQ 227
DB 267 LSQDMTDCEDILPCVPFVSVAKSLSYLGFMFSGTVPVIRLRFKRLQ 313

RESULT 5

US-10-223-084-48
; Sequence 48, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-090-48

Query Match 85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKNGSPYTKNSGFATCVNLPDQCTPNPCDKGTQACQDLMGNFFCLCKAGWG 60
Db 87 PRYQCKRKYGRPEKNPDKFPAKCVNLPDQCTPNPCDKGTQACQDLMGNFFCVCTDGGW 146
Qy 61 GRLCDKVNCSQNGCLQICHNKPCHSFGHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKVNCSQNGCLQICHNKPCHSFGHSGFELSSDGRTCQDIDECADSEACGE 206
Qy 121 ARCKNLPGSYSLCDEGFAYSSQKACRDVDECLQRCCEQVNVNPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSLCDEGTYSKRTQDVDECCQDRCQTCVNSPGSYTCHCDGRGLK 266
Qy 181 LSQDMTCEIDILPCVPFSSVAKSVKSLYLGRMFGSTPVIRLRFKRLQP 227
Db 267 LSPDMTCEIDILPCVPFSSVAKSVKSLYLGRMFGSTPVIRLRFKRLQP 313

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US-10-223-087-48
; Sequence 48, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C4
; CURRENT APPLICATION NUMBER: US/10/223,087
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
;
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT

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; ORGANISM: Murine
US-10-223-087-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

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Db 87 PRYQECMKYGRPEENKPNDFAKCVQNLDPDOCTPNPCDKKGTGTHICODLGMGNFFCVCTDGGW 146
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GRLCDKDVNECSQENGCGCIQICHNKPFGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GRLCDKDVNECVQKNGCGSQVCHNKPFGSFQACACHSGFSLASDQGTQCDIDECTSDTCGD 206
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 ARCKNLPGSYSLCLDEGFAYSSQEKACRDVDECLQRCSEQVQVNSPGSYTCHCDGRGGGLK 180
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 ARCKNLPGSYSLCLDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGGLK 266
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 LSQDMTDCEDILPCVPFVSVAKSVLGLRMFSGTVPVIRLRFKRLQP 227
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 LSPDMTDCEDILPCVPFVSMAKSVLGLRMFSGTVPVIRLRFKRLQP 313
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RESULT 9
US-10-223-083-48
; Sequence 48, Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
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; TYPE: PRT
; ORGANISM: Murine
US-10-223-083-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDICNKYGSPTKNSGFATCVQNLDPDOCTPNPCDRKGTQACODLGMGNFFCLCKAGWG 60
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 PRYQECMKYGRPEENKPNDFAKCVQNLDPDOCTPNPCDKKGTGTHICODLGMGNFFCVCTDGGW 146
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GRLCDKDVNECSQENGCGCIQICHNKPFGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GRLCDKDVNECVQKNGCGSQVCHNKPFGSFQACACHSGFSLASDQGTQCDIDECTSDTCGD 206
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 ARCKNLPGSYSLCLDEGFAYSSQEKACRDVDECLQRCSEQVQVNSPGSYTCHCDGRGGGLK 180
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 ARCKNLPGSYSLCLDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGGLK 266
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 LSQDMTDCEDILPCVPFVSVAKSVLGLRMFSGTVPVIRLRFKRLQP 227
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 LSPDMTDCEDILPCVPFVSMAKSVLGLRMFSGTVPVIRLRFKRLQP 313
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 10
US-10-223-089-48
; Sequence 48, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC9
; CURRENT APPLICATION NUMBER: US/10/223,089
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
```



```
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-089-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDICNKYSGPYTKNSGFATCVQNLDPDOCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 PRYQECMRKYGRPEKNPFAKCVQNLDPDOCTPNPCDRKGTQACODLMGNFFCLCKAGWG 146
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 GRLCDKDVNECSQENGCLQICHNKPGSFHCSCHSGFELSSDGRTCODIDECADSEACGE 120
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPGSFQACACHSGFSLASDGTQCDIDECTDSDTCGD 206
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 ARCKNLPGSYSLCDEGYTYSKKTQDVDECOQDRCEQTCVNSPGSYTCHCDGRGLK 266
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFGTVPVIRLRFKRLQP 227
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 LSPDMTDCEDILPCVPFSPMAKSVKSLYLGRMFGTVPVIRLRFKRLQP 313
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-10-223-081-48
; Sequence 48, Application US/10223081
; Publication No. US20030186866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P2235P1C7
; CURRENT APPLICATION NUMBER: US/10/223,081
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDICNKYSGPYTKNSGFATCVQNLDPDOCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 PRYQECMRKYGRPEKNPFAKCVQNLDPDOCTPNPCDRKGTQACODLMGNFFCLCKAGWG 146
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 GRLCDKDVNECSQENGCLQICHNKPGSFHCSCHSGFELSSDGRTCODIDECADSEACGE 120
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPGSFQACACHSGFSLASDGTQCDIDECTDSDTCGD 206
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 ARCKNLPGSYSLCDEGYTYSKKTQDVDECOQDRCEQTCVNSPGSYTCHCDGRGLK 266
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFGTVPVIRLRFKRLQP 227
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 LSPDMTDCEDILPCVPFSPMAKSVKSLYLGRMFGTVPVIRLRFKRLQP 313
   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-10-223-082-48
; Sequence 48, Application US/10223082
; Publication No. US20030191059A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: F3235P1C3
; CURRENT APPLICATION NUMBER: US/10/223,082
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-082-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKINXGSPYTKNSGFATCVQNLPDQCTPNPCDRKGTCACQDLGMGNFCLCKAGWG 60
Db 87 PRYQECWRKYGREEPKNDPAKVCQNLPDQCTPNPCDKKGTHICQDLGMGNFVCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFCHSGFELSSDRTQDIDECADSEACGE 120
Db 147 GRLCDKDVNSCVQNGGCSQVCHNKPFSQACACHSGFSLASDGTQDIDECTDSPTCGD 206

QY 121 ARCKNLPGSYSLCDGEGFAYSSQEKACRDVDECLQRCBQVQVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYSLCDGEGYTYSSKEKTCQDVDECOQDRCBQTCVNSPGSYTCHCDGRGGLK 266

QY 181 LSQDMPTCEDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQP 227
Db 267 LSPDMPTCEDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQP 313

QY 181 LSQDMPTCEDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQP 227
Db 267 LSPDMPTCEDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQP 313

RESULT 14
US-10-081-056-48
; Sequence 48, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20

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; PRIORITY APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIORITY APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIORITY APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIORITY APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIORITY APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIORITY APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIORITY APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIORITY APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIORITY APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIORITY APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIORITY APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIORITY APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIORITY APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIORITY APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIORITY APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIORITY APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-081-056-48

Query Match 85.8%; Score 1113; DB 15; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKYKGYRPEEKNDPFAKCVQNLDPDQCTPNPCDRKGTOACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYRPEEKNDPFAKCVQNLDPDQCTPNPCDRKGTHICQDLGMGNFFCVCTDGMG 146

QY 61 GRLCDKDVNECSQENGGLQICHNKGSGFCHSGFELSSDGRTCQDIDECADSEACGE 120
DB 147 GRLCDKDVNECVQNGGCSQVCHNKGSPQACACHSGFSLASDQGTQDIDECTDSDTCGD 206

QY 121 ARCKNLPGSYSLCDEGFAYSSOEKACRDVDECLQRCCEQVCSVPSGYSYTCCHCDGRGLK 180
DB 207 ARCKNLPGSYSLCDEGTYSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCCHCDGRGLK 266

QY 181 LSQDMTCELDPCVPFSSVAKSVKSLYLGRMFSGTPIRLRFRKLP 227
DB 267 LSPDMTCELDPCVPFSSVAKSVKSLYLGRMFSGTPIRLRFRKLP 313

RESULT 15
US-10-367-094-31
; Sequence 31, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(697)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-367-094-31

Query Match 85.8%; Score 1113; DB 16; Length 697;
Best Local Similarity 82.8%; Pred. No. 5.1e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKYKGYRPEEKNDPFAKCVQNLDPDQCTPNPCDRKGTOACQDLGMGNFFCLCKAGWG 60
DB 120 PRYQECMRKYRPEEKNDPFAKCVQNLDPDQCTPNPCDRKGTHICQDLGMGNFFCVCTDGMG 179

QY 61 GRLCDKDVNECSQENGGLQICHNKGSGFCHSGFELSSDGRTCQDIDECADSEACGE 120
DB 180 GRLCDKDVNECVQNGGCSQVCHNKGSPQACACHSGFSLASDQGTQDIDECTDSDTCGD 239

QY 121 ARCKNLPGSYSLCDEGFAYSSOEKACRDVDECLQRCCEQVCSVPSGYSYTCCHCDGRGLK 180
DB 240 ARCKNLPGSYSLCDEGTYSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCCHCDGRGLK 299

QY 181 LSQDMTCELDPCVPFSSVAKSVKSLYLGRMFSGTPIRLRFRKLP 227
DB 300 LSPDMTCELDPCVPFSSVAKSVKSLYLGRMFSGTPIRLRFRKLP 346

RESULT 16
US-10-723-860-467
; Sequence 467, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 467
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-467

Query Match 46.4%; Score 601.5; DB 16; Length 650;
Best Local Similarity 43.4%; Pred. No. 1.4e-41;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRYLDCKYKGYRPEEKNDPFAKCVQNLDPDQCTPNPCDRKGTOACQDLGMGNFF 52
DB 57 PRYLDCKYKGYRPEEKNDPFAKCVQNLDPDQCTPNPCDRKGTHICQDLGMGNFFCVCTDGMG 116

QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKGSGFCHSGFELSSDGRTCQD 109
DB 117 CTCKAGWGRLCDKDVNEC---SQENGGLQICHNKGSGFCHSGFELSSDGRTCQD 176

QY 110 DECA-DSEACGAEARCKNLPGSYSLCDEGFAYSSOEKACRDVDECLQRCCEQVCSVPSG 168

Db 177 DECSLKPSICGTAVCKNIPGDFECPECPGYRNILKSKSCEDIDECSENMCQALCVNYPG 236
Qy 169 YTHCDGRGLKLSODMTCEDILPCVPFVSAKSVKSLYLGRMFSGTPVIRLRFK 223
Db 237 YTCYCDGKGGFKLAQDKSCFVWSVCLPLNIDTKYLLYLAEPAGV-VLYLKR 290

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RESULT 17
US-10-952-459-30
; Sequence 30, Application US/10952459
; Publication NO. US20050074805A1
; GENERAL INFORMATION:
; APPLICANT: Kochan, Jarema Peter
; APPLICANT: Martin, Mitchell Lee
; APPLICANT: Rosinski, James Andrew
; TITLE OF INVENTION: Specific Markers for Diabetes
; FILE REFERENCE: 21270US1
; CURRENT APPLICATION NUMBER: US/10/952,459
; CURRENT FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-952-459-30

```

Query Match	46.4%	Score	601.5	DB	17	Length	676
Best Local Similarity	43.4%	Pred. No.	1.4e-4				
Matches	102	Conservative	45	Mismatches	75	Indels	13
Gaps	5						
Qy	1	PRYLDCLNKY-----GSPYTKNS--GFATCQVNLDPQCTPNPCDRKGTQACODLMGNFF	52				
Db	83	PXYLVCLRSFQTGLFTAAKGSTNAYPDLRSCVNAIPQCSPPLCNEGYMSCKDGKASFT	142				
Qy	53	CLCKAGWGBRLCDKVNNEC---SOENGGCLQICHNKGSPHCSCHSGFELSSDGRTCODI	109				
Db	143	CTCKPWQGBKECEPDIINECKDPSNINGGCSQICDNTPGSYHCSCKNGFVMLSNNKDKDV	202				
Qy	110	DECA-DSEACEGARCKNLPGSYSCLCDBEGFAYSISOEKACRDVDBCLQRCBQVCWNSPGS	168				
Db	203	DECSLKPSICGTAVCKNIIPGDFECEGEGYRYNLKSKSCEDIDECSENMAQLCVNTPGG	262				
Qy	169	YTHCDGRGGLKLSQDMDTCEDILPCVPFVSVAKSVKSLYLGRMPSGFTVIRLPK	223				
Db	263	YTVCDGKGGFKLAQDKQSGSEVSVCLPLNLDTKYELLALAEQAGV-VLYLKPR	316				

```

RESULT 18
US-10-367-094-34
; Sequence 34, Application US/10367094
; Publication No. US2004010982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-34

```

```

Query Match      27.8%; Score 361; DB 16; Length 510;
Best Local Similarity 35.7%; Pred. No. 9.7e-22;
Matches 81; Conservative 0; Mismatches 0; Indels 146; Gaps 1;
QV      1  PVLDCINKYGSPTKNSGGATCVNLPDQCTPNPCDRKGTGTAOCODLWGNFFCLCKAGWG 60

```

Db	74	PRYLDCKNGSPYTKNSGFATCVQNLPDQCTPNPCRKGTQA	116
Qy	61	GRLCDKDVNECSQENGCGCLQICHNKPQSGFHCSSHGFEISSLSDGRTCQDIDECADEACGE	120
Db	117	-----	116
Qy	121	ARKNVLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQCVNSPGSVYTHCDGRGGIK	180
Db	117	-----	116
Qy	181	LSQDMTCDILPCVPFSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ	227
Db	117	-----DILPCVPFSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ	154

```

RESULT 19
US-09-855-824-4
; Sequence 4, Application US/09855824
; Publication No. US20030166048A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETORY
; TITLE OF INVENTION: NUCLEIC ACID MOLECUL
; TITLE OF INVENTION: US THEREOF
; FILE REFERENCE: CL001233
; CURRENT APPLICATION NUMBER: US/09/855,824
; CURRENT FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-824-4

```

Query Match	27.6%;	Score	357.5;	DB	10;	Length	911;
Best Local Similarity	38.6%;	Pred. No.	3.4e-21;				
Matches	80;	Conservative	23;	Mismatches	81;	Indels	23;
Gaps	10;						
Qy	14	YTKNSGATCQNLPLDQCTN--PCDRKGTQACQDLDMGNFFCLCKAGW----	GGRLCDKD	67			
Db	232	YALHADGRTCIET-----CAVNVGGCDR-----	TCKDTATGVRCS	CPVGF	TLQPDG	KTC-KD	282
Qy	68	VNECSQNGGCLQICHNKPQSGFHCSHGSELPSSDGRGTCQIDICADSEACEARCKNLP	127				
Db	283	INECLMNVGGDHFRCNRTVSGFECQKGKHLTDERTCQIDICSPFTCDHI-CINSP	341				
Qy	128	GSYSCLCDEGFA-YSSGEKACRDVDECL--QGRCEQVCVNSPGSYTHCDGRGGGLKSQD	184				
Db	342	GSQCLCRGTYLYGTH--CGDVDECSMNVGSCQGCVCNTRGSECVCP--PGRRLHVN	397				
Qy	185	MDTCEDILPCVPFSSVAKSVKSLYLGRM	211				
Db	398	OKDCVENMGCLSRSKASQAQOLSCKGV	424				

```

RESULT 20
US-10-476-542-4
; Sequence 4, Application US/10476542
; Publication No. US20040242473A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRET
; TITLE OF INVENTION: NUCLEIC ACID MOLECUL
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001233-US
; CURRENT APPLICATION NUMBER: US/10/476,542
; CURRENT FILING DATE: 2003-11-03
; PRIORITY APPLICATION NUMBER: PCT/US02/22278
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/855,824
; PRIOR FILING DATE: 2001-05-16

```



```
Db      283 INECLMNGGCDHFCRNTVSGFECGCGKHLLTDERTCQDIDECSEFERTCDHI-CINSP 341
QY      128 GSYSCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
Db      342 GSFQCLCRRGVTLTGTH--CGDVDECSMNNGSCGQCVNTRGSEYECVCP--PGRRLHWN 397
QY      185 MDTCEDILPCVPFSPVSAKSVKSLYLGRM 211
Db      398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

RESULT 23
US-10-231-913-88
; Sequence 88, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 2000-12-12
; PRIOR FILING DATE: 2000-12-12
; PRIOR FILING DATE: 2001-01-08
; PRIOR FILING DATE: 2001-01-24
; PRIOR FILING DATE: 2001-01-24
; PRIOR FILING DATE: 2001-02-20
; PRIOR FILING DATE: 2001-04-24
; PRIOR FILING DATE: 2001-04-24
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-231-913-88

Query Match      27.6%; Score 357.5; DB 15; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY      14 YTKNSGFATCVQNLPDQCTPN--PCDRKGTOACQDLMGNFFCLCKAGW----GGRLCDKD 67
Db      283 YALHADGRTCIET-----CAVNNGGCDR---TCXDTATGVRCSGCVGTLPDQDKTC-KD 282
QY      68 VNECSQENGGLQICHNKPFGSHCSHGSEFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db      283 INECLMNGGCDHFCRNTVSGFECGCGKHLLTDERTCQDIDECSEFERTCDHI-CINSP 341
QY      128 GSYSCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
Db      342 GSFQCLCRRGVTLTGTH--CGDVDECSMNNGSCGQCVNTRGSEYECVCP--PGRRLHWN 397

RESULT 24
US-10-029-020-35
; Sequence 35, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; PRIOR FILING DATE: 2000-12-19
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-29
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2000-12-20
; PRIOR FILING DATE: 2001-09-14
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-020-35

Query Match      27.6%; Score 357.5; DB 15; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY      14 YTKNSGFATCVQNLPDQCTPN--PCDRKGTOACQDLMGNFFCLCKAGW----GGRLCDKD 67
Db      232 YALHADGRTCIET-----CAVNNGGCDR---TCXDTATGVRCSGCVGTLPDQDKTC-KD 282
QY      68 VNECSQENGGLQICHNKPFGSHCSHGSEFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db      283 INECLMNGGCDHFCRNTVSGFECGCGKHLLTDERTCQDIDECSEFERTCDHI-CINSP 341
QY      128 GSYSCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
Db      342 GSFQCLCRRGVTLTGTH--CGDVDECSMNNGSCGQCVNTRGSEYECVCP--PGRRLHWN 397

Query Match      27.6%; Score 357.5; DB 15; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY      185 MDTCEDILPCVPFSPVSAKSVKSLYLGRM 211
Db      398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

RESULT 25
```

```
US-10-016-248-77
; Sequence 77, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-77

Query Match      27.3%; Score 354.5; DB 15; Length 1587;
Best Local Similarity 43.3%; Pred. No. 1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy 29 DOCTNP--CDRKGTOACODLMGNFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db 636 DECTQSPGLCGG--CKNLPGSFRCVCPAGFRGSACEDVDDECAQEPFPCGPGRCNDT 692

Qy 86 PGSFHCSCHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSCLCDEGFAYSSQE 144
Db 693 AGSFHCACAPAGFRSRGPGAPCQDVDECARSPPCTYGRCENTEGSFQCVCPMGFPQNTAG 752

Qy 145 KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db 753 SECEDVDECEHNLACPGQECVNSPGSFQCRCTCPSGHHLHGRCTDVEDCSSGAPPCGP 810

RESULT 26
US-10-016-248-78
; Sequence 78, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-78

Query Match      27.3%; Score 353.5; DB 15; Length 888;
Best Local Similarity 43.3%; Pred. No. 7.1e-21;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy 29 DOCTNP--CDRKGTOACODLMGNFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db 470 DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEDVDDECAQEPFPCGPGRCNDT 526

Qy 86 PGSFHCSCHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSCLCDEGFAYSSQE 144
Db 527 AGSFHCACAPAGFRSRGPGAPCQDVDECARSPPCTYGRCENTEGSFQCVCPMGFPQNTAG 586

Qy 145 KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db 587 SECEDVDECEHNLACPGQECVNSPGSFQCRCTCPSGHHLHGRCTDVEDCSSGAPPCGP 644

US-10-016-248-75
; Sequence 75, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-75

Query Match      27.3%; Score 353.5; DB 15; Length 888;
Best Local Similarity 43.3%; Pred. No. 7.1e-21;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy 29 DOCTNP--CDRKGTOACODLMGNFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db 470 DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEDVDDECAQEPFPCGPGRCNDT 526

Qy 86 PGSFHCSCHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSCLCDEGFAYSSQE 144
Db 527 AGSFHCACAPAGFRSRGPGAPCQDVDECARSPPCTYGRCENTEGSFQCVCPMGFPQNTAG 586

Qy 145 KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db 587 SECEDVDECEHNLACPGQECVNSPGSFQCRCTCPSGHHLHGRCTDVEDCSSGAPPCGP 644
```



```
RESULT 28
US-09-855-824-6
; Sequence 6, Application US/09855824
; Publication No. US20030166048A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: US97800001
; CURRENT APPLICATION NUMBER: US/09/855,824
; CURRENT FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-824-6

Query Match 27.3%; Score 353.5; DB 10; Length 957;
Best Local Similarity 34.9%; Pred. No. 7.6e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDOCTPN--PCDRKGTOA 43
Db 199 PRYRLHADGRSCLEQEGTVLEGTSNATSVADGDKRVKRRLLMETCAVNNGGCDR---T 254

QY 44 CQDLGNFCLCKAGW-----GGRLCDKDVNECSQENGGCLQICHNKPFSFHCSCSHGPFEL 99
Db 255 CKDTSTGVHCSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKNTVGSFDCSCCKGFKL 313

QY 100 SSDGRTCODIDECADSEACGEARCKNLPGSYCLCDEGFA-YSSQEKACRDVDECL--QG 156
Db 314 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGTYLSFTH--CGDTNECSVNNG 370

QY 157 RCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 371 GCQQVCINTVGSYECQC--HPGFKLHWNKDCVEVKVGFPTSMTPRV-SLHCCKSGGG 425

RESULT 29
US-10-476-542-6
; Sequence 6, Application US/10476542
; Publication No. US20040242473A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: US97800001
; CURRENT APPLICATION NUMBER: US/10/476,542
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/US02/22278
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/855,824
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-476-542-6

Query Match 27.3%; Score 353.5; DB 16; Length 957;
Best Local Similarity 34.9%; Pred. No. 7.6e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDOCTPN--PCDRKGTOA 43
Db 199 PRYRLHADGRSCLEQEGTVLEGTSNATSVADGDKRVKRRLLMETCAVNNGGCDR---T 254
```

```
QY 44 CQDLGNFCLCKAGW-----GGRLCDKDVNECSQENGGCLQICHNKPFSFHCSCSHGPFEL 99
Db 255 CKDTSTGVHCSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKNTVGSFDCSCCKGFKL 313

QY 100 SSDGRTCODIDECADSEACGEARCKNLPGSYCLCDEGFA-YSSQEKACRDVDECL--QG 156
Db 314 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGTYLSFTH--CGDTNECSVNNG 370

QY 157 RCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 371 GCQQVCINTVGSYECQC--HPGFKLHWNKDCVEVKVGFPTSMTPRV-SLHCCKSGGG 425

RESULT 30
US-09-747-371-3
; Sequence 3, Application US/09747371
; Patent No. US20020006616A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; TITLE OF INVENTION: No. US20020006616A1el Methods of Diagnosing Breast Cancer, Composi
; TITLE OF INVENTION: Screening for Breast Cancer Modulators
; FILE REFERENCE: A-69038/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/747,371
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/ US/00/06952
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-747-371-3

Query Match 27.3%; Score 353.5; DB 9; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDOCTPN--PCDRKGTOA 43
Db 239 PRYRLHADGRSCLEQEGTVLEGTSNATSVADGDKRVKRRLLMETCAVNNGGCDR---T 294

QY 44 CQDLGNFCLCKAGW-----GGRLCDKDVNECSQENGGCLQICHNKPFSFHCSCSHGPFEL 99
Db 295 CKDTSTGVHCSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKNTVGSFDCSCCKGFKL 353

QY 100 SSDGRTCODIDECADSEACGEARCKNLPGSYCLCDEGFA-YSSQEKACRDVDECL--QG 156
Db 354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGTYLSFTH--CGDTNECSVNNG 410

QY 157 RCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 411 GCQQVCINTVGSYECQC--HPGFKLHWNKDCVEVKVGFPTSMTPRV-SLHCCKSGGG 465

RESULT 31
US-09-930-512-66
; Sequence 66, Application US/09930512
; Publication No. US20040010118A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spytek, Kimberly
; APPLICANT: Spaderna, Steven
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Burgess, Catherine E
; APPLICANT: Majumder, Kumud
; APPLICANT: Shinkets, Richard
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine
; APPLICANT: Szekeres, Edward S
```

APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Liu, Xiaohong
APPLICANT: Gerlach, Valerie L
APPLICANT: Ellerman, Karen
APPLICANT: Smithson, Glennnda
APPLICANT: Peyman, John
APPLICANT: Stone, David
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20040010118a1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-091
CURRENT APPLICATION NUMBER: US/09/930,512
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,692
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/225,837
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/225,693
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/226,236
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/226,353
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/227,085
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/227,395
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/227,492
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/227,600
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/275,952
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 997
TYPE: PRT
ORGANISM: Mus musculus
US-09-930-512-66

Query Match 27.3%; Score 353.5; DB 11; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;
QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDQCTPN--PCDRKGTQA 43
DB 239 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRLMETCAVNGGCDR----T 294
QY 44 QDLMGNFFCLCKAGW----GRLCDKDVNECSQENGGLQICHNKPFSFHCSCSGFEL 99
DB 295 CKDTSTGVHSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKCNKTVGSPDCSCCKGFKL 353
QY 100 SSDGRTCODIDECADSEACEARCKNLPGSYSLCDEGFA-YSSQEKACRDVDECL--QG 156
DB 354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFIACNPGTYLFTFTH--CGDTNECSVNGG 410
QY 157 RCQVQCVNSPGSYTCHDGRGGLKLSQDMDTCDILPCVPFVSVAKSVKSLYLGRMFSG 214
DB 411 GCQVQCVINTVGSVEQC--HPGFKLHNKKDCVEVGFPTSTMTPRV-SLHCGKSGGG 465

RESULT 32
US-10-231-913-90
Sequence 90, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.

APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schloimit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Baha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 90
LENGTH: 997
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-90
Query Match 27.3%; Score 353.5; DB 15; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;
QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDQCTPN--PCDRKGTQA 43
DB 239 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRLMETCAVNGGCDR----T 294
QY 44 QDLMGNFFCLCKAGW----GRLCDKDVNECSQENGGLQICHNKPFSFHCSCSGFEL 99
DB 295 CKDTSTGVHSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKCNKTVGSPDCSCCKGFKL 353
QY 100 SSDGRTCODIDECADSEACEARCKNLPGSYSLCDEGFA-YSSQEKACRDVDECL--QG 156
DB 354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFIACNPGTYLFTFTH--CGDTNECSVNGG 410
QY 157 RCQVQCVNSPGSYTCHDGRGGLKLSQDMDTCDILPCVPFVSVAKSVKSLYLGRMFSG 214
DB 411 GCQVQCVINTVGSVEQC--HPGFKLHNKKDCVEVGFPTSTMTPRV-SLHCGKSGGG 465

RESULT 33
US-10-029-020-37
Sequence 37, Application US/10029020
Publication No. US20040033971A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

```

; FILE REFERENCE: 21402-325
; CURRENT APPLICATION NUMBER: US/10/029,020
; PRIOR FILING DATE: 2001-12-19
; SOFTWARE: PatentIn Ver. 2.1
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-029-020-37

Query Match      27.3%; Score 353.5; DB 15; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY      1  PRY-----LDCINKVGSPTKNSGFATCVQN-----LPOCTPN--PCDRKGTQA 43
DB      239  PRYRLHADGRSCLEOBSGTVLEGTESNATSVADGDKRVKRLMETCAVNGGCDR-----T 294

QY      44  CQDLMGNFCLCKAGH---GGRLCDKDVNCSQBNGGCLQICHNKPFSFCHSCHSGFEL 99
DB      295  CKDTSTGVHSCPTGTLQVDGKTC-KOIDEQOTENGCGNHFCKNTVGSFDCSKKGFKL 353

QY      100  SSGRTCCQDIDECASEAGEARCNKLPGSVYSLCDEGFA-YSSQEKACRDVDECL--QG 156
DB      354  LTDEKSCQDVDECSLERTCDHS-CINHFQTFICACNPGYTLYSFTH--CGDTNCSYVNG 410

QY      157  RCQVQVNSPFSYTHCHDGRGLKLSQDMDTCTDILPCVPFVSVAKSVKSLVLRMFSG 214
DB      411  GCQVVCINTVGSYEQC--HPGFKLHWKDKDVEVKGFPPTSMTPRV-SLHCGSGGG 465

RESULT 34
US-10-016-248-32
; Sequence 32, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-016-248-30

Query Match      27.3%; Score 353.5; DB 15; Length 1356;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

QY      29  DOCTNP--CDRKGTAQCDLMGNFFCLCKAGWGRLCDKDVNCSQBNGGC-LQICHNK 85
DB      560  DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEEDVDECAQEPFPCGFRCDNT 616

QY      86  PGSPHCSCHSGFELSSDGRCTQDIDECADS-EACGEARCNKLPGSVYSLCDEGFAYSSQE 144
DB      617  AGSFHCACPAFGRSRGPGAPQDVDECARSPPTCYGRCENTEGSFQVCPMGFQPNNAAG 676

QY      145  KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDRGGGLKLSQ--DMDTCED-ILPCVP 196
DB      677  SECEDVDECEHNLACPGQECVNSPFSQCRACPSGHHLHGRCTDVEDCSGAPPCGP 734

RESULT 35
US-10-016-248-30
; Sequence 30, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-016-248-30

Query Match      27.3%; Score 353.5; DB 15; Length 1356;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

QY      29  DOCTNP--CDRKGTAQCDLMGNFFCLCKAGWGRLCDKDVNCSQBNGGC-LQICHNK 85
DB      560  DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEEDVDECAQEPFPCGFRCDNT 616

QY      86  PGSPHCSCHSGFELSSDGRCTQDIDECADS-EACGEARCNKLPGSVYSLCDEGFAYSSQE 144
DB      617  AGSFHCACPAFGRSRGPGAPQDVDECARSPPTCYGRCENTEGSFQVCPMGFQPNNAAG 676

QY      145  KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDRGGGLKLSQ--DMDTCED-ILPCVP 196
DB      677  SECEDVDECEHNLACPGQECVNSPFSQCRACPSGHHLHGRCTDVEDCSGAPPCGP 734

```

```
RESULT 36
US-10-112-944-315
; Sequence 315, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pt_Fl_genes Version 5.0
; SEQ ID NO 315
; LENGTH: 1425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-315

Query Match 27.3%; Score 353.5; DB 15; Length 1425;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy 29 DOCTPNP--CDRKGTOACODLMGNFFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db 560 DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEDVDECAQEPFPPCGPGRCDNT 616

Qy 86 PGSFHCCHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSLCDEGFAYSSQE 144
Db 617 AGSFHCACAPAGFRSRGPGAPCQDVDECARSPPCTYGRCENTEGSFQCVCPMGFQPNAA 676

Qy 145 KACRDVDECIQOG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db 677 SECEDVDECEHNLACPGQECVNSPGSFQCRACPSGHHLHGRCTDVEDCSSGAPPCGP 734

; SOFTWARE: Pt_Fl_genes Version 5.0
; SEQ ID NO 315
; LENGTH: 1425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-315

RESULT 37
US-10-016-248-28
; Sequence 28, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
```

```
US-10-016-248-28
; Sequence 26, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-28

Query Match 27.3%; Score 353.5; DB 15; Length 1467;
Best Local Similarity 43.3%; Pred. No. 1.2e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy 29 DOCTPNP--CDRKGTOACODLMGNFFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db 560 DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEDVDECAQEPFPPCGPGRCDNT 616

Qy 86 PGSFHCCHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSLCDEGFAYSSQE 144
Db 617 AGSFHCACAPAGFRSRGPGAPCQDVDECARSPPCTYGRCENTEGSFQCVCPMGFQPNAA 676

Qy 145 KACRDVDECIQOG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db 677 SECEDVDECEHNLACPGQECVNSPGSFQCRACPSGHHLHGRCTDVEDCSSGAPPCGP 734

RESULT 38
US-10-016-248-26
; Sequence 26, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-26
```


; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIAL
; FILE REFERENCE: MPI02-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406.073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-17

Query Match 26.9%; Score 349; DB 15; Length 764;
Best Local Similarity 37.7%; Pred. No. 1.9e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;
QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLMGNFFCLCKAGW-----GGRLCDKD 67
DB 207 YAPHSDDRTCIET-----CAVNGGCDR----TCKDTATGVRCSCPVGFLLQPDGKTC-KD 257
QY 68 VNECSQENGGLQICHNKPGECHSGFELSSDGRTCODIDECADSEAGEARCKNLP 127
DB 258 INECLVNGGCDHFCRNTVSGFCGRKGYKLLTDRTCODIDECSPERTCDHI-CINSP 316
QY 128 GSYSLCLDEGF-AYSSQEKACRDVDEC--LQGRCEQVCVNSPGSYTCHDGRGGLKLSQD 184
DB 317 GSFOCLCHRGYILYGTTH--CGDVDECSMSNGSCDQCQVNTKGSYECVCP--FGRRLHWN 372
QY 185 MDTCEDILPC-----VPPSVAKSVKSLYL 208
DB 373 RKDCVETGKLSRAKTSPPRAQLSCSKAGGVESCF 407

RESULT 42
US-10-406-073-2
; Sequence 2, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMUVES, Lazlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; FILE REFERENCE: MPI02-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406.073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 988
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-2

Query Match 26.9%; Score 349; DB 15; Length 988;
Best Local Similarity 37.7%; Pred. No. 1.9e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;
QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLMGNFFCLCKAGW-----GGRLCDKD 67
DB 232 YAPHSDDRTCIET-----CAVNGGCDR----TCKDTATGVRCSCPVGFLLQPDGKTC-KD 282
QY 68 VNECSQENGGLQICHNKPGECHSGFELSSDGRTCODIDECADSEAGEARCKNLP 127

DB 283 INECLVNGGCDHFCRNTVSGFCGRKGYKLLTDRTCODIDECSPERTCDHI-CINSP 341
QY 128 GSYSLCLDEGF-AYSSQEKACRDVDEC--LQGRCEQVCVNSPGSYTCHDGRGGLKLSQD 184
DB 342 GSFOCLCHRGYILYGTTH--CGDVDECSMSNGSCDQCQVNTKGSYECVCP--FGRRLHWN 397
QY 185 MDTCEDILPC-----VPPSVAKSVKSLYL 208
DB 398 RKDCVETGKLSRAKTSPPRAQLSCSKAGGVESCF 432

RESULT 43
US-10-231-913-18
; Sequence 18, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Payman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 988
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-18

Query Match 26.9%; Score 349; DB 15; Length 988;
Best Local Similarity 37.7%; Pred. No. 1.9e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;
QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLMGNFFCLCKAGW-----GGRLCDKD 67

Db 232 YAPHS DGRTCIET-CAVNNGGCDR---TKD TATGVRGSCPVGFTLQPDGKTC-KD 282
QY 68 VNECSQENGGLQICHNKPGSFCHSGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 283 INECLVNNGGCDHFCRTNVTGSPFCGCRKGKLLTDBERTCQDIDECSEFERTCDHI-CINSP 341
QY 128 GSYSCLCDEGF-AYSSQEKACRDVDC--LQGRCEQVCVNSPGSYTCHDGRGLKLSOD 184
Db 342 GSFQCLCHRGYILYGTTH--CGDVDCSMNSGSCDQGCNTKGSYECVCP--PGRRLHWN 397
QY 185 MDTCEDILPC-----VPFSVAKSVKSLYL 208
Db 398 RKDCVETGKCLSRKSTSPRAQLSCSKAGGVESCF 432

RESULT 44

US-10-406-073-19
; Sequence 19, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruy-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMUVES, Lazslo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIIUM
; FILE REFERENCE: MP102-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406,073
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; TYPE: PRT
; LENGTH: 386
; ORGANISM: Homo sapiens
US-10-406-073-19

Query Match 26.9%; Score 348.5; DB 15; Length 386;
Best Local Similarity 39.8%; Pred. No. 8e-21;
Matches 76; Conservative 20; Mismatches 72; Indels 23; Gaps 10;
QY 14 YTKNSGFATCVQNLDPQCTPN--PCDRKGTQACQDLMGNFFCLCKAGW----GGRLCDKD 67
Db 207 YAPHS DGRTCIET-CAVNNGGCDR---TKD TATGVRGSCPVGFTLQPDGKTC-KD 257
QY 68 VNECSQENGGLQICHNKPGSFCHSGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 258 INECLVNNGGCDHFCRTNVTGSPFCGCRKGKLLTDBERTCQDIDECSEFERTCDHI-CINSP 316
QY 128 GSYSCLCDEGF-AYSSQEKACRDVDC--LQGRCEQVCVNSPGSYTCHDGRGLKLSOD 184
Db 317 GSFQCLCHRGYILYGTTH--CGDVDCSMNSGSCDQGCNTKGSYECVCP--PGRRLHWN 372
QY 185 MDTCEDILPCV 195
Db 373 RKDCVETGKCL 383

RESULT 45

US-10-015-115-57
; Sequence 57, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A

; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 2871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-57
Query Match 26.9%; Score 348.5; DB 15; Length 2871;
Best Local Similarity 42.9%; Pred. No. 5.9e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;
QY 44 QDLMGNFFCLCKAGWG---RLCDKQVNECSQENGGLQICHNKPGSFCHSGFELLS 100
Db 1171 CVNLGKYGQACNPGYHSTPDLFCVDIDECIMNGCETFTCTNSEGSEVSCSQPGFALM 1230
QY 101 SDGRTCQDIDECADSEACGEARCKNLPVSGVSCLCDEGFAYSSQEKACRDVDE----- 152
Db 1231 PDQRSCDIDECEDNPNTCDGQCTNIFGEYRCLCYDGFMAEDMKTCVDVNECDLNPNI 1290
QY 153 CLQGRCEQVCVNSPGSYTCHD---GRGLKLSODMDTCE 189
Db 1291 CLSGTCE----NTRGSEFICHDMGYSGRKKGTGCTDINECE 1327
RESULT 46
US-10-015-115-56
; Sequence 56, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of


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; ORGANISM: Fibrillin-1 Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: A47221
; DATABASE ENTRY DATE: 2000-07-21
US-10-478-451-10

Query Match      26.9%; Score 348.5; DB 16; Length 3002;
Best Local Similarity 42.9%; Pred. No. 6.2e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLNMFCLCKAGWG--RLCDXDVNECSQENGGLQICHNKPQSFHCSCHSGFELS 100
DB 1302 CVNLIGKYQCACNPGYHSTPDLFCVDIIDECSTIMNGGCTFCTNSGSEYECSCQPGFALM 1361
QY 101 SDGRTQDIDECADS-EAGEARCKNLPGSYSLCDGFPAYSSQEKACRDVDE----- 152
DB 1362 PDQRCTDIDCEDNPNICDGGCTNIPGEYRCLCYDGFWASEDMKTCVDVNECDLNPNI 1421
QY 153 CLQGRCEQVCVNSPGSYTCHCD---GRGGLKLSQDMDTCE 189
DB 1422 CLSGTCE---NTKGSFICHCDMGYSKKGKTGCTDINECE 1458

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RESULT 50
US-10-239-663-57
; Sequence 57, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-663-57

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Query Match      26.8%; Score 348; DB 14; Length 387;
Best Local Similarity 41.1%; Pred. No. 8.8e-21;
Matches 74; Conservative 16; Mismatches 60; Indels 30; Gaps 9;

QY 24 VQNLPDQCTPN---PCDRKGTQACQDLNMGFFCLCKAGW-----GGRLCDXDVNECSQENG 77
DB 213 IMSAPETCAVNGGCDR---TCKDTATGVRCSCPVGFTLQPDGKTC-KDINECLVNNGG 267
QY 78 CLQICHNKPQSFHCSGFLSSDGTQDIDECADSEACGEARCKNLPGSYSLCLCDG 137
DB 268 CHFCRNTVGSFECGRKGKGLLTDTERTQDIDECSFERTCDHI-CINSPGFSQCLCHRG 326
QY 138 F-AYSQEKACRDVDE--LQGRCEQVCVNSPGSYTC-----HCDGRGLKL 181
DB 327 YILYGTTH--CGDVDECSMNSGCDQGCYVNTKGSYECVCPGRRRLHWNGKDCVGRGSLLL 384

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Search completed: July 7, 2005, 10:31:22
Job time : 407.132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:49:00 ; Search time 25.7967 Seconds
(without alignments)
224.889 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYLG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A.Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	518	ABO84421	Human can
2	72	100.0	624	ADQ67207	Novel hum
3	72	100.0	678	AAR99414	Human gas
4	72	100.0	678	AAW46463	Human gro
5	72	100.0	678	AAV29794	Human gro
6	72	100.0	678	AAV57383	Amino aci
7	72	100.0	678	ADL83231	Human PRO
8	72	100.0	678	ADM40825	Human Gas
9	72	100.0	678	ADM60275	Human PRO
10	72	100.0	678	ADD48757	Human PRO
11	72	100.0	686	ADM40823	Human Gas
12	69	95.8	673	AAW46462	Murine gr
13	69	95.8	673	AAV29793	Murine gr
14	69	95.8	673	AAV33459	Human PRO
15	69	95.8	673	AAV57382	Amino aci
16	69	95.8	673	ABW48480	Human PRO
17	69	95.8	673	ABW95446	Human ang
18	69	95.8	673	ADD10337	Human sec
19	69	95.8	673	ADD11297	Human sec
20	69	95.8	673	ADD37090	Human sec
21	69	95.8	673	ADH41298	Human sec
22	69	95.8	673	ADH43481	Human PRO
23	69	95.8	673	ADK82826	Human PRO
24	69	95.8	703	ABO84420	Mouse can
25	44	61.1	77	ADC94783	E. faeciu

26	44	61.1	374	4	AAU03812
27	44	61.1	374	8	ADN23180
28	42	58.3	291	7	ADD31762
29	42	58.3	1220	8	ADN07100
30	42	58.3	1220	8	ADS43652
31	42	58.3	4345	4	ABW66417
32	41	56.9	364	6	ABW67414
33	41	56.9	527	8	ADO05107
34	41	56.9	1067	8	ADO05104
35	41	56.9	1173	8	ADS43524
36	41	56.9	1206	1	AAV60679
37	41	56.9	1206	1	AAV60679
38	41	56.9	1235	8	ADP98882
39	41	56.9	3457	2	AAW84560
40	41	56.9	3457	2	AAW84560
41	40	55.6	174	4	ABG08969
42	40	55.6	394	4	ABG02533
43	40	55.6	969	5	ABP73632
44	39	54.2	64	4	AAW89790
45	39	54.2	369	3	AAW27329
46	38	52.8	120	5	ABP04700
47	38	52.8	133	5	ABP62898
48	38	52.8	307	8	ADS43968
49	38	52.8	349	6	ABW53899
50	38	52.8	349	7	ADK64826
51	38	52.8	374	3	AAW04796
52	38	52.8	382	8	ADJ76321
53	38	52.8	393	3	AAW04797
54	38	52.8	406	3	AAW04796
55	37	51.4	62	4	AAW28773
56	37	51.4	62	4	ABW20718
57	37	51.4	62	4	ABW50149
58	37	51.4	225	3	AAW58195
59	37	51.4	258	8	ADN18230
60	37	51.4	266	7	ABO61682
61	37	51.4	307	5	ABW53034
62	37	51.4	307	8	ADN19329
63	37	51.4	316	7	ADC95392
64	37	51.4	334	2	AAW48701
65	37	51.4	334	2	AAW02673
66	37	51.4	384	3	AAW27003
67	37	51.4	433	5	ABW64887
68	37	51.4	456	7	ADL46379
69	37	51.4	461	3	AAW27002
70	37	51.4	480	3	AAW27001
71	37	51.4	506	8	ADS29909
72	37	51.4	512	5	ABW55533
73	37	51.4	529	5	ABW26857
74	37	51.4	771	4	ABW64331
75	37	51.4	812	5	ABG92717
76	37	51.4	1702	2	AAW38095
77	36.5	50.7	54	5	ABP00991
78	36.5	50.7	966	7	ADC83634
79	36	50.0	12	2	AAV17975
80	36	50.0	74	7	ABO62312
81	36	50.0	84	4	ABW15173
82	36	50.0	226	6	ABU35512
83	36	50.0	297	4	AAV17978
84	36	50.0	297	4	AAW46976
85	36	50.0	394	5	AAW16591
86	36	50.0	400	6	ABW73084
87	36	50.0	410	4	AAU35435
88	36	50.0	432	6	ABU26432
89	36	50.0	515	4	ABG12419
90	36	50.0	529	6	ABU49551
91	36	50.0	551	3	ABW15526
92	36	50.0	551	4	AAW82992
93	36	50.0	605	5	ABW47309
94	36	50.0	629	4	AAW94640
95	36	50.0	629	4	AAW02721
96	36	50.0	641	5	ABW57280
97	36	50.0	719	4	ABW68053
98	36	50.0	875	5	ABW09317

AAU03812	G protein
ADN23180	Bacterial
ADD31762	Enterobac
ADN07100	S. cerevi
ADS43652	Bacterial
ABW66417	Drosophi
ABW67414	Photorhab
ADO05107	Rift vall
ADO05104	Rift vall
ADS43524	Bacterial
AAV60679	Sequence
AAV60679	Rift Vall
ADP98882	C. albica
AAW84560	Large pol
AAW84560	Polyprote
ABG08969	Novel hum
ABG02533	Novel hum
ABP73632	Candida a
AAW89790	Human imm
AAW27329	N. tabacu
ABP04700	Human ORF
ABP62898	Human pol
ADS43968	Bacterial
ABW53899	Protein g
ADK64826	Disease c
AAW04796	Arabidops
ADJ76321	Marker ge
AAW04797	Arabidops
AAW04796	Arabidops
AAW28773	Peptide #
ABW50149	Human liv
AAW58195	Arabidops
ADN18230	Bacterial
ABO61682	Klebsiell
ABW53034	Yeast RNA
ADN19329	Bacterial
ADC95392	E. faeciu
AAW48701	G-protein
AAW02673	G-protein
AAW27003	Arabidops
ABW64887	Human pro
ADL46379	UDP-N-ace
AAW27002	Arabidops
AAW27001	Arabidops
ADS29909	Bacterial
ABW55533	Lactococc
ABW26857	Anabaena
ABW64331	Drosophi
ABG92717	Coccidiol
AAW38095	T. litora
ABP00991	Human ORF
ADC83634	LTRPC3-te
AAV17975	Peptide S
ABO62312	Klebsiell
ABW15173	Human ner
AAV17978	Hexulose
ABU35512	Protein e
AAW46976	A. aeolic
AAW16591	Pseudozym
ABW73084	Staphyloc
AAU35435	Haemophil
ABU26432	Protein e
ABG12419	Novel hum
ABU49551	Protein e
ABW15526	Arabidops
AAW82992	Arabidops
ABW47309	Listeria
AAW94640	Human pro
AAW02721	C-termina
ABW57280	Mouse lac
ABW68053	Drosophi
ABW09317	Human TIC

99	36	50.0	876	7	ADB37641	Adb37641	Neural th	172	35	48.6	421	6	ADA76252	Ada76252	Human PRO
100	36	50.0	876	7	ADB37636	Adb37636	Neural th	173	35	48.6	421	6	ADA18902	Ada18902	Human PRO
101	36	50.0	900	2	AY30338	Aay30338	A multifu	174	35	48.6	421	6	ADA61525	Ada61525	Homo sapi
102	36	50.0	900	4	AAB20179	Aab20179	S. cerevi	175	35	48.6	421	6	ADB19310	Adb19310	Novel hum
103	36	50.0	900	4	AAB20178	Aab20178	S. cerevi	176	35	48.6	421	6	ADB27851	Adb27851	Human PRO
104	36	50.0	900	4	AAB20176	Aab20176	Saccharom	177	35	48.6	421	6	ADA86330	Ada86330	Novel hum
105	36	50.0	900	4	AAB20177	Aab20177	S. cerevi	178	35	48.6	421	6	ADA15894	Ada15894	Human PRO
106	36	50.0	900	8	ADS43839	Adsa43839	Bacterial	179	35	48.6	421	6	ADA47680	Ada47680	Human PRO
107	36	50.0	930	7	ADN95169	Adn95169	Human BEC	180	35	48.6	421	6	ADA67475	Ada67475	Human PRO
108	36	50.0	931	5	ABB09319	Abb09319	Human tra	181	35	48.6	421	6	ADB30482	Adb30482	Human PRO
109	36	50.0	931	7	ADB37609	Adb37609	Neural th	182	35	48.6	421	6	ADA85778	Ada85778	Novel hum
110	36	50.0	931	8	ADH51626	Adh51626	Human 156	183	35	48.6	421	6	ADA96990	Ada96990	Human PRO
111	36	50.0	1086	8	ADN23310	Adn23310	Bacterial	184	35	48.6	421	6	ADA79294	Ada79294	Human PRO
112	36	50.0	1145	8	ADN73071	Adn73071	Thale cre	185	35	48.6	421	6	ADA87433	Ada87433	Novel hum
113	36	50.0	15281	2	AAR44929	Aar44929	T. niveum	186	35	48.6	421	6	ADB16635	Adb16635	Human PRO
114	35.5	49.3	116	3	AAG34529	Aag34529	Arabidops	187	35	48.6	421	6	ADA91727	Ada91727	Novel hum
115	35.5	49.3	119	5	ABP33627	Abp33627	Human ORF	188	35	48.6	421	6	ADB14790	Adb14790	Human PRO
116	35.5	49.3	239	3	AAG24805	Aag24805	Arabidops	189	35	48.6	421	6	ADB18751	Adb18751	Novel hum
117	35.5	49.3	239	3	AAG40407	Aag40407	Arabidops	190	35	48.6	421	6	ADA93966	Ada93966	Human PRO
118	35.5	49.3	267	8	ADS43476	Adsa43476	Bacterial	191	35	48.6	421	6	ADB19862	Adb19862	Novel hum
119	35	48.6	50	8	ABO56052	Abos6052	Human gen	192	35	48.6	421	6	ADB13174	Adb13174	Human PRO
120	35	48.6	78	5	ABP11021	Abp11021	Human ORF	193	35	48.6	421	6	ABO43299	Abos43299	Novel hum
121	35	48.6	93	8	ADI57735	Adi57735	Human bre	194	35	48.6	421	6	ADA74428	Ada74428	Human PRO
122	35	48.6	209	4	ABG16149	Abg16149	Novel hum	195	35	48.6	421	6	ADB24661	Adb24661	Human PRO
123	35	48.6	217	3	AAG31815	Aag31815	Arabidops	196	35	48.6	421	6	ADA82185	Ada82185	Human PRO
124	35	48.6	223	3	AAG31814	Aag31814	Arabidops	197	35	48.6	421	6	ADA75148	Ada75148	Human PRO
125	35	48.6	279	7	ABO84175	Abos84175	Pseudomon	198	35	48.6	421	6	ADA85226	Ada85226	Novel hum
126	35	48.6	303	6	ADA33592	Ada33592	Acinetoba	199	35	48.6	421	6	ADA84674	Ada84674	Novel hum
127	35	48.6	332	7	ABO60744	Abos60744	Klebsiell	200	35	48.6	421	6	ADB29930	Adb29930	Human PRO
128	35	48.6	358	3	AAG31813	Aag31813	Arabidops	201	35	48.6	421	6	ADA80458	Ada80458	Human PRO
129	35	48.6	361	8	ABM84676	Abm84676	Human dia	202	35	48.6	421	6	ADA75700	Ada75700	Human PRO
130	35	48.6	361	8	ABM82804	Abm82804	Human dia	203	35	48.6	421	6	ADA46925	Ada46925	Human PRO
131	35	48.6	362	7	ADD49055	Add49055	Human NOV	204	35	48.6	421	6	ADB25221	Adb25221	Human PRO
132	35	48.6	366	8	ADS30288	Ads30288	Bacterial	205	35	48.6	421	6	ADA93397	Ada93397	Human PRO
133	35	48.6	367	4	ABB52489	Abb52489	Escherich	206	35	48.6	421	6	ADB26747	Adb26747	Human PRO
134	35	48.6	379	2	AAR64159	Aar64159	Human ela	207	35	48.6	421	6	ADB31034	Adb31034	Human PRO
135	35	48.6	379	2	AAR94367	Aar94367	Human ela	208	35	48.6	421	6	ADA60962	Ada60962	Homo sapi
136	35	48.6	379	7	ADD49057	Add49057	Human NOV	209	35	48.6	421	6	ADB24109	Adb24109	Human PRO
137	35	48.6	379	7	ADJ69755	Adj69755	Human hea	210	35	48.6	421	6	ADA96438	Ada96438	Human PRO
138	35	48.6	379	8	AUG25245	Aug25245	Human leu	211	35	48.6	421	6	ADA81010	Ada81010	Human PRO
139	35	48.6	379	8	ADJ66663	Adj66663	Nipl prot	212	35	48.6	421	6	ADA95886	Ada95886	Human PRO
140	35	48.6	379	8	ADJ66641	Adj66641	Leukocyte	213	35	48.6	421	6	ADB26195	Adb26195	Human PRO
141	35	48.6	379	8	ADJ75603	Adj75603	Marker ge	214	35	48.6	421	6	ADB21680	Adb21680	Novel hum
142	35	48.6	379	8	ADN04567	Adn04567	Antipsori	215	35	48.6	421	7	ADA77459	Ada77459	Human PRO
143	35	48.6	379	8	ADQ30590	Adq30590	Pancreas	216	35	48.6	421	7	ADB18199	Adb18199	Human PRO
144	35	48.6	379	8	ADP24496	Adp24496	PRO polyp	217	35	48.6	421	7	ADA86882	Ada86882	Novel hum
145	35	48.6	382	8	ADN25725	Adn25725	Bacterial	218	35	48.6	421	7	ADA87985	Ada87985	Novel hum
146	35	48.6	386	6	ADA36269	Ada36269	Acinetoba	219	35	48.6	421	7	ADA46373	Ada46373	Novel hum
147	35	48.6	391	1	AAP70479	Aap70479	Sequence	220	35	48.6	421	7	ADB28403	Adb28403	Human PRO
148	35	48.6	391	2	AAR25305	Aar25305	HRSV majo	221	35	48.6	421	7	ADB28955	Adb28955	Human PRO
149	35	48.6	391	2	AAR24184	Aar24184	Bovine RS	222	35	48.6	421	7	ADA76907	Ada76907	Human PRO
150	35	48.6	391	2	AAR50001	Aar50001	HRSV majo	223	35	48.6	421	7	ADA89537	Ada89537	Novel hum
151	35	48.6	391	5	ABG99060	Abg99060	N protein	224	35	48.6	421	7	ADA97542	Ada97542	Human PRO
152	35	48.6	391	8	ADJ97186	Adj97186	Human res	225	35	48.6	421	7	ADB27299	Adb27299	Human PRO
153	35	48.6	391	8	ADJ97187	Adj97187	Human res	226	35	48.6	421	7	ADB22232	Adb22232	Novel hum
154	35	48.6	396	6	ADN49106	Adn49106	Bovine re	227	35	48.6	421	7	ADA66923	Ada66923	Human PRO
155	35	48.6	397	2	AAR21328	Aar21328	Sequence	228	35	48.6	421	7	ADB22784	Adb22784	Human PRO
156	35	48.6	410	6	ADU40655	Adu40655	Protein e	229	35	48.6	421	7	ADB23557	Adb23557	Human PRO
157	35	48.6	413	7	ADU05967	Adu05967	Bacterial	230	35	48.6	421	7	ADA92279	Ada92279	Novel hum
158	35	48.6	421	2	AY05767	Ay05767	Human ost	231	35	48.6	421	7	ADB15342	Adb15342	Human PRO
159	35	48.6	421	3	AY088377	Ay088377	PRO216 (o	232	35	48.6	421	7	ADB38594	Adb38594	Novel hum
160	35	48.6	421	3	AAB33417	Aab33417	Human PRO	233	35	48.6	421	7	ADB38042	Adb38042	Novel hum
161	35	48.6	421	3	AAB24435	Aab24435	Human PRO	234	35	48.6	421	7	ADB66514	Adb66514	Novel hum
162	35	48.6	421	4	AAB12322	Aab12322	Human PRO	235	35	48.6	421	7	ADB89594	Adb89594	Human PRO
163	35	48.6	421	4	AAB20340	Aab20340	Human PRO	236	35	48.6	421	7	ADB90326	Adb90326	Human PRO
164	35	48.6	421	5	AAB081955	Aab081955	Human PRO	237	35	48.6	421	7	ADB39427	Adb39427	Novel hum
165	35	48.6	421	6	ABO17766	Abos17766	Human PRO	238	35	48.6	421	7	ADB47050	Adb47050	Novel hum
166	35	48.6	421	6	ABU81020	Abu81020	Human PRO	239	35	48.6	421	7	ADB86657	Adb86657	Human PRO
167	35	48.6	421	6	ABU66720	Abu66720	Human PRO	240	35	48.6	421	7	ADB77262	Adb77262	Novel hum
168	35	48.6	421	6	ABU59801	Abu59801	Novel sec	241	35	48.6	421	7	ADB34419	Adb34419	Human PRO
169	35	48.6	421	6	ABO24991	Abos24991	Human sec	242	35	48.6	421	7	ADB35523	Adb35523	Human PRO
170	35	48.6	421	6	ABU66996	Abu66996	Human sec	243	35	48.6	421	7	ADB33867	Adb33867	Human PRO
171	35	48.6	421	6	ADA45821	Ada45821	Novel hum	244	35	48.6	421	7	ADB34971	Adb34971	Human PRO

245	35	48.6	421	7	ADB36075	Human	PRO	Adb36075	Human	PRO	318	35	48.6	421	7	ADN16510	Novel	hum	Adn16510	Novel	hum
246	35	48.6	421	7	ADB46470	Novel	hum	Adb46470	Novel	hum	319	35	48.6	421	7	ADN15329	Novel	hum	Adn15329	Novel	hum
247	35	48.6	421	7	ADC50343	Novel	hum	Adc50343	Novel	hum	320	35	48.6	421	7	ADN14777	Novel	hum	Adn14777	Novel	hum
248	35	48.6	421	7	ADC71890	Novel	hum	Adc71890	Novel	hum	321	35	48.6	421	7	ADIC64003	Novel	hum	Adc64003	Novel	hum
249	35	48.6	421	7	ADC59869	Novel	hum	Adc59869	Novel	hum	322	35	48.6	421	7	ADIC81039	Novel	hum	Adc81039	Novel	hum
250	35	48.6	421	7	ADC52876	Novel	hum	Adc52876	Novel	hum	323	35	48.6	421	8	ADD76487	Human	PRO	Add76487	Human	PRO
251	35	48.6	421	7	ADC57230	Novel	hum	Adc57230	Novel	hum	324	35	48.6	421	8	ADD87851	Human	PRO	Add87851	Human	PRO
252	35	48.6	421	7	ADC60421	Novel	hum	Adc60421	Novel	hum	325	35	48.6	421	8	ADD86255	Human	PRO	Add86255	Human	PRO
253	35	48.6	421	7	ADC50896	Novel	hum	Adc50896	Novel	hum	326	35	48.6	421	8	ADE75703	Human	PRO	Ade75703	Human	PRO
254	35	48.6	421	7	ADC65423	Human	PRO	Adc65423	Human	PRO	327	35	48.6	421	8	ADE23279	Human	PRO	Ade23279	Human	PRO
255	35	48.6	421	7	ADC54521	Novel	hum	Adc54521	Novel	hum	328	35	48.6	421	8	ADE23831	Human	PRO	Ade23831	Human	PRO
256	35	48.6	421	7	ADC53482	Novel	hum	Adc53482	Novel	hum	329	35	48.6	421	8	ADE24474	Human	PRO	Ade24474	Human	PRO
257	35	48.6	421	7	ADC59005	Novel	hum	Adc59005	Novel	hum	330	35	48.6	421	8	ADD87299	Human	PRO	Add87299	Human	PRO
258	35	48.6	421	7	ADC55883	Novel	hum	Adc55883	Novel	hum	331	35	48.6	421	8	ADE89165	Human	PRO	Ade89165	Human	PRO
259	35	48.6	421	7	ADC58453	Novel	hum	Adc58453	Novel	hum	332	35	48.6	421	8	ADE18304	Human	PRO	Ade18304	Human	PRO
260	35	48.6	421	7	ADC01127	Novel	hum	Adc01127	Novel	hum	333	35	48.6	421	8	ADE88613	Human	PRO	Ade88613	Human	PRO
261	35	48.6	421	7	ADC90119	Novel	hum	Adc90119	Novel	hum	334	35	48.6	421	8	ADE94633	Human	PRO	Ade94633	Human	PRO
262	35	48.6	421	7	ADC69538	Human	PRO	Adc69538	Human	PRO	335	35	48.6	421	8	ADE91044	Human	PRO	Ade91044	Human	PRO
263	35	48.6	421	7	ADC48427	Human	PRO	Adc48427	Human	PRO	336	35	48.6	421	8	ADE95185	Human	PRO	Ade95185	Human	PRO
264	35	48.6	421	7	ADD09956	Human	PRO	Adc09956	Human	PRO	337	35	48.6	421	8	ADE93295	Human	PRO	Ade93295	Human	PRO
265	35	48.6	421	7	ADD04531	Novel	hum	Adc04531	Novel	hum	338	35	48.6	421	8	ADF74876	Human	PRO	Ade74876	Human	PRO
266	35	48.6	421	7	ADC80487	Novel	hum	Adc80487	Novel	hum	339	35	48.6	421	8	ADF92191	Novel	hum	Ade92191	Novel	hum
267	35	48.6	421	7	ADD10994	Human	PRO	Adc10994	Human	PRO	340	35	48.6	421	8	ADE90492	Human	PRO	Ade90492	Human	PRO
268	35	48.6	421	7	ADC47875	Human	PRO</														

391	35	48.6	421	8	ADI14637	Adi14637 Novel hum	464	35	48.6	775	6	ADB24479	ADB24479 Human PRO
392	35	48.6	421	8	ADI18232	Adi18232 Novel hum	465	35	48.6	775	6	ADA82003	ADA82003 Human PRO
393	35	48.6	421	8	ADJ63513	Adj63513 Novel hum	466	35	48.6	775	6	ADA74966	ADA74966 Human PRO
394	35	48.6	421	8	ADJ77408	Adj77408 Human PRO	467	35	48.6	775	6	ADA85044	ADA85044 Novel hum
395	35	48.6	421	8	ADJ65530	Adj65530 Human PRO	468	35	48.6	775	6	ADA84492	ADA84492 Novel hum
396	35	48.6	421	8	ADM27666	Adm27666 Human PRO	469	35	48.6	775	6	ADB29748	ADB29748 Human PRO
397	35	48.6	421	8	ADM42390	Adm42390 Human PRO	470	35	48.6	775	6	ADA80276	ADA80276 Human PRO
398	35	48.6	421	8	ADM28252	Adm28252 Human PRO	471	35	48.6	775	6	ADA75518	ADA75518 Human PRO
399	35	48.6	421	8	ADQ18584	Adq18584 Human sof	472	35	48.6	775	6	ADA46743	ADA46743 Human PRO
400	35	48.6	421	8	ADQ195734	Adq195734 Human PRO	473	35	48.6	775	6	ADB25039	ADB25039 Human PRO
401	35	48.6	421	8	ADI96286	Adi96286 Novel hum	474	35	48.6	775	6	ADA93215	ADA93215 Human PRO
402	35	48.6	421	8	ADT94397	Adt94397 Human PRO	475	35	48.6	775	6	ADB26565	ADB26565 Human PRO
403	35	48.6	437	3	AAB343755	Aab343755 Human can	476	35	48.6	775	6	ADB30852	ADB30852 Human PRO
404	35	48.6	444	7	ADG40032	Adg40032 Murine Sp	477	35	48.6	775	6	ADA60780	ADA60780 Homo sapi
405	35	48.6	445	7	ABO75589	Abg75589 Pseudomon	478	35	48.6	775	6	ADB23927	ADB23927 Human PRO
406	35	48.6	451	8	ADN04632	Adn04632 Antipisori	479	35	48.6	775	6	ADA96256	ADA96256 Human PRO
407	35	48.6	451	8	ADP24649	Adp24649 PRO polyp	480	35	48.6	775	6	ADA80828	ADA80828 Human PRO
408	35	48.6	452	2	AY09553	AY09553 Streptoco	481	35	48.6	775	6	ADA95704	ADA95704 Human PRO
409	35	48.6	452	5	ABP25517	Abp25517 Streptoco	482	35	48.6	775	6	ADB26013	ADB26013 Human PRO
410	35	48.6	452	6	ABU46730	Abu46730 Protein e	483	35	48.6	775	6	ADB21498	ADB21498 Novel hum
411	35	48.6	457	6	ABP76802	Abp76802 N. gonorr	484	35	48.6	775	7	ADA77277	ADA77277 Human PRO
412	35	48.6	457	6	ABP80055	Abp80055 N. gonorr	485	35	48.6	775	7	ADB18017	ADB18017 Human PRO
413	35	48.6	460	4	ABE67576	ABE67576 Drosoephil	486	35	48.6	775	7	ADA86700	ADA86700 Novel hum
414	35	48.6	460	7	ABO70261	ABO70261 Pseudomon	487	35	48.6	775	7	ADA87803	ADA87803 Novel hum
415	35	48.6	465	6	ADA34854	Ada34854 Acinetoba	488	35	48.6	775	7	ADA46191	ADA46191 Novel hum
416	35	48.6	469	5	ABG93131	Abg93131 S. cerevi	489	35	48.6	775	7	ADB28221	ADB28221 Human PRO
417	35	48.6	469	6	ABR52710	Abg52710 Protein a	490	35	48.6	775	7	ADB28773	ADB28773 Human PRO
418	35	48.6	469	7	ADK61927	Adk61927 Disease t	491	35	48.6	775	7	ADA76725	ADA76725 Human PRO
419	35	48.6	516	5	ABN93350	ABn93350 Herbicida	492	35	48.6	775	7	ADA88355	ADA88355 Novel hum
420	35	48.6	517	8	ADN10645	Adn10645 Nicotiana	493	35	48.6	775	7	ADA97360	ADA97360 Human PRO
421	35	48.6	529	5	ABB47666	Abb47666 Listeria	494	35	48.6	775	7	ADB27117	ADB27117 Human PRO
422	35	48.6	529	6	ABU32537	Abu32537 Protein e	495	35	48.6	775	7	ADB22050	ADB22050 Novel hum
423	35	48.6	606	7	ADH86208	Adh86208 Enterococ	496	35	48.6	775	7	ADA66741	ADA66741 Human PRO
424	35	48.6	662	8	ADN74701	Adn74701 Thale cre	497	35	48.6	775	7	ADB22602	ADB22602 Human PRO
425	35	48.6	715	6	ABU40115	Abu40115 Protein e	498	35	48.6	775	7	ADB23375	ADB23375 Human PRO
426	35	48.6	715	5	ABN91351	ABn91351 Herbicida	499	35	48.6	775	7	ADA92097	ADA92097 Novel hum
427	35	48.6	735	4	AAU36496	Aau36496 Pseudomon	500	35	48.6	775	7	ADB15160	ADB15160 Human PRO
428	35	48.6	735	6	ABU38864	Abu38864 Protein e	501	35	48.6	775	7	ADB38412	ADB38412 Novel hum
429	35	48.6	759	8	ADS43027	Ads43027 Bacterial	502	35	48.6	775	7	ADB37860	ADB37860 Novel hum
430	35	48.6	771	8	ADS24420	Ads24420 Bacterial	503	35	48.6	775	7	ADB66332	ADB66332 Novel hum
431	35	48.6	772	4	ABB12438	Abb12438 Human bon	504	35	48.6	775	7	ADB89412	ADB89412 Human PRO
432	35	48.6	775	4	AAU12231	Aau12231 Human PRO	505	35	48.6	775	7	ADB90144	ADB90144 Human PRO
433	35	48.6	775	4	ABB71228	Abb71228 Drosoephil	506	35	48.6	775	7	ADB39245	ADB39245 Novel hum
434	35	48.6	775	6	ABO17675	Abc17675 Novel hum	507	35	48.6	775	7	ADB46868	ADB46868 Novel hum
435	35	48.6	775	6	ABU80929	Abu80929 Human PRO	508	35	48.6	775	7	ADB86475	ADB86475 Human PRO
436	35	48.6	775	6	ABU66629	Abu66629 Human PRO	509	35	48.6	775	7	ADB77080	ADB77080 Novel hum
437	35	48.6	775	6	ABU59710	Abu59710 Novel sec	510	35	48.6	775	7	ADB34237	ADB34237 Human PRO
438	35	48.6	775	6	ABO24900	ABO24900 Human sec	511	35	48.6	775	7	ADB35341	ADB35341 Human PRO
439	35	48.6	775	6	ABU66905	ABu66905 Human sec	512	35	48.6	775	7	ADB33685	ADB33685 Human PRO
440	35	48.6	775	6	ADA45639	Ada45639 Novel hum	513	35	48.6	775	7	ADB34789	ADB34789 Human PRO
441	35	48.6	775	6	ADA76070	Ada76070 Human PRO	514	35	48.6	775	7	ADB35893	ADB35893 Human PRO
442	35	48.6	775	6	ADA18720	Ada18720 Human PRO	515	35	48.6	775	7	ADB46288	ADB46288 Novel hum
443	35	48.6	775	6	ADA63343	Ada63343 Homo sapi	516	35	48.6	775	7	ADC50161	ADC50161 Novel hum
444	35	48.6	775	6	ADB19128	Adb19128 Novel hum	517	35	48.6	775	7	ADC71708	ADC71708 Novel hum
445	35	48.6	775	6	ADB27669	Adb27669 Human PRO	518	35	48.6	775	7	ADC52694	ADC52694 Novel hum
446	35	48.6	775	6	ADA86148	Ada86148 Novel hum	519	35	48.6	775	7	ADC52687	ADC52687 Novel hum
447	35	48.6	775	6	ADB15712	Adb15712 Human PRO	520	35	48.6	775	7	ADC57048	ADC57048 Novel hum
448	35	48.6	775	6	ADA47498	Ada47498 Human PRO	521	35	48.6	775	7	ADC60239	ADC60239 Novel hum
449	35	48.6	775	6	ADA67293	Ada67293 Human PRO	522	35	48.6	775	7	ADC50714	ADC50714 Novel hum
450	35	48.6	775	6	ADB30300	Adb30300 Human PRO	523	35	48.6	775	7	ADC5241	ADC5241 Human PRO
451	35	48.6	775	6	ADA85596	Ada85596 Novel hum	524	35	48.6	775	7	ADC54339	ADC54339 Novel hum
452	35	48.6	775	6	ADA96808	Ada96808 Human PRO	525	35	48.6	775	7	ADC53300	ADC53300 Novel hum
453	35	48.6	775	6	ADA79112	Ada79112 Human PRO	526	35	48.6	775	7	ADC58823	ADC58823 Novel hum
454	35	48.6	775	6	ADA87251	Ada87251 Novel hum	527	35	48.6	775	7	ADC55701	ADC55701 Novel hum
455	35	48.6	775	6	ADB16453	Adb16453 Human PRO	528	35	48.6	775	7	ADC58271	ADC58271 Novel hum
456	35	48.6	775	6	ADA91545	Ada91545 Novel hum	529	35	48.6	775	7	ADD02945	ADD02945 Novel hum
457	35	48.6	775	6	ADB14608	Adb14608 Human PRO	530	35	48.6	775	7	ADC89937	ADC89937 Novel hum
458	35	48.6	775	6	ADB18569	Adb18569 Novel hum	531	35	48.6	775	7	ADC69356	ADC69356 Human PRO
459	35	48.6	775	6	ADA93784	Ada93784 Human PRO	532	35	48.6	775	7	ADC48245	ADC48245 Human PRO
460	35	48.6	775	6	ADB19680	Adb19680 Novel hum	533	35	48.6	775	7	ADD09774	ADD09774 Human PRO
461	35	48.6	775	6	ADB12992	Adb12992 Human PRO	534	35	48.6	775	7	ADD04349	ADD04349 Novel hum
462	35	48.6	775	6	ABO43208	ABO43208 Novel hum	535	35	48.6	775	7	ADC80305	ADC80305 Novel hum
463	35	48.6	775	6	ADA74246	Ada74246 Human PRO	536	35	48.6	775	7	ADD10812	ADD10812 Human PRO

537	35	48.6	775	7	ADC47693	Adc47693	Human	PRO	610	35	48.6	775	8	ADG91457	Ade91457	Novel	hum
538	35	48.6	775	7	ADC79753	Adc79753	Novel	PRO	611	35	48.6	775	8	ADG02036	Adg02036	Human	PRO
539	35	48.6	775	7	ADD09222	AdD09222	Human	PRO	612	35	48.6	775	8	ADG21822	Adg21822	Novel	hum
540	35	48.6	775	7	ADD40935	AdD40935	Novel	hum	613	35	48.6	775	8	ADG19892	Adg19892	Human	PRO
541	35	48.6	775	7	ADD52074	AdD52074	Human	PRO	614	35	48.6	775	8	ADf97798	Adf97798	Human	PRO
542	35	48.6	775	7	ADD52814	AdD52814	Human	PRO	615	35	48.6	775	8	ADG24015	Adg24015	Novel	hum
543	35	48.6	775	7	ADD53366	AdD53366	Novel	hum	616	35	48.6	775	8	ADf98369	Adf98369	Human	PRO
544	35	48.6	775	7	ADD51522	AdD51522	Human	PRO	617	35	48.6	775	8	ADG03200	Adg03200	Human	PRO
545	35	48.6	775	7	ADD02321	AdD02321	Human	PRO	618	35	48.6	775	8	ADf98921	Adf98921	Human	PRO
546	35	48.6	775	7	ADD01755	AdD01755	Human	PRO	619	35	48.6	775	8	ADf16506	Adf16506	Human	PRO
547	35	48.6	775	7	ADD53937	AdD53937	Novel	hum	620	35	48.6	775	8	ADG04965	Adg04965	Human	PRO
548	35	48.6	775	7	ADD92254	AdD92254	Human	PRO	621	35	48.6	775	8	ADG19232	Adg19232	Human	PRO
549	35	48.6	775	7	ADD91150	AdD91150	Human	PRO	622	35	48.6	775	8	ADG13069	Adg13069	Human	PRO
550	35	48.6	775	7	ADG03764	AdG03764	Human	PRO	623	35	48.6	775	8	ADG08126	Adg08126	Novel	hum
551	35	48.6	775	7	ADG32061	AdG32061	Novel	hum	624	35	48.6	775	8	ADG15296	Adg15296	Human	PRO
552	35	48.6	775	7	ADG21993	AdG21993	Human	PRO	625	35	48.6	775	8	ADf96694	Adf96694	Human	PRO
553	35	48.6	775	7	ADG79217	AdG79217	Human	PRO	626	35	48.6	775	8	ADG05879	Adg05879	Human	PRO
554	35	48.6	775	7	ADG41753	AdG41753	Human	PRO	627	35	48.6	775	8	ADG23463	Adg23463	Novel	hum
555	35	48.6	775	7	ADG17570	AdG17570	Human	PRO	628	35	48.6	775	8	ADG03752	Adg03752	Human	PRO
556	35	48.6	775	7	ADD91702	AdD91702	Human	PRO	629	35	48.6	775	8	ADG24653	Adg24653	Novel	hum
557	35	48.6	775	7	ADG33165	AdG33165	Novel	hum	630	35	48.6	775	8	ADG06950	Adg06950	Novel	hum
558	35	48.6	775	7	ADG33717	AdG33717	Novel	hum	631	35	48.6	775	8	ADG07502	Adg07502	Novel	hum
559	35	48.6	775	7	ADD79769	AdD79769	Human	PRO	632	35	48.6	775	8	ADG54997	Adg54997	Novel	hum
560	35	48.6	775	7	ADD92806	AdD92806	Human	PRO	633	35	48.6	775	8	ADG60661	Adg60661	Novel	hum
561	35	48.6	775	7	ADG19226	AdG19226	Human	PRO	634	35	48.6	775	8	ADG61765	Adg61765	Novel	hum
562	35	48.6	775	7	ADG18674	AdG18674	Human	PRO	635	35	48.6	775	8	ADG81966	Adg81966	Human	PRO
563	35	48.6	775	7	ADG42870	AdG42870	Human	PRO	636	35	48.6	775	8	ADG57205	Adg57205	Novel	hum
564	35	48.6	775	7	ADD95659	AdD95659	Human	PRO	637	35	48.6	775	8	ADG56653	Adg56653	Novel	hum
565	35	48.6	775	7	ADG22545	AdG22545	Human	PRO	638	35	48.6	775	8	ADG55549	Adg55549	Novel	hum
566	35	48.6	775	7	ADD78663	AdD78663	Human	PRO	639	35	48.6	775	8	ADG58309	Adg58309	Novel	hum
567	35	48.6	775	7	ADG32813	AdG32813	Novel	hum	640	35	48.6	775	8	ADG70675	Adg70675	Novel	hum
568	35	48.6	775	7	ADG42305	AdG42305	Human	PRO	641	35	48.6	775	8	ADG57757	Adg57757	Novel	hum
569	35	48.6	775	7	ADD80321	AdD80321	Human	PRO	642	35	48.6	775	8	ADG53341	Adg53341	Novel	hum
570	35	48.6	775	7	ADG89349	AdG89349	Human	PRO	643	35	48.6	775	8	ADG71227	Adg71227	Novel	hum
571	35	48.6	775	7	ADG40633	AdG40633	Human	PRO	644	35	48.6	775	8	ADG81414	Adg81414	Human	PRO
572	35	48.6	775	7	ADG04432	AdG04432	Human	PRO	645	35	48.6	775	8	ADH30376	Adh30376	Human	PRO
573	35	48.6	775	7	ADG92561	AdG92561	Human	PRO	646	35	48.6	775	8	ADH11743	Adh11743	Novel	hum
574	35	48.6	775	7	ADG21270	AdG21270	Novel	hum	647	35	48.6	775	8	ADG52165	Adg52165	Novel	hum
575	35	48.6	775	7	ADG22911	AdG22911	Novel	hum	648	35	48.6	775	8	ADG53893	Adg53893	Novel	hum
576	35	48.6	775	7	ADf97246	Adf97246	Human	PRO	649	35	48.6	775	8	ADG80862	Adg80862	Human	PRO
577	35	48.6	775	7	ADG80310	AdG80310	Human	PRO	650	35	48.6	775	8	ADG56101	Adg56101	Novel	hum
578	35	48.6	775	7	ADG79758	AdG79758	Human	PRO	651	35	48.6	775	8	ADH12367	Adh12367	Novel	hum
579	35	48.6	775	7	ADH55050	AdH55050	Novel	hum	652	35	48.6	775	8	ADG61213	Adg61213	Novel	hum
580	35	48.6	775	7	ADH55602	AdH55602	Novel	hum	653	35	48.6	775	8	ADH28300	Adh28300	Human	PRO
581	35	48.6	775	7	ADf63821	Adf63821	Novel	hum	654	35	48.6	775	8	ADG54445	Adg54445	Novel	hum
582	35	48.6	775	7	ADf64770	Adf64770	Novel	hum	655	35	48.6	775	8	ADG59485	Adg59485	Novel	hum
583	35	48.6	775	7	ADf63269	Adf63269	Novel	hum	656	35	48.6	775	8	ADf80909	Adf80909	Human	PRO
584	35	48.6	775	7	ADH81583	AdH81583	Novel	hum	657	35	48.6	775	8	ADG09652	Adg09652	Novel	hum
585	35	48.6	775	7	ADH81131	AdH81131	Novel	hum	658	35	48.6	775	8	ADf15223	Adf15223	Novel	hum
586	35	48.6	775	7	ADH822300	AdH822300	Novel	hum	659	35	48.6	775	8	ADG09000	Adg09000	Novel	hum
587	35	48.6	775	7	ADN15699	AdN15699	Novel	hum	660	35	48.6	775	8	ADf14455	Adf14455	Novel	hum
588	35	48.6	775	7	ADN16328	AdN16328	Novel	hum	661	35	48.6	775	8	ADf18050	Adf18050	Novel	hum
589	35	48.6	775	7	ADN15147	AdN15147	Novel	hum	662	35	48.6	775	8	ADf06531	Adf06531	Human	hum
590	35	48.6	775	7	ADN14595	AdN14595	Novel	hum	663	35	48.6	775	8	ADf63331	Adf63331	Novel	hum
591	35	48.6	775	8	ADH80857	AdH80857	Novel	hum	664	35	48.6	775	8	ADf77226	Adf77226	Human	PRO
592	35	48.6	775	8	ADH76305	AdH76305	Human	PRO	665	35	48.6	775	8	ADf65348	Adf65348	Human	PRO
593	35	48.6	775	8	ADH87669	AdH87669	Human	PRO	666	35	48.6	775	8	ADm27484	Adm27484	Human	PRO
594	35	48.6	775	8	ADH86073	AdH86073	Human	PRO	667	35	48.6	775	8	ADm42208	Adm42208	Human	PRO
595	35	48.6	775	8	ADf75521	Adf75521	Human	PRO	668	35	48.6	775	8	ADm28070	Adm28070	Human	PRO
596	35	48.6	775	8	ADG23097	AdG23097	Human	PRO	669	35	48.6	775	8	ADf95552	Adf95552	Human	PRO
597	35	48.6	775	8	ADG23649	AdG23649	Human	PRO	670	35	48.6	775	8	ADf96104	Adf96104	Novel	hum
598	35	48.6	775	8	ADG24292	AdG24292	Human	PRO	671	35	48.6	775	8	ADJ49896	AdJ49896	Human	PRO
599	35	48.6	775	8	ADH87117	AdH87117	Human	PRO	672	35	48.6	775	8	ADJ49896	AdJ49896	Oil-assoc	
600	35	48.6	775	8	ADH88983	AdH88983	Human	PRO	673	35	48.6	936	6	ABU29398	Abu29398	Protein e	
601	35	48.6	775	8	ADf18122	Adf18122	Human	PRO	674	35	48.6	1987	7	ABU63358	Abu63358	Tumour-as	
602	35	48.6	775	8	ADH88431	AdH88431	Human	PRO	675	35	48.6	2013	7	ABU63356	Abu63356	Human	Sin
603	35	48.6	775	8	ADH94451	AdH94451	Human	PRO	676	35	48.6	2014	7	ABU63356	Abu63356	Human	Sin
604	35	48.6	775	8	ADH90862	AdH90862	Human	PRO	677	35	48.6	2014	5	AAE24137	Aae24137	Amino aci	
605	35	48.6	775	8	ADH95003	AdH95003	Human	PRO	678	35	48.6	2014	6	ABP60434	Abp60434	Human	ste
606	35	48.6	775	8	ADH93113	AdH93113	Human	PRO	679	35	48.6	2014	7	ABU63359	Abu63359	Human	Sin
607	35	48.6	775	8	ADf34694	Adf34694	Human	PRO	680	35	48.6	2040	6	ABU63357	Abu63357	Human	Sin
608	35	48.6	775	8	ADG92009	AdG92009	Novel	hum	681	35	48.6	2041	6	ABP60435	Abp60435	Human	ste
609	35	48.6	775	8	ADG90310	AdG90310	Human	PRO	682	34.5	47.9	61	4	AAW92318	Aam92318	Human	dig

683	34.5	47.9	123	4	AAU32762	Aau32762 Novel hum	756	34	47.2	188	3	AAG29990	Aag29990 Arabidops
684	34.5	47.9	223	5	ABG26207	Aag26207 Arabidops	757	34	47.2	196	4	AAU27541	Aau27541 Human G-p
685	34.5	47.9	223	3	ABG1073	Abg1073 Herbicida	758	34	47.2	200	5	AAM49451	Aam49451 Escherich
686	34.5	47.9	225	8	ADM91017	Adm91017 Human pha	759	34	47.2	201	7	ADF04028	Adf04028 Bacterial
687	34.5	47.9	225	8	ADM91016	Adm91016 Human pha	760	34	47.2	204	7	RAE02389	Rae02389 Soybean l
688	34.5	47.9	241	4	AGM80951	Agm80951 Human nfp	761	34	47.2	222	7	ADH86261	Adh86261 Enterococ
689	34.5	47.9	241	5	ABG93769	Abg93769 Human G p	762	34	47.2	232	7	ADF04579	Adf04579 Bacterial
690	34.5	47.9	248	4	AAU29731	Aau29731 Novel hum	763	34	47.2	237	7	ADH04579	Adh04579 Bacterial
691	34.5	47.9	273	5	ABB83167	Abb83167 Murine re	764	34	47.2	252	4	AAB92903	Aab92903 Human pro
692	34.5	47.9	308	5	ABB83165	Abb83165 Human ren	765	34	47.2	252	5	ABB89797	Abb89797 Human pol
693	34.5	47.9	332	5	AAE23417	Aae23417 Human G-p	766	34	47.2	252	5	ABB97568	Abb97568 Novel hum
694	34.5	47.9	335	2	AAU59720	Aau59720 Secreted	767	34	47.2	254	5	ABP70050	Abp70050 Human NOV
695	34.5	47.9	335	7	ADM77895	Adm77895 Human pro	768	34	47.2	254	5	ABP70052	Abp70052 Human NOV
696	34.5	47.9	335	6	ADP19551	Adp19551 Human sec	769	34	47.2	254	5	ABP70051	Abp70051 Human NOV
697	34.5	47.9	339	6	ABJ37891	Abj37891 NOXV prot	770	34	47.2	254	5	ABP70053	Abp70053 Human NOV
698	34.5	47.9	344	8	ADO30378	Ado30378 Mouse GPC	771	34	47.2	254	5	ABP70054	Abp70054 Human NOV
699	34.5	47.9	344	8	ADO30380	Ado30380 Mouse GPC	772	34	47.2	267	2	AAU04290	Aau04290 Streptoco
700	34.5	47.9	344	8	ADO30390	Ado30390 Mouse GPC	773	34	47.2	293	8	ABM83498	Abm83498 Human dia
701	34.5	47.9	345	8	ADO29665	Ado29665 Mouse GPC	774	34	47.2	293	8	ABM83497	Abm83497 Human dia
702	34.5	47.9	346	8	ADL04725	Adl04725 M. catarr	775	34	47.2	300	4	AAU22928	Aau22928 Novel hum
703	34.5	47.9	348	3	AAB18764	Aab18764 Amino aci	776	34	47.2	302	3	AAG50629	Aag50629 Arabidops
704	34.5	47.9	348	5	ABB98168	Abb98168 Human AXO	777	34	47.2	302	3	AAG16856	Aag16856 Arabidops
705	34.5	47.9	348	6	ABP81735	Abp81735 Human tra	778	34	47.2	313	2	AAU38657	Aay38657 Neisseria
706	34.5	47.9	348	7	ADC54042	Adc54042 Human reg	779	34	47.2	313	2	AAU38656	Aay38656 Neisseria
707	34.5	47.9	348	7	ADE71022	Adc54042 TA3 amino	780	34	47.2	313	6	ABP78726	Abp78726 N. gonorr
708	34.5	47.9	348	7	ADL00349	Adl00349 Polypepti	781	34	47.2	313	6	ABP80805	Abp80805 N. gonorr
709	34.5	47.9	348	8	ADO29148	Ado29148 Mouse nov	782	34	47.2	317	4	ABB62682	Abb62682 Drosophil
710	34.5	47.9	348	8	ADO29147	Ado29147 Human nov	783	34	47.2	321	3	AAG29989	Aag29989 Arabidops
711	34.5	47.9	350	2	AAW64539	Aaw64539 Human epi	784	34	47.2	321	5	ABBS1991	Abbs1991 Herbicida
712	34.5	47.9	350	4	AAW90553	Aaw90553 Human sec	785	34	47.2	324	7	ADF07935	Adf07935 Bacterial
713	34.5	47.9	350	4	AAW90589	Aaw90589 Human sec	786	34	47.2	330	2	AAW48698	Aaw48698 G-protein
714	34.5	47.9	350	4	AAW88347	Aab88347 Human mem	787	34	47.2	330	2	AAW02670	Aaw02670 G-protein
715	34.5	47.9	350	5	ABB89154	Abb89154 Human pol	788	34	47.2	335	5	ABW55117	Abw55117 Streptoco
716	34.5	47.9	350	5	ABB83164	Abb83164 Human ren	789	34	47.2	335	5	ABW54611	Abw54611 S. pneumo
717	34.5	47.9	350	5	ABG65467	Abg65467 Human alb	790	34	47.2	335	7	ADC45191	Adc45191 S. pneumo
718	34.5	47.9	350	5	ABG65466	Abg65466 Human alb	791	34	47.2	353	3	AAG47267	Aag47267 Arabidops
719	34.5	47.9	350	8	ADL78734	Adl78734 Albumin f	792	34	47.2	353	3	AAG11237	Aag11237 Arabidops
720	34.5	47.9	350	8	ADL78733	Adl78733 Albumin f	793	34	47.2	353	3	AAG20688	Aag20688 Arabidops
721	34.5	47.9	350	8	ADR67233	Adr67233 Human bla	794	34	47.2	353	3	AAG47251	Aag47251 Arabidops
722	34.5	47.9	362	4	AAU31747	Aau31747 Novel hum	795	34	47.2	356	3	AAG11236	Aag11236 Arabidops
723	34.5	47.9	586	7	ADF70504	Adf70504 Orphan re	796	34	47.2	356	3	AAG47266	Aag47266 Arabidops
724	34.5	47.9	593	4	ABG17986	Abg17986 Novel hum	797	34	47.2	364	2	AAR39215	Aar39215 Mutant PD
725	34.5	47.9	632	4	ABG03498	Abg03498 Novel hum	798	34	47.2	365	2	AAR39214	Aar39214 Mutant PD
726	34.5	47.9	653	4	ABG04236	Abg04236 Novel hum	799	34	47.2	368	3	AAG47250	Aag47250 Arabidops
727	34.5	47.9	783	4	ABB58228	Abb58228 Drosophil	800	34	47.2	371	6	ABU01547	Abu01547 S. pneumo
728	34.5	47.9	783	8	ADS96518	Ads96518 Drosophil	801	34	47.2	371	8	ADK47300	Adk47300 Streptoco
729	34.5	47.9	833	4	ABG19903	Abg19903 Novel hum	802	34	47.2	374	2	AAR39221	Aar39221 Mutant PD
730	34.5	47.9	852	4	ABG23160	Abg23160 Novel hum	803	34	47.2	378	8	ADR96187	Adr96187 Novel S.
731	34.5	47.9	852	4	ABG14257	Abg14257 Novel hum	804	34	47.2	390	3	AAG50628	Aag50628 Arabidops
732	34.5	47.9	1062	4	ABG01394	Abg01394 Novel hum	805	34	47.2	390	3	AAG16855	Aag16855 Arabidops
733	34.5	47.9	1083	4	ABG07867	Abg07867 Novel hum	806	34	47.2	390	7	ADC17135	Adc17135 Human Adl
734	34.5	47.9	1083	4	ABG06607	Abg06607 Novel hum	807	34	47.2	391	3	AAG16854	Aag16854 Arabidops
735	34.5	47.9	1093	4	ABG15860	Abg15860 Novel hum	808	34	47.2	391	3	AAG50627	Aag50627 Arabidops
736	34.5	47.9	1293	4	ABG07498	Abg07498 Novel hum	809	34	47.2	391	6	ABU35437	Abu35437 Protein e
737	34.5	47.9	1955	8	ADD44356	Ad44356 Bacterial	810	34	47.2	395	2	AAR39218	Aar39218 Mutant PD
738	34	47.2	27	7	ADD15761	Add15761 Peptide 1	811	34	47.2	403	2	AAR39220	Aar39220 Mutant PD
739	34	47.2	34	4	AAU21290	Aau21290 Human nov	812	34	47.2	404	2	AAR39222	Aar39222 Mutant PD
740	34	47.2	72	7	ADH88357	Adh88357 Enterococ	813	34	47.2	405	2	AAR39213	Aar39213 Mutant PD
741	34	47.2	76	4	AGT07732	Ag70732 S cerevis	814	34	47.2	405	6	ABM67471	Abm67471 Photorhab
742	34	47.2	84	5	ABB75892	Abb75892 Human ATP	815	34	47.2	407	4	AAE02395	Aae02395 Soybean l
743	34	47.2	113	7	ADD69210	Ad69210 Human ant	816	34	47.2	410	2	AAR39212	Aar39212 E. coli p
744	34	47.2	119	7	ADD69209	Ad69209 Human ant	817	34	47.2	410	2	AAR50093	Aar50093 wild-type
745	34	47.2	123	6	AAU51127	Aau51127 Propionib	818	34	47.2	410	4	AAU34698	Aau34698 E. coli c
746	34	47.2	123	6	ABM47646	Abm47646 Propionib	819	34	47.2	411	2	AAR39219	Aar39219 Mutant PD
747	34	47.2	123	6	ABR63613	Ab63613 Human gly	820	34	47.2	412	2	AAR39217	Aar39217 Mutant PD
748	34	47.2	134	4	ABG11800	Abg11800 Novel hum	821	34	47.2	414	2	AAR39216	Aar39216 Mutant PD
749	34	47.2	151	6	ABR41492	Ab41492 Human DIT	822	34	47.2	414	6	ABM67234	Abm67234 Photorhab
750	34	47.2	154	2	AAW98259	Aaw98259 H. pylori	823	34	47.2	415	8	ADL04914	Adl04914 M. catarr
751	34	47.2	155	7	ADP58675	Adp58675 Human pol	824	34	47.2	416	7	ADF04735	Adf04735 Bacterial
752	34	47.2	156	8	ADN48052	Adn48052 Thermococ	825	34	47.2	421	2	AAW36010	Aaw36010 Polyamide
753	34	47.2	167	8	ADL06084	Adl06084 M. catarr	826	34	47.2	427	4	AAU38150	Aau38150 Salmonell
754	34	47.2	179	6	ABM65143	Abm65143 Propionib	827	34	47.2	427	7	ABO65505	Ab65505 Klebsiell
755	34	47.2	185	3	AAG29991	Aag29991 Arabidops	828	34	47.2	443	3	AAG50474	Aag50474 Arabidops

829	34	47.2	446	2	AAV04289	Streptococ	902	34	47.2	854	4	AAW42224	AAW42224 Soybean r
830	34	47.2	450	2	AAW29454	Streptococ	903	34	47.2	877	4	AAW42214	AAW42214 Soybean r
831	34	47.2	450	2	AAW68551	S. pneumo	904	34	47.2	877	4	AAW42223	AAW42223 Soybean r
832	34	47.2	450	4	AAU37805	Streptococ	905	34	47.2	877	4	AAW42231	AAW42231 Soybean r
833	34	47.2	450	4	AAU38040	Streptococ	906	34	47.2	877	4	AAW42227	AAW42227 Soybean r
834	34	47.2	450	6	ABU01072	S. pneumo	907	34	47.2	877	4	AAW42225	AAW42225 Soybean r
835	34	47.2	450	6	ABU01072	S. pneumo	907	34	47.2	877	4	AAW42221	AAW42221 Soybean r
836	34	47.2	450	7	ADD15557	Protein e	908	34	47.2	877	4	AAW42222	AAW42222 Soybean r
837	34	47.2	450	7	ADD15557	Streptococ	909	34	47.2	877	4	AAW42229	AAW42229 Soybean r
838	34	47.2	450	7	ADD15555	Streptococ	910	34	47.2	877	4	AAW42219	AAW42219 Soybean r
839	34	47.2	450	8	ADK46343	Streptococ	911	34	47.2	877	4	AAW42217	AAW42217 Soybean r
840	34	47.2	451	5	ABP30250	Streptococ	912	34	47.2	884	4	ABG22489	Novel hum
841	34	47.2	456	4	AAU35043	Enterococ	913	34	47.2	884	4	ABG30084	Novel hum
842	34	47.2	456	6	ABU14562	Protein e	914	34	47.2	919	6	ABU21774	Protein e
843	34	47.2	456	6	ADL46377	Protein e	915	34	47.2	1081	5	ABP27331	Streptococ
844	34	47.2	456	8	ADO07009	UDP-N-ace	916	34	47.2	1081	8	ADK99301	Streptococ
845	34	47.2	456	8	ADO07009	Activator	917	34	47.2	1164	2	AAW33113	Thermococ
846	34	47.2	457	4	AAU23562	Novel hum	918	34	47.2	1374	5	ABP26112	Streptococ
847	34	47.2	462	8	ADR95741	Novel S.	919	34	47.2	1535	5	ABP73813	Candida a
848	34	47.2	462	8	ADS21900	Bacterial	920	34	47.2	1615	4	AAU03536	Human pro
849	34	47.2	463	8	ADO07006	E faecali	921	34	47.2	1879	5	ADL16684	Human nov
850	34	47.2	466	5	ABP27384	Streptococ	922	34	47.2	1879	8	ADN42338	Human nov
851	34	47.2	474	6	ABU33574	Protein e	923	34	47.2	2652	5	ABG31321	Predicted
852	34	47.2	487	6	ABM69249	Phototrab	924	34	47.2	2652	8	ADL02250	Human OCP
853	34	47.2	487	8	ADR94568	Novel S.	925	34	47.2	2764	4	ABM66967	Drosophil
854	34	47.2	496	5	ABP65142	Hypoxia-r	926	34	47.2	2802	4	AAE05485	Drosophil
855	34	47.2	496	6	ABP96793	Human COP	927	34	47.2	2802	4	ABM63789	Drosophil
856	34	47.2	496	7	ADE55870	Human PRO	928	34	47.2	2802	5	ABB08077	Drosophil
857	34	47.2	496	7	ADD45246	Human PRO	929	34	47.2	2828	5	ADL17071	Human NOV
858	34	47.2	496	8	ADL82965	Human PRO	930	34	47.2	2845	5	ABP70049	Human NOV
859	34	47.2	496	8	ADL019284	Human PRO	931	34	47.2	2853	6	ABR40110	Human cel
860	34	47.2	496	8	ADO19282	Human PRO	932	33.5	46.5	137	4	AAU18143	Novel hum
861	34	47.2	496	8	ADO19282	Human PRO	933	33.5	46.5	137	4	AAU18098	Novel hum
862	34	47.2	496	8	ADQ76758	Human glu	934	33.5	46.5	137	4	AAU18697	Renal and
863	34	47.2	496	8	ADR14665	Human NF-	935	33.5	46.5	137	4	AAU18650	Renal and
864	34	47.2	496	8	ADP25408	PRO polyp	936	33.5	46.5	137	4	AAU21589	Novel hum
865	34	47.2	502	4	ABP96833	Putative	937	33.5	46.5	137	4	AAU21746	Novel hum
866	34	47.2	509	6	ABM71923	Staphyloc	938	33.5	46.5	137	4	AAW99966	Human exp
867	34	47.2	512	5	ABP25416	Streptococ	939	33.5	46.5	137	4	AAW99938	Human exp
868	34	47.2	543	4	ABAB48036	S. pneumo	940	33.5	46.5	137	4	AAW99965	Human exp
869	34	47.2	543	6	ABU01445	S. pneumo	941	33.5	46.5	137	4	AAW91804	Human hum
870	34	47.2	543	8	ADM92154	S. pneumo	942	33.5	46.5	137	4	AAW98975	Human hum
871	34	47.2	544	5	ABP74066	Candida a	943	33.5	46.5	137	4	ABM10183	Human CDN
872	34	47.2	547	8	ADK47203	Streptococ	944	33.5	46.5	137	4	ABM10420	Human CDN
873	34	47.2	578	2	AAW75085	Oxaliy-Co	945	33.5	46.5	137	4	AAW42390	Human pol
874	34	47.2	578	2	AAW22882	Human oxa	946	33.5	46.5	137	4	AAU87136	Novel cen
875	34	47.2	579	5	ABB48472	Listeria	947	33.5	46.5	137	4	AAU87136	Novel cen
876	34	47.2	587	3	AAV99819	Corn prot	948	33.5	46.5	137	4	AAU18418	Human end
877	34	47.2	587	8	ADH62812	Lactobaci	949	33.5	46.5	137	4	AAU18295	Human end
878	34	47.2	593	8	ADH62811	Lactobaci	950	33.5	46.5	137	4	ADG15142	Human 7 t
879	34	47.2	632	4	AG93218	C glutami	951	33.5	46.5	137	4	ADG15164	Human 7 t
880	34	47.2	632	4	AG93218	Human dia	952	33.5	46.5	137	5	ABJ05725	Novel hum
881	34	47.2	685	2	AAV25683	Cockroach	953	33.5	46.5	137	5	ABJ05770	Novel hum
882	34	47.2	685	7	ADC34931	Cockroach	954	33.5	46.5	137	5	ABP66770	Human pol
883	34	47.2	686	8	ADH22525	Human tra	955	33.5	46.5	137	5	ABP67007	Human pol
884	34	47.2	758	4	AAW84848	Human dia	956	33.5	46.5	137	6	ABU97312	Human pol
885	34	47.2	758	5	AAU03389	Altenaria	957	33.5	46.5	137	6	ABU97265	Human pol
886	34	47.2	763	5	ABG92715	Listeria	958	33.5	46.5	137	7	ADC46230	Human neo
887	34	47.2	764	6	ABM50119	Listeria	959	33.5	46.5	137	7	ADC46387	Human neo
888	34	47.2	764	6	AAW60568	Down-regu	960	33.5	46.5	137	8	ADI54768	Novel hum
889	34	47.2	764	6	ADL10955	Human CDN	961	33.5	46.5	137	8	ADI54451	Novel hum
890	34	47.2	792	8	ADG47981	Human col	962	33.5	46.5	236	6	ABU18169	Protein e
891	34	47.2	805	8	ADH34349	Novel Lac	963	33.5	46.5	319	6	ABU18118	Protein e
892	34	47.2	827	4	ADH34349	Bacterial	964	33.5	46.5	322	7	AAW72332	Human OR-
893	34	47.2	830	4	ABM60840	Drosophil	965	33.5	46.5	322	7	ABG67653	Klebsiell
894	34	47.2	854	4	ABM10122	Soy bean	966	33.5	46.5	343	2	AAW59907	Human HNH
895	34	47.2	854	4	AAW42220	Soybean r	967	33.5	46.5	343	6	AAO19904	Human TN4
896	34	47.2	854	4	AAW42228	Soybean r	968	33.5	46.5	343	6	ABP81702	Human G p
897	34	47.2	854	4	AAW42222	Soybean r	969	33.5	46.5	343	8	ADO29418	Human GFC
898	34	47.2	854	4	AAW42226	Soybean r	970	33.5	46.5	347	8	ADO29145	Mouse nov
899	34	47.2	854	4	AAW42230	Soybean r	971	33.5	46.5	455	4	ABG04587	Novel hum
900	34	47.2	854	4	AAW42218	Soybean r	972	33.5	46.5	497	4	ABM57922	Drosophil
901	34	47.2	854	4	AAW42232	Soybean r	973	33.5	46.5	815	7	ADB37640	Neural th
							974	33.5	46.5	876	7	ADB37596	Neural th

975 33.5 46.5 876 7 ADB37574
 976 33.5 46.5 893 7 ADB37638
 977 33.5 46.5 930 2 AAW55961
 978 33.5 46.5 930 6 ABB99469
 979 33.5 46.5 930 7 ADB37583
 980 33.5 46.5 930 7 ADB37619
 981 33.5 46.5 930 7 ADB37591
 982 33.5 46.5 930 7 ADB37631
 983 33 45.8 27 2 AAR81819
 984 33 45.8 45 4 AAM95235
 985 33 45.8 45 4 ABB95932
 986 33 45.8 61 4 AAU86767
 987 33 45.8 61 7 ADB60101
 988 33 45.8 67 4 AAM16772
 989 33 45.8 67 4 ABB35758
 990 33 45.8 67 4 AAM29259
 991 33 45.8 67 4 ABB21182
 992 33 45.8 67 4 ABB21182
 993 33 45.8 67 4 AAM68948
 994 33 45.8 67 4 AAM56566
 995 33 45.8 67 4 AAG50611
 996 33 45.8 67 4 AAM04489
 997 33 45.8 67 5 ABB38532
 998 33 45.8 68 5 ABB04063
 999 33 45.8 73 5 ABE20834
 1000 33 45.8 73 5 ABB64680

ALIGNMENTS

RESULT 1
 ASO8421
 ID ABO84421 standard; protein; 518 AA.
 XX ABO84421;
 AC ABO84421;
 DT 18-NOV-2004 (first entry)
 DE Human cancer-associated protein HP7-153.1.
 XX Human; cancer-associated protein; cytostatic; cancer; leukaemia;
 KW Lymphoma; CAP.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO2004074320-A2.
 FN WO2004074320-A2.
 XX 02-SEP-2004.
 PD 02-SEP-2004.
 XX 17-FEB-2004; 2004WO-US004730.
 PF 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX (SAGR-) SAGRES DISCOVERY INC.
 PA Morris DW, Morris DW, Malandro MS;
 PI WPI; 2004-652914/63.
 DR N-PSDB; ABB32567.
 DR N-PSDB; ABB32567.
 XX New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX claim 18; seqid 54; 310pp; English.
 PS The invention relates to an isolated nucleic acid comprising at least 10

CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 72; DB 8; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 124 VPFSVAKSVKSLYL 138

RESULT 2
 ADQ67207
 ID ADQ67207 standard; protein; 624 AA.
 XX ADQ67207;
 AC ADQ67207;
 DT 07-OCT-2004 (first entry)
 DE Novel human protein sequence #2180.
 XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX Homo sapiens.
 OS Homo sapiens.
 PN EPI440981-A2.
 PD 28-JUL-2004.
 XX 21-JAN-2004; 2004EP-00001196.
 PF 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX
DR WPI; 2004-535376/52.
DR N-PSDB; ADQ65019.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 4368; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.
XX
SQ Sequence 624 AA;
Query Match 100.0%; Score 72; DB 8; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 15
Db 230 VPFSVAKSVKSLYL 244
RESULT 3
AAR99414
ID AAR99414 standard; protein; 678 AA.
XX
AC AAR99414;
XX
DT 04-DEC-1996 (first entry)
XX
DE Human gas6 protein, an S protein homologue and axl receptor ligand.
XX
KW Axl receptor ligand; human protein S homologue; growth factor;
KW myeloid cell proliferation; myeloid malignancy; regulation; prevention;
KW recombinant production.
XX
OS Homo sapiens.
XX
PN US5538861-A.
XX
PD 23-JUL-1996.
XX
PF 29-JUL-1994; 94US-00282141.
XX
PR 29-JUL-1994; 94US-00282141.
XX
PA (AMGE/) AMGEN INC.
PA (SCHN/) SCHNEIDER C.
XX
PI Manfioletti G, Varnum BC, Schneider C, Avanzi G, Brancolini C;
XX
DR WPI; 1996-353825/35.
DR N-PSDB; AAT41544.
XX
PT DNA encoding gas6, the axl receptor ligand - useful to regulate growth of
PT myeloid cells and malignancies.
XX
PS Claim 1; Col 19-22; 36pp; English.
XX
CC AAR99414 is the gas6 protein (from the growth arrest specific gene number
CC 6). The gas6 protein has homology to human protein S which functions as a
CC cofactor in a protease cascade that regulates coagulation. Gas6
CC expression, as with gas1 and gas2, is associated with cell growth arrest
CC which suggests a possible role of gas6 in the regulation of cell growth.
CC In fact the gas6 protein is an axl receptor: (axlr) ligand and a growth

CC factor for any cells expressing axlr e.g. bone marrow, spleen, thymus,
CC ovary, heart, intestine and lung cells. The axl receptor is involved in
CC myeloid cell proliferation and myeloid malignancies, so gas6 may regulate
CC growth of such cells
XX
SQ Sequence 678 AA;
Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298
RESULT 4
AAW46463
ID AAW46463 standard; protein; 678 AA.
XX
AC AAW46463;
XX
DT 15-MAY-1998 (first entry)
XX
DE Human growth arrest specific-gene 6 (gas6) protein.
XX
KW Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
KW receptor tyrosine kinase; regulation; protease cascade; insulin;
KW growth regulation; serum-free culture medium; human; Schwann cell;
KW receptor activator; erbB receptor; heregulin; cAMP level; proliferation;
KW treatment; nervous system injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 49..89 /note= "A domain of gas6"
FT Domain 90..117 /note= "B domain of gas6 comprising a thrombin sensitive
FT loop"
FT Domain 118..278 /note= "C domain of gas6, contains 4 epidermal growth
FT factor-like repeats"
FT Domain 279..678 /note= "D domain of gas6, homologous to steroid binding
FT hormone"
FT Domain 314..471 /note= "G domain 1"
FT Domain 503..671 /note= "G domain 2"
XX
PN US5714385-A.
XX
PD 03-FEB-1998.
XX
PF 10-MAY-1995; 95US-00435434.
XX
PR 10-MAY-1995; 95US-00435434.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Mather JP, Li R;
XX
DR WPI; 1998-129864/12.
XX
PT Medium for culturing human Schwann cells - is serum-free and contains Rse
PT receptor activator and other mitogens.
XX
PS Disclosure; Fig 2; 51pp; English.
XX
CC The present sequence represents a human growth arrest specific-gene 6
CC (gas6) protein which is able to activate the Rsa and Axl receptor. Rse is
CC a receptor tyrosine kinase that is preferentially expressed in the adult

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; PRO; B cell related disorder; cancer;
 KW Immune-mediated inflammatory disease; human.
 XX Homo sapiens.
 OS WO2004024097-A2.
 XX 25-MAR-2004.
 XX 15-SEP-2003; 2003WO-US029097.
 XX 16-SEP-2002; 2002US-0411392P.
 XX (GETH) GENENTECH INC.
 PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
 PI Wu TD;
 PS WPI; 2004-329389/30.
 DR N-PSDB; ADL83230.
 XX New PRO polypeptide, useful for diagnosing and treating a B cell related
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
 PS Claim 10; Fig 433; 695pp; English.
 XX The present invention relates to PRO proteins and their coding sequences.
 CC The PRO proteins are useful for diagnosing and treating a B cell related
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
 CC antigen unresponsiveness, selective IgA deficiency, selective IGM
 CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
 CC hyper IGM, transient hypogammaglobulinemia of infancy, Burkitt's
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
 CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 CC coding sequences are useful as hybridization probes in chromosome and
 CC gene mapping, in preparing PRO proteins, or in generating transgenic
 CC animals or knockout animals, which in turn are useful in the development
 CC and screening of therapeutically useful reagents.
 XX Sequence 678 AA;
 SQ
 Query Match 100.0%; Score 72; DB 8; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 15
 DB 284 VPFSVAKSVKSLYL 298
 RESULT 8
 ADM40825
 ID ADM40825 standard; protein; 678 AA.
 XX ADM40825;
 XX 01-JUL-2004 (first entry)
 XX Human Gas6 protein SEQ ID NO:3.
 XX growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
 KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
 KW receptor internalisation; cell proliferation; cell apoptosis prevention;
 KW signaling molecule; cell marker; human.
 XX

OS Homo sapiens.
 XX WO2004029209-A2.
 XX 08-APR-2004.
 XX 24-SEP-2003; 2003WO-US030330.
 XX 24-SEP-2002; 2002US-0413157P.
 XX (CENZ) CENTOCOR INC.
 PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
 XX WPI; 2004-316097/29.
 XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
 PT manufacturing medicines or for identifying inhibitors of Gas6 and its
 PT receptors.
 XX Disclosure; SEQ ID NO 3; 28pp; English.
 XX The present invention describes an isolated growth arrest specific gene 6
 CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
 CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
 CC ID NO:2, ADM40824), or a polyhistidine sequence. The variant Gas6
 CC polypeptide has 75% identity to native human Gas6 protein. Also
 CC described: (1) a recombinant DNA molecule encoding the amino acid
 CC sequence of the polypeptide described above; (2) a vector comprising the
 CC above nucleic acid; (3) a host cell comprising the vector, where the host
 CC cell is of mammalian origin; and (4) a composition comprising the
 CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
 CC activity. The composition is useful for manufacturing medicines or for
 CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
 CC may also be used for Gas6-dependent receptor phosphorylation, receptor
 CC internalisation, cell proliferation, prevention of cell apoptosis, or
 CC induction of signaling molecules or cell markers. The present sequence
 CC represents the human Gas6 protein from the present invention.
 XX Sequence 678 AA;
 SQ
 Query Match 100.0%; Score 72; DB 8; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 15
 DB 284 VPFSVAKSVKSLYL 298
 RESULT 9
 ADM60275
 ID ADM60275 standard; protein; 678 AA.
 XX ADM60275;
 XX 18-NOV-2004 (first entry)
 XX Human growth arrest-specific 6 (GAS6) protein.
 XX angiogenesis modulator; tumorigenesis modulator; angiogenesis; Ax1;
 KW tubulin cofactor D; transglutaminase 2; cytosine deaminase;
 KW peptidase M41; paraplegin; CD13 aminopeptidase; PPK-1; zip kinase; Gas6;
 KW SRm160; non-muscle myosin heavy chain; calmodulin 2; symporter;
 KW semaphorin; zinc finger helicase; plexin-A2; deoxycytidylate deaminase;
 KW sugar transporter; tumorigenesis; antiangiogenic; cytostatic;
 KW cerebroprotective; vasotropic; antiinfertility; cardiant;
 KW antibody therapy; antisense therapy; RNA interference therapy;
 KW RNAi therapy; cancer; stroke; infertility; heart disease; human.
 XX Homo sapiens.
 OS WO2004039955-A2.
 XX

XX 13-MAY-2004.
 XX 29-OCT-2003; 2003WO-US034281.
 XX 29-OCT-2002; 2002US-0421989P.
 XX 17-OCT-2003; 2003US-0512251P.
 XX (RIGE-) RIGEL PHARM INC.
 XX Lorens JB, Atchison RE, Frieria A, Holland S;
 XX WPI; 2004-376181/35.
 XX N-PSDB; ADN60274.
 XX Identifying a compound that modulates angiogenesis or tumorigenesis,
 XX useful in diagnosing and treating angiogenesis, cancer, stroke,
 XX infertility and heart disease, comprises contacting the compound with
 XX angiogenesis polypeptide.
 XX Disclosure; Page 65; 105pp; English.
 XX The present invention describes a method for identifying a compound that
 XX modulates angiogenesis or tumorigenesis. The method comprises: (a)
 XX contacting the compound with angiogenesis polypeptide, e.g. Axi, tubulin
 XX cofactor D, transglutaminase 2, cytosine deaminase, peptidase M41
 XX (paraplegin), CD13 aminopeptidase, PPK-1, zip kinase, Gas6, SRm160, non-
 XX muscle myosin heavy chain, calmodulin 2, novel symporter, novel
 XX semaphorin, novel zinc finger helicase (FLJ22611), plexin-A2,
 XX deoxycytidylate deaminase or novel sugar transporter; (b) determining the
 XX functional effector of the compound upon the angiogenesis polypeptide or
 XX the physical effect of the compound upon the target polypeptide or its
 XX fragment or inactive variant; and (c) determining the chemical or
 XX phenotypic effect of the compound upon a cell comprising the target
 XX polypeptide or its fragment or inactive variant, thus identifying a
 XX compound that modulates cell cycle arrest. Also described is a method of
 XX modulating angiogenesis in a subject. The angiogenesis or tumorigenesis
 XX modulating compound has antiangiogenic, cytostatic, cerebroprotective,
 XX vasotrophic, antiinfertility and cardiac activities, and can be used in
 XX antibody, antisense and RNA interference (RNAi) therapies. The method is
 XX useful in identifying a compound that modulates angiogenesis. The methods
 XX and compounds or compositions are useful in diagnosing and treating
 XX angiogenesis, cancer, stroke, infertility and heart disease. The present
 XX sequence represents a human growth arrest-specific 6 (GAS6) protein,
 XX which is used in the exemplification of the present invention.
 XX Sequence 678 AA;
 XX
 XX Query Match 100.0%; Score 72; DB 8; Length 678;
 XX Best Local Similarity 100.0%; Pred. No. 0.00032;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 VPFSVAKSVKSLYLIG 15
 XX 284 VPFSVAKSVKSLYLIG 298
 XX
 XX RESULT 10
 XX ADD48757
 XX ID ADD48757 standard; protein; 678 AA.
 XX AC ADD48757;
 XX AC ADD48757;
 XX DT 02-DEC-2004 (revised)
 XX DT 29-JAN-2004 (first entry)
 XX DT Human Protein L13720, SEQ ID NO 14467.
 XX DE Human; pain; neuronal tissue; gene therapy;
 XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
 XX KW spared nerve injury; SNI; Chung.
 XX OS Homo sapiens.

OS Unidentified.
 XX WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; L13720.
 XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX Example 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 XX human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell
 XX comprising the vector, a method for identifying a nucleotide sequence
 XX which is differentially regulated in an animal subjected to pain and a
 XX kit to perform the method, an array, a method for identifying an agent
 XX that increases or decreases the expression of the polynucleotide sequence
 XX that is differentially expressed in neuronal tissue of a first animal
 XX subjected to pain, a method for identifying a compound which regulates
 XX the expression of a polynucleotide sequence which is differentially
 XX expressed in an animal subjected to pain, a method for identifying a
 XX compound that regulates the activity of one or more of the
 XX polynucleotides, a method for producing a pharmaceutical composition, a
 XX method for identifying a compound or small molecule that regulates the
 XX activity in an animal of one or more of the polypeptides given in the
 XX specification, a method for identifying a compound useful in treating
 XX pain and a pharmaceutical composition comprising the one or more
 XX polypeptides or their antibodies. The polynucleotide or the compound that
 XX modulates its activity is useful for preparing a medicament for treating
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 XX therapy). The sequence presented is a human protein (described in Table 3
 XX of the specification) which is differentially expressed during pain.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic form directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 679 AA;
 XX
 XX Query Match 100.0%; Score 72; DB 7; Length 679;
 XX Best Local Similarity 100.0%; Pred. No. 0.00032;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 VPFSVAKSVKSLYLIG 15
 XX 284 VPFSVAKSVKSLYLIG 298
 XX
 XX RESULT 11
 XX ADM40823
 XX ID ADM40823 standard; protein; 686 AA.
 XX AC ADM40823;
 XX AC ADM40823;
 XX DT 01-JUL-2004 (first entry)
 XX DE Human Gas6 protein with a C-terminal epitope tag SEQ ID NO:1.

XX growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
 KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
 KW receptor internalisation; cell proliferation; cell apoptosis prevention;
 KW signaling molecule; cell marker; human.
 OS Homo sapiens.
 XX WO2004029209-A2.
 XX 08-APR-2004.
 XX 24-SEP-2003; 2003WO-US030330.
 XX 24-SEP-2002; 2002US-0413157P.
 XX (CENZ) CENTOCOR INC.
 XX Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
 XX WPI; 2004-316097/29.
 XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
 PT manufacturing medicines or for identifying inhibitors of Gas6 and its
 PT receptors.
 XX Claim 2; SEQ ID NO 1; 28pp; English.
 XX The present invention describes an isolated growth arrest specific gene 6
 CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
 CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
 CC ID NO:2, AWM40824), or a polyhistidine sequence. The variant Gas6
 CC polypeptide has 75% identity to native human Gas6 protein. Also
 CC described: (1) a recombinant DNA molecule encoding the amino acid
 CC sequence of the polypeptide described above; (2) a vector comprising the
 CC above nucleic acid; (3) a host cell comprising the vector, where the host
 CC cell is of mammalian origin; and (4) a composition comprising the
 CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
 CC activity. The composition is useful for manufacturing medicines or for
 CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
 CC may also be used for Gas6-dependent receptor phosphorylation, receptor
 CC internalisation, cell proliferation, prevention of cell apoptosis, or
 CC induction of signaling molecules or cell markers. The present sequence
 CC represents the human Gas6 protein with an epitope tag fused at the C-
 CC terminus, from the present invention.
 XX Sequence 686 AA;
 SQ
 Query Match 100.0%; Score 72; DB 8; Length 686;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYLK 15
 DB 284 VPFSVAKSVKSLYLK 298
 |||||
 RESULT 12
 AA46462
 ID AA46462 standard; protein; 673 AA.
 XX AA46462;
 AC
 XX 15-MAY-1998 (first entry)
 DT
 XX Murine growth arrest specific-gene 6 (gas6) protein.
 DE
 XX Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
 KW receptor tyrosine kinase; regulation; protease cascade; insulin;
 KW growth regulation; serum-free culture medium; human; Schwann cell;
 KW receptor activator; erbB receptor; heregulin; cAMP level; proliferation;
 KW treatment; nervous system injury.

OS Mus sp.
 XX US5714385-A.
 XX 03-FEB-1998.
 PD
 XX 10-MAY-1995; 95US-00435434.
 PF
 XX 10-MAY-1995; 95US-00435434.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Chen J, Mather JP, Li R;
 PI
 XX WPI; 1998-129864/12.
 DR
 XX Medium for culturing human Schwann cells - is serum-free and contains Rse
 XX receptor activator and other mitogens.
 PT
 XX Disclosure; Fig 2; 51pp; English.
 PS
 XX The present sequence represents a murine growth arrest specific-gene 6
 CC (gas6) protein which is able to activate the Rse and Axl receptor. Rse is
 CC a receptor tyrosine kinase that is preferentially expressed in the adult
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise cAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries
 XX Sequence 673 AA;
 SQ
 Query Match 95.8%; Score 69; DB 2; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYLK 15
 DB 281 VPFSVAKSVKSLYLK 295
 |||||
 RESULT 13
 AA429793
 ID AA429793 standard; protein; 673 AA.
 XX AA429793;
 AC
 XX 15-NOV-1999 (first entry)
 DT
 XX Murine growth arrest-specific gene 6 protein.
 DE
 XX Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; Gas6;
 KW growth arrest-specific gene 6; proliferation; differentiation;
 KW glial cell; Schwann cell; fusion protein.
 XX
 OS Mus sp.
 XX US5955420-A.
 PN
 XX 21-SEP-1999.
 PD
 XX 10-MAY-1995; 95US-00438864.
 PF
 XX 10-MAR-1995; 95US-00402253.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX

PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
 XX WPI; 1999-539585/45.
 XX
 XX Activation of the Rse receptor on a cell, useful for promoting cell
 PT proliferation and differentiation.
 XX
 XX Disclosure; Fig 2; 48pp; English.
 XX
 XX A method has been developed for activating the Rse receptor on a cell.
 CC The method comprises exposing the receptor to the exogenous growth arrest
 CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
 CC cell proliferation and cell differentiation. The present sequence
 CC represents murine gas6 given in the present invention
 XX
 XX Sequence 673 AA;
 SQ

Query Match 95.8%; Score 69; DB 2; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
 Db 281 VPFSMAKSVKSLYLIG 295
 ||||:|||||||

RESULT 14
 AAB33459
 ID AAB33459 standard; protein; 673 AA.
 XX
 XX AAB33459;
 AC
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO21 protein UNQ21 SEQ ID NO:231.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; anti rheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antianemic; hepatotropic; virucide; antiporiatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200053758-A2.
 FN
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US005841.
 XX
 XX 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99WO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US000356.
 PR 18-FEB-2000; 2000WO-US0004341.
 PR 18-FEB-2000; 2000WO-US0004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff JC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 XX WPI; 2000-572271/53.
 DR N-PSDB; AAC58624.
 DR
 XX

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 Claim 33; Fig 92; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Sequence 673 AA;

Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
 Db 281 VPFSMAKSVKSLYLIG 295
 ||||:|||||||

RESULT 15

AAY57382
 ID AAY57382 standard; protein; 673 AA.
 AC AAY57382;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of murine gas6 (m gas6) protein.
 XX
 KW Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
 KW central nervous system; peripheral nervous system; injury; trauma;
 KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 KW protein S.
 XX
 OS Mus sp.
 XX
 PN US6033660-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 10-MAY-1995; 95US-00438862.
 XX
 PR 10-MAY-1995; 95US-00438862.
 XX
 PA (GETH) GENENTECH INC.
 XX
 FI Mather JP, Chen J, Li R;
 XX
 DR WPI; 2000-246046/21.
 XX
 PT Repairing nervous system injuries in mammals, by administering human
 PT Schwann cells that have been propagated in medium supplemented with
 PT mitogens.
 XX
 PS Disclosure; Fig 2; 52pp; English.
 XX
 CC The invention relates to a method for treating nervous system injuries in
 CC mammals by administering human Schwann cells (SC) that have been cultured
 CC in serum-free medium. The serum-free medium is a nutrient solution
 CC supplemented with two mitogens, one of which, is a Res/Axl receptor
 CC activator, to increase survival and proliferation of SC. The method is
 CC used to treat (or prevent) central or peripheral nervous system injury,
 CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
 CC or lesions associated with nutritional deficiencies, systemic disease,
 CC toxins or demyelination. Culturing cells in the specified medium allows
 CC proliferation of adult SC for use in autologous transplants. The present
 CC sequence represents a murine gas6 (m gas6) protein, having 43% sequence
 CC identity to human protein S. Gas6 is demonstrated to be a potent growth/
 CC survival factor for SCs in defined serum-free culture
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 VPFSVAKSVKSLYL 15
 Db 281 VPFSVAKSVKSLYL 295
 RESULT 16
 ABB84840
 ID ABB84840 standard; protein; 673 AA.
 XX
 AC ABB84840;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO21 protein sequence SEQ ID NO:48.
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006656.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88095.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides;
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 48; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL8259 to ABL8267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 673 AA;

Query Match 95.8%; Score 69; DB 5; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
 Db 281 VPFSMAKSVKSLYLIG 295
 ||||:|||||||

RESULT 17
 ABB95446
 ID ABB95446 standard; protein; 673 AA.

XX AC ABB95446;
 XX DT 19-JUL-2002 (first entry)
 XX DE Human angiogenesis related protein PRO21 SEQ ID NO: 48.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytostatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.

XX OS Homo sapiens.
 XX WO200208284-A2.
 XX PD 31-JAN-2002.

XX PF 09-JUL-2001; 2001WO-US021735.
 XX PR 20-JUL-2000; 2000US-0219556P.
 XX PR 25-JUL-2000; 2000US-0220624P.
 XX PR 25-JUL-2000; 2000US-0220664P.
 XX PR 28-JUL-2000; 2000WO-US020710.
 XX PR 02-AUG-2000; 2000US-0222699P.
 XX PR 17-AUG-2000; 2000US-00643657.
 XX PR 23-AUG-2000; 2000WO-US023522.
 XX PR 24-AUG-2000; 2000WO-US023328.
 XX PR 07-SEP-2000; 2000US-0230978P.
 XX PR 18-SEP-2000; 2000US-00684610.
 XX PR 18-SEP-2000; 2000US-00665350.
 XX PR 24-OCT-2000; 2000US-0242922P.
 XX PR 08-NOV-2000; 2000US-00709238.
 XX PR 08-NOV-2000; 2000WO-US030952.
 XX PR 10-NOV-2000; 2000WO-US030873.
 XX PR 01-DEC-2000; 2000WO-US032678.
 XX PR 20-DEC-2000; 2000US-00747259.
 XX PR 20-DEC-2000; 2000WO-US034956.
 XX PR 22-JAN-2001; 2001US-00767609.
 XX PR 28-FEB-2001; 2001US-00796498.
 XX PR 28-FEB-2001; 2001WO-US006520.
 XX PR 01-MAR-2001; 2001WO-US006666.
 XX PR 09-MAR-2001; 2001US-00802706.
 XX PR 14-MAR-2001; 2001US-00808689.
 XX PR 22-MAR-2001; 2001US-00816748.
 XX PR 05-APR-2001; 2001US-00828366.
 XX PR 10-MAY-2001; 2001US-00854208.
 XX PR 10-MAY-2001; 2001US-00854280.
 XX PR 25-MAY-2001; 2001US-00866028.
 XX PR 25-MAY-2001; 2001US-00866034.
 XX PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI: 2002-171999/22.
 DR N-PSDB; ABL95584.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 48; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention

XX Sequence 673 AA;

Query Match 95.8%; Score 69; DB 5; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
 Db 281 VPFSMAKSVKSLYLIG 295
 ||||:|||||||

RESULT 18
 ADD10337
 ID ADD10337 standard; protein; 673 AA.

XX AC ADD10337;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human secreted/transmembrane PRO polypeptide #24.

XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.

XX OS Homo sapiens.

PN US2003105011-A1.
 XX
 PD
 XX
 XX
 XX 05-JUN-2003.
 XX
 XX 16-AUG-2002; 2002US-00223084.
 XX
 XX 15-SEP-2000; 2000US-0232887P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2003-810831/76.
 DR N-PSDB; ADD10336.
 DR
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 PT
 XX Claim 11; SEQ ID NO 48; 493pp; English.
 PS
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 7; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYLGL 15
 Db 281 VPFSMAKSVKSLYLGL 295
 ||||:|||||
 ||||:|||||
 RESULT 19
 ADD11297
 ID ADD11297 standard; protein; 673 AA.
 XX
 XX ADD11297;
 XX
 XX 01-JAN-2004 (first entry)
 DT
 XX Human secreted/transmembrane PRO polypeptide #24.
 DE
 XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 XX US2003105013-A1.
 PN

XX 05-JUN-2003.
 PD
 XX
 XX 16-AUG-2002; 2002US-00223090.
 XX
 XX 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2003-801242/75.
 DR N-PSDB; ADD11296.
 DR
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, useful for treating a cardiovascular, endothelial, or
 PT angiogenic disorder in a mammal, such as cancer or age-related macular
 PT degeneration.
 PT
 XX Claim 11; SEQ ID NO 48; 493pp; English.
 PS
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 7; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYLGL 15
 Db 281 VPFSMAKSVKSLYLGL 295
 ||||:|||||
 ||||:|||||
 RESULT 20
 ADD37090
 ID ADD37090 standard; protein; 673 AA.
 XX
 XX ADD37090;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Human secreted/transmembrane PRO polypeptide #24.
 DE
 XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 XX US2003105012-A1.
 PN

PD 05-JUN-2003.
XX 16-AUG-2002; 2002US-00223088.
XX
XX 15-SEP-2000; 2000US-0232887P.
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
XX (GETH) GENENTECH INC.
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2003-829354/77.
DR N-PSDB; ADD37089.
XX
XX New isolated nucleic acids encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
XX Claim 11; SEQ ID NO 48; 492pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;
Query Match 95.8%; Score 69; DB 7; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295
RESULT 21
ADE41298
ID ADE41298 standard; protein; 673 AA.
XX
XX ADE41298;
AC
XX 29-JAN-2004 (first entry)
DT
XX Human secreted/transmembrane PRO polypeptide #24.
DE
XX human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
XX US2003100497-A1.
PN
XX 29-MAY-2003.
PD

XX 16-AUG-2002; 2002US-00223085.
XX
XX 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2004-008957/01.
DR N-PSDB; ADE41297.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or
PT PRO214, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and for treating disorders involving
PT angiogenesis.
XX
XX Claim 11; SEQ ID NO 48; 492pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;
Query Match 95.8%; Score 69; DB 8; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295
RESULT 22
ADH43481
ID ADH43481 standard; protein; 673 AA.
XX
XX ADH43481;
AC
XX 25-MAR-2004 (first entry)
DT
XX Human PRO polypeptide #24.
DE
XX Human; PRO; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
KW cell apoptosis; cell tube formation; angiogenesis;
KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
KW age-related macular degeneration; cytostatic; cardiac;
KW cerebroprotective; ophthalmological; vulnary.
XX
OS Homo sapiens.
XX
XX US2003224984-A1.
PN
XX 04-DEC-2003.
PD

XX 26-NOV-2002; 2002US-00305654.
 XX 20-JUN-2001; 2001WO-US019692.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NP;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Ye W;
 PI Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2004-042166/04.
 DR N-PSDB; ADH43480.
 XX
 XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 PT for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
 PT or age-related macular degeneration.
 XX
 XX Claim 11; SEQ ID NO 48; 492pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the PRO
 CC polynucleotides encoding them. The invention also relates to treating
 CC cardiovascular, endothelial or angiogenic disorders in mammals,
 CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
 CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
 CC stimulating angiogenesis or smooth muscle cell growth by administering
 CC polypeptides of the invention. The PRO polypeptides and polynucleotides
 CC are useful for treating cardiovascular, endothelial or angiogenic
 CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
 CC cancer or age-related macular degeneration. The PRO polynucleotides are
 CC useful as hybridisation probes in chromosome and gene mapping and in
 CC generating antisense RNA and DNA, and for chromosome identification and
 CC tissue typing. The PRO polypeptides and polynucleotides are also useful
 CC in gene therapy and as molecular weight markers for protein
 CC electrophoresis purposes. This sequence represents a human PRO
 CC polypeptide of the invention.
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 8; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSAKSVKSLYL 15
 Db 281 VPFSAKSVKSLYL 295
 RESULT 23
 ID ADK82826
 ADK82826 standard; protein; 673 AA..
 XX
 AC ADK82826;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PRO polypeptide #24.
 XX
 KW Human; PRO; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
 KW cell apoptosis; cell tube formation; angiogenesis;
 KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
 KW age-related macular degeneration; cytostatic; cardiant;
 KW cerebroprotective; ophthalmological; vulnary.
 XX
 OS Homo sapiens.
 XX
 XX US2004043927-A1.
 XX
 XX 04-MAR-2004.
 PD
 XX 20-FEB-2002; 2002US-00081056.
 XX
 XX

PR 19-SEP-1997; 97US-00333821.
 PR 29-JAN-1998; 98US-00015089.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 19-NOV-1998; 98US-00180997.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-00218517.
 PR 05-JAN-1999; 99WO-US000106.
 PR 12-FEB-1999; 99US-00214186.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 09-MAR-1999; 99US-00254460.
 PR 12-MAR-1999; 99US-00267213.
 PR 02-APR-1999; 99WO-US0284291.
 PR 12-JUN-1999; 99WO-US012252.
 PR 14-JUN-1999; 99US-00332928.
 PR 14-JUN-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 15-OCT-1999; 99US-00403154.
 PR 18-OCT-1999; 99US-00403296.
 PR 18-OCT-1999; 99US-00403297.
 PR 10-NOV-1999; 99US-00423741.
 PR 12-NOV-1999; 99US-00423843.
 PR 29-NOV-1999; 99US-00423844.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 05-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001US-00796498.
 PR

PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00828366.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918595.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 04-SEP-2001; 2001US-00946374.
 PR 07-SEP-2001; 2001US-00948901.
 PR 15-NOV-2001; 2001US-00002796.
 PR 30-NOV-2001; 2001US-00001054.
 PR 06-DEC-2001; 2001US-00006867.
 PR 19-DEC-2001; 2001US-00028072.
 PR 15-JAN-2002; 2002US-00052586.
 PR 17-JAN-2002; 2002US-00053107.
 PR 18-JAN-2002; 2002US-00052594.
 PR 08-FEB-2002; 2002US-00072068.
 PR 09-APR-2002; 2002US-00119480.
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski FU, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2004-225727/21.
 DR N-PSDB; ABD82825.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 11; SEQ ID NO 48; 494pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the PRO
 CC polynucleotides encoding them. The invention also relates to treating
 CC cardiovascular, endothelial or angiogenic disorders in mammals,
 CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
 CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
 CC stimulating angiogenesis or smooth muscle cell growth by administering
 CC polypeptides of the invention. The PRO polypeptides and polynucleotides
 CC are useful for treating cardiovascular, endothelial or angiogenic
 CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
 CC cancer or age-related macular degeneration. The PRO polynucleotides are
 CC useful as hybridisation probes in chromosome and gene mapping and in
 CC generating antisense RNA and DNA, and for chromosome identification and
 CC tissue typing. The PRO polypeptides and polynucleotides are also useful
 CC in gene therapy and as molecular weight markers for protein
 CC electrophoresis purposes. This sequence represents a human PRO
 CC polypeptide of the invention. Note: The sequence data for this patent is
 CC also available in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 673 AA;

Query Match 95.8%; Score 69; DB 8; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
 Db 281 VPFSVAKSVKSLYL 295
 AC ABO84420;
 XX
 DT 18-NOV-2004 (first entry)
 DE Mouse cancer-associated protein MP7-153.1.
 XX
 KW Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;
 XX lymphoma; CAP.
 OS Mus musculus.
 XX
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388938.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 FI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD32565.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS disclosure; seqid 51; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and

CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 703 AA;

Query Match 95.8%; Score 69; DB 8; Length 703;
Best Local Similarity 93.3%; Pred. NO. 0.0012;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 314 VPFSMAKSVKSLYL 328
||||:|||||

RESULT 25
ADC94783
ID ADC94783 standard; protein; 77 AA.
XX AC ADC94783;
XX DT 01-JAN-2004 (first entry)
XX DE E. faecium protein sequence SEQ ID 4410.
XX KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX OS Enterococcus faecium.
XX PN US6583275-B1.
XX PD 24-JUN-2003.
XX PF 30-JUN-1998; 98US-00107532.
XX PR 02-JUL-1997; 97US-0051571P.
XX PR 14-MAY-1998; 98US-0085598P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Doucette-Stamm LA, Bush D;
XX WPI; 2003-799836/75.
XX DR N-PSDB; ADC91129.
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX Example 1; SEQ ID NO 4410; 243pp; English.

CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids are useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.

XX SQ Sequence 77 AA;

Query Match 61.1%; Score 44; DB 7; Length 77;
Best Local Similarity 57.1%; Pred. No. 4;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 44 IPISIAKKEVILYL 57
:|:|:|:|:|

RESULT 26
AAU03812
ID AAU03812 standard; protein; 374 AA.
XX AC AAU03812;
XX DT 12-SEP-2001 (first entry)
XX DE G protein-coupled receptor-like (GPCR-like) receptor protein #11.
XX KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW fruitfly.
XX OS Homo sapiens.
XX PN WO200138533-A2.
XX PD 31-MAY-2001.
XX PF 24-NOV-2000; 2000WO-US032225.
XX PR 24-NOV-1999; 99US-0167523P.
XX PA (PHAA) PHARMACIA & UPJOHN.
XX PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX WPI; 2001-343952/36.
XX DR N-PSDB; AAS07211.
XX Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX Claim 6; Page 121-122; 219pp; English.
XX The sequence represents a G protein-coupled receptor-like (GPCR-like)
CC receptor protein. GPCR-like receptors and their associated nucleic acids
CC may be used to identify candidate compounds for their ability to modulate
CC the activity of GPCRs. The sequences therefore are useful for treating
CC and preventing infection by endoparasitic and ectoparasitic invertebrate
CC parasites, especially helminths and insects, and particularly ailments
CC related to aberrant neurological and neuromuscular function

XX SQ Sequence 374 AA;

Query Match 61.1%; Score 44; DB 4; Length 374;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 13
Db 142 LPFAIAASVNSLY 154
:|:|:|:|:|

RESULT 27
ADN23180
ID ADN23180 standard; protein; 374 AA.
XX

XX 17-JUN-2004 (first entry)
XX S. cerevisiae histidine kinase Slnp protein.
XX Histidine kinase; fungal infection; antifungal drug; yeast; Slnp.
XX Saccharomyces cerevisiae.
XX Key Location/Qualifiers
XX Region 556..703
XX /note="H-box"
XX Binding-site 859..920
XX /note="ATP-binding domain"
XX Region 1081..1207
XX /note="D-box"
XX US6716625-B1.
XX 06-APR-2004.
XX 09-AUG-2000; 2000US-00636728.
XX 16-APR-1997; 97US-00843530.
XX 22-JUN-1999; 99US-0038156.
XX (SELI/) SELITRENNIKOFF C.
XX (POTT/) POTT G.
XX Selitrennikoff C, Pott G;
XX WPI; 2004-303092/28.
XX New fungal histidine kinase polypeptides and nucleic acids, e.g. FOS-1 or
XX COS-1, useful for eradicating, mitigating or preventing fungal
XX infections, and in identifying antifungal drugs.
XX Example 10; SEQ ID NO 32; 124pp; English.
XX The invention relates to histidine kinases of Aspergillus and other
XX fungal species and their corresponding nucleic acid sequences. The
XX histidine kinase polypeptides and nucleic acids are useful for
XX eradicating, mitigating or preventing fungal infections and in
XX identifying antifungal drugs. The present sequence is Saccharomyces
XX cerevisiae histidine kinase Slnp protein. This sequence is used in the
XX exemplification of the invention.
XX Sequence 1220 AA;
SQ Query Match 58.3%; Score 42; DB 8; Length 1220;
Best Local Similarity 81.8%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKS 11
DB 955 VKFSVAKSIKS 965
RESULT 30
ADS43652
ID ADS43652 standard; protein; 1220 AA.
XX AC
XX ADS43652;
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #22082.
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAO/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 22082; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 1220 AA;
SQ Query Match 58.3%; Score 42; DB 8; Length 1220;
Best Local Similarity 81.8%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKS 11
DB 955 VKFSVAKSIKS 965
RESULT 31
ABB66417
ID ABB66417 standard; protein; 4345 AA.
XX AC
XX ABB66417;
XX 26-MAR-2002 (first entry)
XX

DE Drosophila melanogaster polypeptide SEQ ID NO 26043.
XX
KW Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL10520.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.

XX Disclosure; SEQ ID NO 26043; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 4345 AA;

Query Match 58.3%; Score 42; DB 4; Length 4345;
Best Local Similarity 63.6%; Pred. No. 8.4e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSL 12

Db 2115 PFAVAKNIKSI 2125

RESULT 32

ABM67414
ID ABM67414 standard; protein; 364 AA.

XX ABM67414;

DT 20-NOV-2003 (first entry)

XX Photorhabdus luminescens protein sequence #511.

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.

XX Photorhabdus luminescens.

OS WO200294867-A2.

XX 28-NOV-2002.

XX 07-FEB-2002; 2002WO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

PR (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 511; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins

XX Sequence 364 AA;

Query Match 56.9%; Score 41; DB 6; Length 364;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14

Db 78 VPTRVASAIKIYIL 91

RESULT 33

ADO05107
ID ADO05107 standard; protein; 527 AA.

XX ADO05107;

DT 12-AUG-2004 (first entry)

XX Rift valley fever virus (RVFV) GN surface envelope glycoprotein SeqID 5.
XX virus-like particle; VLP; viral core protein; VCP;
KW viral surface envelope glycoprotein; immunogenic; virucidal; vaccine;
KW infection; HIV; Ebola virus.

OS Rift Valley fever virus.

XX WO2004042001-A2.

XX 21-MAY-2004.

XX 19-MAY-2003; 2003WO-US015930.

XX 17-MAY-2002; 2002US-0381557P.

PR 11-MAR-2003; 2003US-0454115P.

PR 11-MAR-2003; 2003US-0454139P.
 PR 14-MAR-2003; 2003US-0454584P.
 PR 16-MAY-2003; 2003US-0381557P.
 XX
 XX
 PA (UYEM-) UNIV EMORY.

XX Compans RW, Yang C, Yao Q, Kang S;
 XX
 XX
 DR WPI; 2004-400659/37.

XX New virus-like particles for enhancing immune responses or for treating

PT or preventing viral infections (e.g. HIV), comprises a viral core
 PT protein, a viral surface envelope glycoprotein and, optionally, an
 PT adjuvant molecule.

XX Disclosure; SEQ ID NO 5; 74pp; English.

XX This invention relates to novel virus-like particles (VLPs).
 CC Specifically, it refers to VLPs that comprise a viral core protein (VCP)
 CC that can self-assemble into a VLP core, at least one viral surface
 CC envelope glycoprotein expressed on the surface of the VLP, (where the
 CC viral protein and the viral surface envelope glycoprotein are from
 CC different viruses) and optionally at least one adjuvant molecule
 CC expressed on the surface of the VLP. The present invention describes the
 CC development of immunogenic compositions comprising the VLP and a
 CC pharmaceutical carrier in order to generate an immunological response in
 CC the host or treat an appropriate condition. Accordingly, the methods and
 CC virucidal compositions thereof are useful for enhancing an immune
 CC response (e.g. antibody production, cytotoxic T-cell activity or cytokine
 CC activity) and for developing vaccines to treat and/or prevent viral
 CC infections such as those caused by HIV or Ebola virus. This polypeptide
 CC sequence is a Rift valley fever virus surface envelope glycoprotein of
 CC the invention.

XX Sequence 527 AA;

Query Match 56.9%; Score 41; DB 8; Length 527;
 Best Local Similarity 57.1%; Pred. No. 1.2e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
 |||:|:|:|:|:
 DB 190 VPFAVFKNSKKVYL 203

RESULT 34

ADO05104
 ID ADO05104 standard; protein; 1067 AA.

XX AC ADO05104;

XX DT 12-AUG-2004 (first entry)

DE Rift valley fever virus (RVFV) surface envelope glycoprotein SeqID 2.

XX virus-like particle; VLP; viral core protein; VCP;

KW viral surface envelope glycoprotein; immunogenic; virucidal; vaccine;

KW infection; HIV; Ebola virus.

XX Rift valley fever virus.

XX WO2004042001-A2.

XX PD 21-MAY-2004.

XX PF 19-MAY-2003; 2003WO-US015930.

XX PR 17-MAY-2002; 2002US-0381557P.

PR 11-MAR-2003; 2003US-0454115P.

PR 11-MAR-2003; 2003US-0454139P.

PR 14-MAR-2003; 2003US-0454584P.

PR 16-MAY-2003; 2003US-0381557P.

XX

PA (UYEM-) UNIV EMORY.

XX Compans RW, Yang C, Yao Q, Kang S;

XX WPI; 2004-400659/37.

XX New virus-like particles for enhancing immune responses or for treating
 or preventing viral infections (e.g. HIV), comprises a viral core
 PT protein, a viral surface envelope glycoprotein and, optionally, an
 PT adjuvant molecule.

XX Disclosure; SEQ ID NO 2; 74pp; English.

XX This invention relates to novel virus-like particles (VLPs).
 CC Specifically, it refers to VLPs that comprise a viral core protein (VCP)
 CC that can self-assemble into a VLP core, at least one viral surface
 CC envelope glycoprotein expressed on the surface of the VLP, (where the
 CC viral protein and the viral surface envelope glycoprotein are from
 CC different viruses) and optionally at least one adjuvant molecule
 CC expressed on the surface of the VLP. The present invention describes the
 CC development of immunogenic compositions comprising the VLP and a
 CC pharmaceutical carrier in order to generate an immunological response in
 CC the host or treat an appropriate condition. Accordingly, the methods and
 CC virucidal compositions thereof are useful for enhancing an immune
 CC response (e.g. antibody production, cytotoxic T-cell activity or cytokine
 CC activity) and for developing vaccines to treat and/or prevent viral
 CC infections such as those caused by HIV or Ebola virus. This polypeptide
 CC sequence is a Rift valley fever virus surface envelope glycoprotein of
 CC the invention.

XX Sequence 1067 AA;

Query Match 56.9%; Score 41; DB 8; Length 1067;
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14

DB 213 VPFAVFKNSKKVYL 226
 |||:|:|:|:|:

RESULT 35

ADS43524
 ID ADS43524 standard; protein; 1173 AA.

XX AC ADS43524;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #21954.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

ADP98825 in a pharmaceutical carrier; an antibody preparation which binds the polypeptide; methods for evaluating a compound against a target gene product encoded by any of ADP98516-ADP98825; identifying an antimycotic compound; a computer or a computer readable medium that comprises at least one of the nucleotide sequences mentioned in the specification or at least one amino acid sequence selected from ADP9826-ADP99135; a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicide activity. The compositions may be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated with Candida albicans. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This sequence represents the protein of a Candida albicans fungal specific gene of the invention. NOTE: This sequence was downloaded from an electronic sequence listing provided on the WIPO website.

XX SQ Sequence 1235 AA;

Query Match 56.9%; Score 41; DB 8; Length 1235;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSLYL 14
Db 52 PFNVDSLQTIYL 64
|||:||||:|

RESULT 39
AAR62504
ID AAR62504 standard; protein; 3457 AA.

XX AC AAR62504;

DT 25-MAR-2003 (revised)
DT 18-MAY-1995 (first entry)

XX DE Large polyprotein sequence of Maize Chlorotic Dwarf Virus.

KW MCDV; maize chlorotic dwarf virus; coat protein; plasmid vector;
KW plant resistance; viral infection resistance; maize plant;
KW maize dwarf mosaic virus; MDMV.

XX OS Maize chlorotic dwarf virus.

XX FH Key Location/Qualifiers

FT Region 439..829

FT /note= "antigenic region of cp2"

FT /label= dipeptide cleavage site

FT /note= "may be used by animal picornavirus 3C proteases"

FT Peptide 897..1098

FT /note= "putative cp3 region, one of the structural

FT proteins"

FT Peptide 897..911

FT /note= "N-terminus of cp3"

FT /label= dipeptide cleavage site

FT /note= "may be used by animal picornavirus 3C proteases"

FT Peptide 1099..1113

FT /note= "N-terminus of cp1"

FT Region 1205..1483

FT /note= "antigenic region of cpl"

XX WO9421796-A2.

PN 29-SEP-1994.

XX

PF 22-MAR-1994; 94WO-US003028.

XX PR 24-MAR-1993; 93US-00038768.

XX (PION-) PIONEER HI-BRED INT INC.

PA (USDA) US SEC OF AGRIC.

XX PI

Roth BA, Townsend R, McMullen MD;

XX WPI; 1994-317016/39.

DR N-PSDB; AAO74694.

XX DNA encoding maize chlorotic dwarf virus proteins - used to provide

plants with resistance to the virus and related viral infections.

XX Disclosure; Page 18-32; 40pp; English.

XX This sequence shows the large polyprotein of the Maize Chlorotic Dwarf

Virus (MCDV). When cleaved it contains 3 structural proteins, cpl, cp2

and cp3. Depending on the exact location of cp2, the MCDV genome, can

encode upto 78 kD of protein 5' of the capsid proteins (for which there

are no corresponding animal picornavirus protein). The DNA is used for

imparting resistance to MCDV or viruses to which MCDV infection or

resistance provides cross-resistance, including maize dwarf mosaic

strain A. Any or all of the three coat protein genes from MCDV can be

used to provide protection for plants. (Updated on 25-MAR-2003 to correct

CC PN field.)

XX SQ Sequence 3457 AA;

Query Match 56.9%; Score 41; DB 2; Length 3457;

Best Local Similarity 66.7%; Pred. No. 9.9e+02;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSL 12

Db 1386 VPFSIAKTAKVL 1397

||||:|

RESULT 40

AAR84560

ID AAR84560 standard; protein; 3457 AA.

XX AC AAR84560;

XX 31-MAR-1999 (first entry)

XX Polyprotein encoded by the MCDV-T positive strand RNA genome.

XX Maize chlorotic dwarf virus strain Tennessee; MCDV-Tn; MCDV-M1;

XX coat protein; transgenic plant; resistance; MCDV-Tn infection.

XX Maize chlorotic dwarf virus.

XX US5866780-A.

XX 02-FEB-1999.

XX 04-APR-1995; 95US-00416603.

XX 04-APR-1995; 95US-00416603.

XX (NOVS) NOVARTIS FINANCE CORP.

XX Habera L, Law M, Reddick BB;

XX WPI; 1999-142034/12.

XX N-PSDB; AAX03390.

XX cDNA of maize chlorotic dwarf virus strain MCDV-Tn - and chimeric genes

for producing e.g. MCDV-Tn-resistant transgenic plants.

XX Disclosure; Col 115-132; 73pp; English.

XX The present sequence represents the polyprotein encoded by contiguous
 CC sequence of the maize chlorotic dwarf virus strain T (MCDV-T) genome. The
 CC specification describes a MCDV strain that is distinct from known MCDV-T
 CC and MCDV-M1 isolates, called MCDV tennessee (MCDV-Tn). The specification
 CC also provides the sequences for 3 MCDV-Tn coat proteins, which may be
 CC expressed in transgenic plants to confer resistance to MCDV-Tn infection.
 CC The coat proteins can also be produced recombinantly
 XX

SQ Sequence 3457 AA;
 Query Match 56.9%; Score 41; DB 2; Length 3457;
 Best Local Similarity 66.7%; Pred. No. 9.9e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
 |||||:
 Db 1386 VPFSIAKTAQVL 1397

RESULT 41
 ABG08969
 ID ABG08969 standard; protein; 174 AA.
 XX
 AC ABG08969;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #8960.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS73156.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 39328; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 174 AA;
 Query Match 55.6%; Score 40; DB 4; Length 174;
 Best Local Similarity 53.3%; Pred. No. 53;
 Matches 8; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 VPFSVAKSVKSLYL 15
 :|||:
 Db 97 LPFTIAKRIK--YL 109

RESULT 42
 ABG02533
 ID ABG02533 standard; protein; 394 AA.
 XX
 AC ABG02533;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #2524.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS66720.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 32892; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 394 AA;
Query Match 55.6%; Score 40; DB 4; Length 394;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYLIG 15
Db 279 IPTTISEVTSILRG 293
RESULT 43
ID ABP73632 standard; protein; 969 AA.
AC ABP73632;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans essential protein SEQ ID NO 7469.
XX
DE Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlseen KL;
XX
DR WPI; 2002-566694/60.
XX
DR N-PSDB; ABZ32182.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 44; SEQ ID NO 7469; 167pp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division

CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an
CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office
XX
SQ Sequence 969 AA;
Query Match 55.6%; Score 40; DB 5; Length 969;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYLIG 15
Db 792 LPFGVAKESKSKELG 806
RESULT 44
ID AAM89790 standard; protein; 64 AA.
XX
AC AAM89790;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:17383.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184654P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.

```
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PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0231977P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2000US-0254097P.
PR 05-JAN-2001; 2000US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-483426/52.
XX N-PSDB; AAK62571.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 11; SEQ ID NO 17383; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK67694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 64 AA;
XX
XX Query Match 54.2%; Score 39; DB 4; Length 64;
XX Best Local Similarity 53.8%; Pred. No. 27;
XX Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1 VPFSVAKSVKSLY 13
XX ||| :|: |||
XX Db 29 VPFLSKKIKSKY 41
XX
XX RESULT 45
```

AAB27329
ID AAB27329 standard; protein; 369 AA.
XX
AC AAB27329;
XX
DT 25-JAN-2001 (first entry)
XX
XX N. tabacum NIM1 homologue SEQ ID NO: 74.
XX
XX Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW potato.
XX
XX Nicotiana tabacum.
XX
XX WO200053762-A2.
XX
XX 14-SEP-2000.
XX
XX 07-MAR-2000; 2000WO-EP001978.
XX
XX 09-MAR-1999; 99US-00265149.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX
XX WPI; 2000-594322/56.
DR N-PSDB; AAA97234.
XX
XX Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are homologs
PT of Arabidopsis NIM1 gene.
XX
XX Claim 1; Page 151-152; 152pp; English.
XX
XX The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC protein and gene can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize
XX
XX Sequence 369 AA;
Query Match 54.2%; Score 39; DB 3; Length 369;
Best Local Similarity 53.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLY 13
Db 237 VPFEVAENIKLIW 249
RESULT 46
ABP04700
ID ABP04700 standard; protein; 120 AA.
XX
AC ABP04700;
XX
XX 24-JUN-2002 (first entry)
DT
XX
DE Human ORFX protein sequence SEQ ID NO:9382.
XX

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
XX Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US010836.
XX
XX 30-MAY-2000; 2000US-0206132P.
XX
XX 29-AUG-2000; 2000US-0228716P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach MD;
XX
XX WPI; 2002-106308/14.
XX
XX N-PSDB; ABN20452.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.
XX
XX Disclosure; SEQ ID NO 9382; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification) . ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative diseases, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 120 AA;
Query Match 52.8%; Score 38; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 SVAKSVKSLYIG 15
Db 95 AVSKKDKSLYIG 106
RESULT 47
ABP62898
ID ABP62898 standard; protein; 133 AA.
XX

AC ABP62898;
 XX 14-OCT-2002 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 335.
 DE
 XX Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 XX
 OS Homo sapiens.
 XX
 XX WO200218424-A2.
 PN
 XX 07-MAR-2002.
 PD
 XX 31-AUG-2001; 2001WO-US027093.
 PF
 XX 01-SEP-2000; 2000US-00654935.
 PR
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
 FI
 XX WPI; 2002-583321/62.
 DR
 XX N-PSDB; ABQ93377.
 DR
 XX New polynucleotide and polypeptides, useful for treatment and diagnosis
 of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies.
 PT
 XX
 PS Claim 20; SEQ ID NO 335; 284pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated polynucleotide (I) comprising one of
 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 CC (I) is useful for gene therapy of diseases and (II) can be used for
 CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 133 AA;
 SQ
 Query Match 52.8%; Score 38; DB 5; Length 133;
 Best Local Similarity 34.8%; Pred. No. 92;
 Matches 8; Conservative 5; Mismatches 2; Indels 8; Gaps 1;
 QY 1 VPFSVAKS-----VKSLYLIG 15
 :|||:|
 DB 73 IPFEVSGEPQPKWLRSLRFLIG 95
 :|||:|
 RESULT 48
 ADS43968
 ID ADS43968 standard; protein; 307 AA.
 XX
 AC ADS43968;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Bacterial polypeptide #22398.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 XX US20032333675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 FI
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 22398; 122pp; English.
 PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 307 AA;
 SQ
 Query Match 52.8%; Score 38; DB 8; Length 307;
 Best Local Similarity 52.6%; Pred. No. 2.4e+02;
 Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
 QY 1 VPFSVAK-----SVKSLYLIG 15
 :|||:|
 DB 137 VPFEIKIRMQDVKSYYLG 155
 :|||:|
 RESULT 49
 ABR53899


```
ID ABR53899 standard; protein; 349 AA.
XX
AC ABR53899;
XX
XX 20-JUN-2003 (first entry)
XX
DE Protein sequence #SEQ ID 2663.
XX
XX Multiprotein complex; eukaryote; drug target; diagnosis.
XX
OS Saccharomyces cerevisiae.
XX
XX EP1258494-A1.
XX
XX 20-NOV-2002.
XX
XX 20-DEC-2001; 2001EP-00130253.
XX
XX 15-MAY-2001; 2001EP-00111774.
XX
XX (CELL-) CELLZOME AG.
XX
XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
XX Marzioch M, Schultz JD, Superti-Furga GD;
XX
XX WPI; 2003-250078/25.
XX N-PSDB; ACC61941.
XX
XX New isolated protein complexes useful for diagnosing a disease or
XX disorder, or as a target for an active agent of a pharmaceutical,
XX preferably a drug target in the treatment or prevention of disease or
XX disorder.
XX
XX Disclosure; SEQ ID NO 2663; 17pp + Sequence Listing; English.
XX
XX The invention relates to multiprotein complexes from eukaryotes. Proteins
XX of the invention and DNA sequences encoding them are given in records
XX ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
XX obtainable by using a protein as a bait and isolating the set of proteins
XX which is attached thereto from cells. Such protein complexes may comprise
XX up to 30 distinct proteins. Protein complexes of the invention are useful
XX for diagnosing a disease or disorder, or as a target for an active agent
XX of a pharmaceutical, preferably a drug target in the treatment or
XX prevention of a disease or disorder. Note: The sequence data for this
XX patent is not represented in the printed specification, but is based on
XX sequence information supplied by the European Patent Office. The complete
XX document is available on CD-ROM
XX
XX Sequence 349 AA;
XX
XX Query Match 52.8%; Score 38; DB 6; Length 349;
XX Best Local Similarity 66.7%; Pred. No. 2.7e+02;
XX Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4 SVAKSVKSLYLIG 15
XX :|: |||||
XX Db 307 AVSKDKSLYLIG 318
XX
XX RESULT 50
XX ADK64826
XX ID ADK64826 standard; protein; 349 AA.
XX
XX AC ADK64826;
XX
XX XX 06-MAY-2004 (first entry)
XX
XX DE Disease treating protein complex-derived protein #1603.
XX
XX KW protein complex; drug target; diagnosis.
XX
XX OS Unidentified.
XX
XX
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PN EPI338608-A2.
XX
XX 27-AUG-2003.
XX
XX 20-DEC-2002; 2002EP-00102902.
XX
XX 20-DEC-2001; 2001EP-00130253.
XX
XX (CELL-) CELLZOME AG.
XX
XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
XX Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
XX Michon A, Leutwein C, Rick J;
XX
XX WPI; 2003-638460/61.
XX N-PSDB; ADK64827.
XX
XX New proteins and protein complexes from eukaryotes, useful as targets in
XX drug screening, or in diagnosing or screening for the presence of a
XX disease or disorder, or a predisposition for developing a disease or
XX disorder in a subject.
XX
XX Disclosure; SEQ ID NO 3205; 13pp; English.
XX
XX The invention relates to novel protein complexes comprising a first and a
XX second protein, or its derivative, fragment, homologue or variant. The
XX proteins are selected from given protein complexes, which are not defined
XX in the specification. The variants are encoded by nucleic acids that
XX hybridize to the nucleic acids encoding the proteins under low stringency
XX conditions. The protein complexes are useful as targets for an active
XX agent of a pharmaceutical. These protein complexes are particularly
XX useful as drugs targets for the treatment or preventing of a disease or
XX disorder. The complexes and methods above are useful in diagnosing or
XX screening for the presence of a disease or disorder or a predisposition
XX for developing a disease or disorder in a subject. These are also useful
XX in screening for a drug for treatment or prevention of a disease or
XX disorder. The molecule that modulates the amount, activity or protein
XX components of the complex is useful for the manufacture of a medicament
XX for the treatment or prevention of a disease or disorder. This sequence
XX corresponds to a protein of the invention. (Note: the sequence data for
XX this patent did not form part of the printed specification but was
XX obtained from the EPO in electronic format).
XX
XX Sequence 349 AA;
XX
XX Query Match 52.8%; Score 38; DB 7; Length 349;
XX Best Local Similarity 66.7%; Pred. No. 2.7e+02;
XX Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4 SVAKSVKSLYLIG 15
XX :|: |||||
XX Db 307 AVSKDKSLYLIG 318
XX
XX Search completed: July 7, 2005, 09:27:29
XX Job time : 66.7967 secs
XX
```

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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:53:50 ; Search time 4.03846 Seconds
(without alignments)
357.377 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	678	2 B48089	growth arrest-spec
2	69	95.8	673	2 A48089	growth arrest-spec
3	69	95.8	674	2 I55476	growth potentiatin
4	44	61.1	374	2 S28285	hypothetical prote
5	42	58.3	252	2 H72469	hypothetical prote
6	42	58.3	292	2 S35915	beta-lactamase (EC
7	42	58.3	1220	2 S48387	SLN1 protein - yea
8	41	56.9	354	2 C64352	hypothetical prote
9	41	56.9	1173	2 S48877	Ca2+-transporting
10	41	56.9	1197	1 VGVURF	M polyprotein - Ri
11	41	56.9	1206	1 VGVURV	M polyprotein - Ri
12	40	55.6	250	2 D70335	hypothetical prote
13	40	55.6	415	1 A48359	glutamy1-trNA redu
14	39	54.2	421	2 T08268	conserved hypotet
15	39	54.2	461	2 T48015	hypothetical prote
16	39	54.2	1262	2 T25168	hypothetical prote
17	38	52.8	307	2 S60949	probable phosphate
18	38	52.8	317	2 C75012	hypothetical prote
19	38	52.8	330	2 B83902	transcription repr
20	38	52.8	349	2 S59308	probable membrane
21	38	52.8	390	2 T03841	patatin homolog -
22	38	52.8	401	2 T51407	proline-rich prote
23	38	52.8	508	1 PKRWA	H+-transporting tw
24	38	52.8	615	2 T29550	hypothetical prote
25	38	52.8	661	2 I56258	RP105 - mouse
26	37.5	52.1	296	2 G70446	hypothetical prote
27	37	51.4	258	1 OYECHP	imidazoleglycerol-
28	37	51.4	258	2 B90982	imidazoleglycerol-
29	37	51.4	258	2 H85827	imidazoleglycerol-

30	37	51.4	258	2 B54052	cyclase hiaF - Kle
31	37	51.4	259	2 T37185	probable GntR-fam1
32	37	51.4	271	2 S47620	beta-lactamase - P
33	37	51.4	300	2 S51044	beta-lactamase - P
34	37	51.4	300	2 A55792	beta-lactamase (EC
35	37	51.4	307	2 S53908	hypothetical prote
36	37	51.4	418	2 A53120	intracellular coag
37	37	51.4	435	2 AG1028	prelin imported
38	37	51.4	506	2 G31090	H+-transporting tw
39	37	51.4	506	2 AE1807	ATP synthase chain
40	37	51.4	513	2 C86897	hypothetical prote
41	37	51.4	533	2 E97854	H+-transporting tw
42	37	51.4	1702	2 S42459	DNA-directed DNA p
43	36.5	50.7	437	2 T00127	hypothetical prote
44	36	50.0	81	2 C91278	hypothetical prote
45	36	50.0	81	2 C86119	hypothetical prote
46	36	50.0	81	2 D65233	hypothetical 9.6 k
47	36	50.0	90	2 AH1054	conserved hypotet
48	36	50.0	149	2 C90217	hypothetical prote
49	36	50.0	166	2 AB2147	hypothetical prote
50	36	50.0	226	2 A64209	ribosomal protein
51	36	50.0	297	2 A70347	UDP-N-acetylenolp
52	36	50.0	356	2 T22882	hypothetical prote
53	36	50.0	366	2 E97304	iron-regulated ABC
54	36	50.0	397	2 D89768	hypothetical prote
55	36	50.0	409	2 C82072	D-3-phosphoglycra
56	36	50.0	410	1 C64070	phosphoglycerate d
57	36	50.0	432	2 F81400	glutamy1-trNA redu
58	36	50.0	455	2 G70089	hypothetical prote
59	36	50.0	486	2 D64474	hypothetical prote
60	36	50.0	506	1 FWEGA	H+-transporting tw
61	36	50.0	529	2 C82076	general secretion
62	36	50.0	529	2 AH1463	conserved membrane
63	36	50.0	551	2 H86260	protein T12C24.30
64	36	50.0	605	2 AC1139	internalin protein
65	36	50.0	611	2 AB1497	internalin protein
66	36	50.0	641	2 A54407	alpha-mannosidase
67	36	50.0	899	2 F88391	protein R06B10.4 (
68	36	50.0	900	1 S25322	beta-functional beta-
69	36	50.0	1086	2 T33893	hypothetical prote
70	36	50.0	1232	2 B39432	ATP-dependent deox
71	36	50.0	15281	2 S41309	cyclosporin synthe
72	35.5	49.3	239	2 H84886	probable VAMP-asso
73	35.5	49.3	382	2 S71669	finger protein MIG
74	35	48.6	255	2 H75346	hypothetical prote
75	35	48.6	298	2 F69502	hypothetical prote
76	35	48.6	304	2 AG1820	esterase imported
77	35	48.6	345	2 D97222	HD-GYP hydrolase d
78	35	48.6	358	2 T02383	hypothetical prote
79	35	48.6	379	2 S27383	elastase inhibitor
80	35	48.6	382	2 S09139	coii intron protei
81	35	48.6	382	2 G70946	probable dioxigena
82	35	48.6	388	2 E72354	probable hexosyltr
83	35	48.6	391	1 JQ1533	nucleocapsid prote
84	35	48.6	391	1 VHNZ1	nucleocapsid prote
85	35	48.6	391	1 VHNZ3	nucleocapsid prote
86	35	48.6	391	1 VHNZB4	nucleocapsid prote
87	35	48.6	393	1 VHNZPM	nucleocapsid prote
88	35	48.6	398	2 G90260	conserved hypotet
89	35	48.6	414	2 C82954	hypothetical prote
90	35	48.6	446	2 H83098	hypothetical prote
91	35	48.6	452	2 JCE561	UDP-N-acetylmuram
92	35	48.6	467	1 VHNZ	nucleocapsid prote
93	35	48.6	469	2 S48370	probable phosphogl
94	35	48.6	470	2 T52440	PRM1 homolog limpo
95	35	48.6	476	2 A83387	probable transport
96	35	48.6	489	2 H84106	teichuronopeptide
97	35	48.6	494	2 S57539	probable membrane
98	35	48.6	499	2 C71111	phenylalanine-tRNA
99	35	48.6	503	2 S78321	H+-transporting tw
100	35	48.6	529	2 AH1101	conserved membrane
101	35	48.6	547	2 I39593	exea protein - Aer
102	35	48.6	563	2 D90531	excinuclease ABC s

103	35	48.6	573	1	S33212	INDAI protein - fu	176	34	47.2	763	2	AH1097	alpha-glucosidase
104	35	48.6	599	2	T17534	hypothetical prote	177	34	47.2	764	2	A47456	down-regulated in
105	35	48.6	605	2	S10197	NADH2 dehydrogenas	178	34	47.2	805	2	S64238	kinesin-related pr
106	35	48.6	663	2	T47802	hypothetical prote	179	34	47.2	1052	2	T37133	hypothetical prote
107	35	48.6	719	2	F96577	hypothetical prote	180	34	47.2	1325	2	S62497	probable nucleopor
108	35	48.6	735	2	A83006	hypothetical prote	181	34	47.2	2052	2	T37711	probable n-end-rec
109	35	48.6	759	1	C64345	replication licens	182	34	47.2	2764	2	T13945	neurofibromin - fr
110	35	48.6	776	2	S39865	late competence pr	183	34	47.2	2802	2	T13947	neurofibromin - fr
111	35	48.6	915	2	T21147	hypothetical prote	184	34	47.2	2802	2	T13947	reverse transcript
112	35	48.6	1008	2	C97726	acriflavin resista	185	33.5	46.5	120	2	S22049	hypothetical prote
113	35	48.6	1067	2	T18196	pol protein - silk	186	33.5	46.5	336	2	C64410	3-phosphoshikimate
114	35	48.6	1685	2	T43217	RNA polymerase (EC	187	33.5	46.5	427	2	C84966	DNA topoisomerase
115	35	48.6	5327	2	T13564	microtubule-associ	188	33	45.8	81	2	A41949	hypothetical prote
116	34.5	47.9	223	2	T51727	C-8, 7 sterol isome	189	33	45.8	85	2	T18143	hypothetical prote
117	34.5	47.9	314	2	T33862	hypothetical prote	190	33	45.8	111	2	H72561	hypothetical prote
118	34.5	47.9	330	2	T08667	hypothetical prote	191	33	45.8	122	2	S36276	Ig heavy chain v r
119	34.5	47.9	422	2	H96591	hypothetical prote	192	33	45.8	140	2	D72322	conserved hypothet
120	34.5	47.9	457	2	H84716	hypothetical prote	193	33	45.8	144	2	G75149	hypothetical prote
121	34.5	47.9	1955	2	T41170	probable 1,3-beta-	194	33	45.8	153	2	S23222	miGA protein - She
122	34.5	47.9	2163	2	T51397	hypothetical prote	195	33	45.8	153	2	H71248	hypothetical prote
123	34	47.2	75	2	S50353	hypothetical prote	196	33	45.8	179	2	S45551	hypothetical prote
124	34	47.2	76	2	S61601	hypothetical prote	197	33	45.8	193	2	T36285	probable hydrolase
125	34	47.2	101	2	S45387	hypothetical prote	198	33	45.8	222	2	F71309	probable phosphogl
126	34	47.2	110	2	S38067	hypothetical prote	199	33	45.8	224	2	D90235	hypothetical prote
127	34	47.2	110	2	S50345	hypothetical prote	200	33	45.8	230	2	C97104	hypothetical prote
128	34	47.2	136	2	PH1559	Ig heavy chain v r	201	33	45.8	232	1	R5BS1	ribosomal protein
129	34	47.2	184	2	AF2247	hypothetical prote	202	33	45.8	234	2	E71905	hypothetical prote
130	34	47.2	190	2	D88957	protein ZK697.8 [i	203	33	45.8	236	2	E90153	conserved hypothet
131	34	47.2	251	2	H64212	hypothetical prote	204	33	45.8	240	2	R97782	ABC transporter At
132	34	47.2	251	2	AH3314	hypothetical membr	205	33	45.8	245	2	S21507	polyhedrin - lacke
133	34	47.2	258	2	H84941	hisF protein [limp	206	33	45.8	254	2	F71654	ABC transporter At
134	34	47.2	258	2	AC0188	histidine biosynth	207	33	45.8	257	2	E82238	imidazoleglycerol-
135	34	47.2	284	2	T18253	probable mitochond	208	33	45.8	263	2	A54543	beta-lactamase (EC
136	34	47.2	286	2	AG3220	hydrolase [impor	209	33	45.8	271	2	C69352	imidazoleglycerol-
137	34	47.2	291	2	JP0074	beta-lactamase (EC	210	33	45.8	275	2	D64933	NAD synthase (EC 6
138	34	47.2	294	2	S19006	beta-lactamase (EC	211	33	45.8	275	2	F90934	NAD synthetase [im
139	34	47.2	307	2	D69521	hypothetical prote	212	33	45.8	275	2	B85783	NAD synthetase, pr
140	34	47.2	313	2	G81782	adhesin MafA2 NMA2	213	33	45.8	279	2	T40445	phosphatidic acid
141	34	47.2	321	2	E84747	probable cinnamoyl	214	33	45.8	290	2	C96776	hypothetical prote
142	34	47.2	364	2	T34221	lir-1 protein - Ca	215	33	45.8	291	2	S42075	beta-lactamase (EC
143	34	47.2	370	2	E71306	probable polynucle	216	33	45.8	292	2	C70421	conserved hypothet
144	34	47.2	371	2	C95130	conserved hypothet	217	33	45.8	295	2	AG0547	probable carboxyvi
145	34	47.2	375	2	E98001	glycerate kinase [218	33	45.8	296	2	C64760	probable carboxyph
146	34	47.2	397	2	E95580	hypothetical prote	219	33	45.8	296	2	D85527	probable phosphono
147	34	47.2	410	1	DESCPG	phosphoglycerate d	220	33	45.8	296	2	A90677	probable phosphono
148	34	47.2	410	2	AD0874	D-3-phosphoglyc	221	33	45.8	297	1	WZECN	N-acetylneuraminat
149	34	47.2	410	2	D85947	D-3-phosphoglyc	222	33	45.8	297	2	AE0908	N-acetylneuraminat
150	34	47.2	410	2	H91101	D-3-phosphoglyc	223	33	45.8	297	2	E85986	N-acetylneuraminat
151	34	47.2	412	2	AD3611	phosphoglycerate d	224	33	45.8	297	2	B91141	N-acetylneuraminat
152	34	47.2	412	2	AG3637	cis,cis-muconate t	225	33	45.8	297	2	H64234	cytadherence acces
153	34	47.2	413	2	AC0112	phosphoglycerate d	226	33	45.8	298	2	A83545	carboxyphosphonen
154	34	47.2	421	2	JN0257	site-specific DNA-	227	33	45.8	303	2	F71680	hypothetical prote
155	34	47.2	427	2	B86266	hypothetical prote	228	33	45.8	305	2	E70410	hypothetical prote
156	34	47.2	445	2	A71699	UDP-N-acetylmuram	229	33	45.8	311	2	JN0520	beta-lactamase (EC
157	34	47.2	447	2	C84306	hypothetical prote	230	33	45.8	311	2	H64157	sufi protein homol
158	34	47.2	450	2	H95079	UDP-N-acetylmuram	231	33	45.8	313	2	G91262	probable carboxydr
159	34	47.2	450	2	C97947	UDP-N-acetylmuram	232	33	45.8	313	2	B86103	probable carboxydr
160	34	47.2	451	2	D47691	UDP-N-acetylmuram	233	33	45.8	321	2	G95920	probable epimerase
161	34	47.2	480	2	E75433	hypothetical prote	234	33	45.8	321	2	S10006	hypothetical prote
162	34	47.2	496	2	A31986	glucose transporte	235	33	45.8	339	1	S47643	alcohol dehydrogen
163	34	47.2	500	2	D75049	phenylalanine-tRNA	236	33	45.8	339	2	T34406	hypothetical prote
164	34	47.2	508	2	A89817	hypothetical prote	237	33	45.8	340	2	T46112	hypothetical prote
165	34	47.2	518	1	S40218	glycine hydroxymet	238	33	45.8	348	2	AG1041	Vi polysaccharide
166	34	47.2	543	2	G95118	RNA methyltransfer	239	33	45.8	348	2	C36892	Vi polysaccharide
167	34	47.2	543	2	D79988	conserved hypothet	240	33	45.8	350	2	D37298	uncharacterized co
168	34	47.2	561	2	C84721	hypothetical prote	241	33	45.8	351	2	T43493	hypothetical prote
169	34	47.2	575	2	C88346	protein F42G4.3a [242	33	45.8	354	1	RGHYO1	GTP-binding regula
170	34	47.2	579	2	AB1414	ABC transporter (A	243	33	45.8	354	1	RGHYO2	GTP-binding regula
171	34	47.2	579	2	A11789	ABC transporter (A	244	33	45.8	354	1	RGBOO1	GTP-binding regula
172	34	47.2	603	2	T22111	hypothetical prote	245	33	45.8	354	1	RGHUO1	GTP-binding regula
173	34	47.2	628	2	S44629	F22B7.10 protein -	246	33	45.8	354	1	RGHUO2	GTP-binding regula
174	34	47.2	632	2	B55225	stress-sensitive r	247	33	45.8	354	1	RGMSO1	GTP-binding regula
175	34	47.2	693	2	F82245	conserved hypothet	248	33	45.8	354	1	RGMSO2	GTP-binding regula

249	33	45.8	354	1	RGRT01	GTP-binding regula	322	32.5	45.1	494	2	S39607	transcription fact
250	33	45.8	354	1	RGRT02	G-protein - regula	323	32.5	45.1	542	2	S39608	transcription fact
251	33	45.8	354	2	S40509	G-protein - chicke	324	32.5	45.1	628	1	A33333	transcription fact
252	33	45.8	355	2	T34405	hypothetical prote	325	32.5	45.1	628	1	A39262	transcription fact
253	33	45.8	359	2	A46046	serine proteinase	326	32.5	45.1	630	1	A46149	transcription fact
254	33	45.8	374	2	T24162	hypothetical prote	327	32.5	45.1	631	1	A36749	transcription fact
255	33	45.8	379	2	T17979	pectin lyase (EC 4	328	32.5	45.1	634	1	S35574	transcription fact
256	33	45.8	380	2	E84748	probable protein p	329	32.5	45.1	702	2	A34434	arylphorin alpha c
257	33	45.8	382	2	T37836	probable protein f	330	32.5	45.1	841	2	D84513	probable ribosome
258	33	45.8	382	2	S62499	hypothetical prote	331	32	44.4	86	2	S54593	ribosomal protein
259	33	45.8	397	2	T33510	hypothetical prote	332	32	44.4	102	2	PH1262	Ig heavy chain V r
260	33	45.8	399	2	A55577	formaldehyde dehyd	333	32	44.4	108	2	G72717	hypothetical prote
261	33	45.8	403	2	C75405	streptomycin biosy	334	32	44.4	121	2	T24096	hypothetical prote
262	33	45.8	417	2	AF3448	hypothetical membr	335	32	44.4	126	2	PH1424	Ig heavy chain V r
263	33	45.8	418	2	A47281	pigment epithelial	336	32	44.4	130	2	G72609	hypothetical prote
264	33	45.8	426	2	F70723	probable transferra	337	32	44.4	133	2	A75039	hypothetical prote
265	33	45.8	434	2	F90184	cobyrinic acid A,C	338	32	44.4	134	2	PH1422	Ig heavy chain V r
266	33	45.8	448	2	AC2373	L-sorbose dehydr	339	32	44.4	137	2	S02155	NADH2 dehydrogenas
267	33	45.8	462	2	A40362	anthranilate synth	340	32	44.4	149	2	B72735	hypothetical prote
268	33	45.8	464	2	C82046	sensor protein Cpx	341	32	44.4	155	2	D75147	Iso ribosomal prot
269	33	45.8	475	2	C86863	N-acetylmuramoyl-L	342	32	44.4	155	2	B71187	probable ribosomal
270	33	45.8	479	2	G96605	hypothetical prote	343	32	44.4	157	2	F90219	Iso ribosomal prot
271	33	45.8	483	2	F71619	hypothetical prote	344	32	44.4	180	2	AD0134	probable prophage
272	33	45.8	510	2	B71017	hypothetical prote	345	32	44.4	184	2	C83911	hypothetical prote
273	33	45.8	527	2	S49827	probable membrane	346	32	44.4	188	2	F82569	dihydrofolate redu
274	33	45.8	534	2	B97352	polylacturonase	347	32	44.4	190	2	G70239	conserved hypotet
275	33	45.8	537	2	AH1277	probable transport	348	32	44.4	218	2	S74867	hypothetical prote
276	33	45.8	537	2	CH1640	probable transport	349	32	44.4	246	1	JQ1868	polyhedrin - Spodo
277	33	45.8	563	1	C64420	N-methylhydantoina	350	32	44.4	246	1	PYNVSF	polyhedrin - Spodo
278	33	45.8	583	2	T12574	phosphoglucosylase	351	32	44.4	254	2	T48732	2,5-diketo-D-gluco
279	33	45.8	590	2	T20537	hypothetical prote	352	32	44.4	254	2	C86277	F14L17.7 protein -
280	33	45.8	613	2	T33266	hypothetical prote	353	32	44.4	256	2	D69952	conserved hypotet
281	33	45.8	638	2	S36546	E1 protein - human	354	32	44.4	258	1	OYEBHF	cyclase hlsf - Sal
282	33	45.8	668	2	H86729	excinuclease ABC s	355	32	44.4	258	2	A10764	cyclase hlsf [impo
283	33	45.8	690	2	C83958	DNA topoisomerase	356	32	44.4	258	2	I64070	cyclase hlsf HI047
284	33	45.8	699	2	E97594	elongation factor	357	32	44.4	259	2	C43260	triose-phosphate i
285	33	45.8	699	2	AC2816	translation elonga	358	32	44.4	259	2	T24131	hypothetical prote
286	33	45.8	747	2	T22916	hypothetical prote	359	32	44.4	261	2	AH2031	hypothetical prote
287	33	45.8	819	2	D85440	Cu2+-transporting	360	32	44.4	266	2	D84953	pseudouridyate sy
288	33	45.8	822	2	T41941	glycoprotein B - h	361	32	44.4	266	2	AE02386	amino acid ABC tra
289	33	45.8	830	2	B44439	protein kinase (EC	362	32	44.4	274	2	A80468	diaminopimelate ep
290	33	45.8	842	2	H44339	hypothetical prote	363	32	44.4	278	2	CB3114	hypothetical prote
291	33	45.8	856	2	A44339	protein kinase (EC	364	32	44.4	278	2	C98173	hypothetical prote
292	33	45.8	857	2	A42861	protein kinase RTK	365	32	44.4	281	2	G24723	tryptophan synthas
293	33	45.8	925	2	A72096	ct234 hypotetrical	366	32	44.4	287	2	D87465	D-alanine aminotra
294	33	45.8	925	2	E81573	conserved hypotet	367	32	44.4	289	2	H96588	hypothetical prote
295	33	45.8	925	2	E86527	CT234 hypotetrical	368	32	44.4	290	2	A70208	conserved hypotet
296	33	45.8	977	2	T38412	hypothetical prote	369	32	44.4	291	2	S62730	cyclin D1 - zebra
297	33	45.8	1003	2	T28654	transposase - pseu	370	32	44.4	293	2	H82634	site-specific DNA-
298	33	45.8	1019	2	F70342	cation efflux syst	371	32	44.4	294	2	AD1910	ABC transporter pe
299	33	45.8	1038	2	A71437	probable resistanc	372	32	44.4	300	2	D87497	MtTB family protei
300	33	45.8	1074	2	G96504	probable En/Spm-li	373	32	44.4	300	2	B99709	probable transcrip
301	33	45.8	1088	2	E86312	FlIA6.9 protein -	374	32	44.4	300	2	F85559	probable transcrip
302	33	45.8	1100	2	G83376	probable trehalose	375	32	44.4	300	2	A64794	YbdO protein - Esc
303	33	45.8	1258	2	D75453	5-methyltetrahydro	376	32	44.4	303	2	C97029	transcription regu
304	33	45.8	1278	2	A47462	probable DNA-direc	377	32	44.4	304	2	AF0730	probable membrane
305	33	45.8	1304	2	G85188	disease resistance	378	32	44.4	306	2	C64015	hypothetical prote
306	33	45.8	1317	2	H85189	disease resistance	379	32	44.4	307	2	B96745	unknown protein T9
307	33	45.8	1385	2	T13987	t1r protein - frui	380	32	44.4	309	2	H98832	hypothetical prote
308	33	45.8	1389	2	T13852	gene wheeler prote	381	32	44.4	316	1	PNBSLC	beta-lactamase (EC
309	33	45.8	1422	2	B71437	probable resistanc	382	32	44.4	321	1	RSUBP0	acidic ribosomal p
310	33	45.8	1737	2	A37491	hypothetical helic	383	32	44.4	323	2	H90282	hypothetical prote
311	33	45.8	1983	2	AC1922	two-component hybr	384	32	44.4	323	2	AB1659	hypothetical prote
312	33	45.8	2133	2	T42763	coagulation factor	385	32	44.4	329	2	T05728	probable cadmium-t
313	33	45.8	2413	2	S34670	splicing factor PR	386	32	44.4	332	2	T23503	hypothetical prote
314	33	45.8	2467	2	D71437	probable resistanc	387	32	44.4	335	2	T50393	probable mitochond
315	33	45.8	5147	1	IJFTM	cadherin-related c	388	32	44.4	336	2	G90421	alcohol dehydrogen
316	32.5	45.1	218	2	B82226	thiopurine methylt	389	32	44.4	337	2	T52358	probable CELL Divi
317	32.5	45.1	365	2	E69220	conserved hypotet	390	32	44.4	338	2	C64551	oligopeptide ABC t
318	32.5	45.1	394	2	B70411	fimbrial assembly	391	32	44.4	339	2	A82441	ABC transporter, p
319	32.5	45.1	407	2	T00989	hypothetical prote	392	32	44.4	341	2	T33221	hypothetical prote
320	32.5	45.1	464	2	AB1480	PTS system, fructo	393	32	44.4	345	2	A97783	tRNA pseudouridine
321	32.5	45.1	464	2	AG1119	PTS system, fructo	394	32	44.4	353	2	I51572	maternal protein -

395	32	44.4	356	2	B89919	hypothetical prote	468	32	44.4	568	2	T03950	probable glucose-6
396	32	44.4	365	1	GNVSSC	genome polyprotein	469	32	44.4	581	2	T05550	hypothetical prote
397	32	44.4	366	2	A71880	probable outer mem	470	32	44.4	584	2	B82834	hypothetical prote
398	32	44.4	371	2	E71932	probable outer mem	471	32	44.4	586	1	JC4219	pyruvate kinase (E
399	32	44.4	372	2	A34261	alanine dehydrogen	472	32	44.4	592	2	D97171	uncharacterized co
400	32	44.4	378	2	A32862	serpin - pig	473	32	44.4	594	2	F82895	hypothetical prote
401	32	44.4	378	2	AG2833	hypothetical prote	474	32	44.4	596	2	D87710	TPR domain protein
402	32	44.4	378	2	C97611	hypothetical prote	475	32	44.4	606	2	H71065	hypothetical prote
403	32	44.4	378	2	H69505	conserved hypotet	476	32	44.4	610	2	T32917	hypothetical prote
404	32	44.4	380	1	GNVSMB	genome polyprotein	477	32	44.4	619	2	S40938	hypothetical prote
405	32	44.4	392	2	A95954	probable membrane	478	32	44.4	626	2	JQ2322	starch synthase (E
406	32	44.4	392	2	E95133	hypothetical prote	479	32	44.4	654	2	T14202	NAH2 dehydrogenas
407	32	44.4	392	2	A99002	hypothetical prote	480	32	44.4	664	2	F70483	glycine-tRNA ligas
408	32	44.4	392	2	G83909	hypothetical prote	481	32	44.4	665	2	D90092	hypothetical prote
409	32	44.4	394	1	VXRP8R	inner capsid prote	482	32	44.4	714	2	T31819	hypothetical prote
410	32	44.4	395	1	A43386	inner capsid prote	483	32	44.4	767	2	E85079	hypothetical prote
411	32	44.4	395	1	VXPKCR	inner capsid prote	484	32	44.4	777	2	T41075	hypothetical WD-re
412	32	44.4	400	2	A49099	penicillin-binding	485	32	44.4	783	2	T45899	receptor protein k
413	32	44.4	403	2	E83366	hypothetical prote	486	32	44.4	792	2	S63141	hypothetical prote
414	32	44.4	403	2	G71236	hypothetical prote	487	32	44.4	796	2	A97731	bifunctional penic
415	32	44.4	406	2	H71308	hypothetical prote	488	32	44.4	813	2	D71378	probable DNA gyras
416	32	44.4	407	2	H75515	tetracycline-efflu	489	32	44.4	814	2	D82101	oxidoreductase, ac
417	32	44.4	408	2	B82507	sodium/glutamate s	490	32	44.4	822	2	E97839	ATP-dependent heli
418	32	44.4	410	2	E70475	folypolyglutamate	491	32	44.4	833	2	T10695	transcription fact
419	32	44.4	415	2	A32853	plasmidogen activa	492	32	44.4	859	2	B64430	DNA-directed RNA p
420	32	44.4	416	2	T03243	PLO/LFY protein ho	493	32	44.4	862	2	B53689	homeotic protein C
421	32	44.4	418	2	A41044	chromosomal protei	494	32	44.4	862	2	S64821	probable membrane
422	32	44.4	423	2	AG1973	hypothetical prote	495	32	44.4	863	2	S37088	phycobilisome anch
423	32	44.4	425	2	E84631	probable serine ca	496	32	44.4	878	2	T21621	hypothetical prote
424	32	44.4	427	2	T39113	probable flavohemo	497	32	44.4	880	2	B45956	beta-glucosidase (
425	32	44.4	427	2	T36167	hypothetical prote	498	32	44.4	882	2	F86164	hypothetical prote
426	32	44.4	441	2	A55542	sensor kinase regB	499	32	44.4	940	2	AD1374	internalin protein
427	32	44.4	442	2	E57041	transcription regu	500	32	44.4	975	2	S33121	homeotic protein C
428	32	44.4	444	2	G69905	glucuronate permease	501	32	44.4	1008	2	T33672	hypothetical prote
429	32	44.4	449	2	C71959	glutamyl tRNA redu	502	32	44.4	1011	2	C84524	probable disease r
430	32	44.4	449	2	G64549	glutamyl-tRNA redu	503	32	44.4	1032	2	H64100	acriflavine resist
431	32	44.4	451	2	F97230	probable maltodext	504	32	44.4	1105	2	F71079	hypothetical prote
432	32	44.4	453	2	D84018	two-component resp	505	32	44.4	1126	1	WMFM12	125K protein - alf
433	32	44.4	454	2	F75571	chromosomal replic	506	32	44.4	1131	2	T38744	hypothetical prote
434	32	44.4	463	2	T04996	male sterility pro	507	32	44.4	1142	2	A45031	cysteine-rich fibr
435	32	44.4	464	2	C84428	probable ribophori	508	32	44.4	1175	2	S52417	E-selectin ligand-
436	32	44.4	465	2	B85358	SERINE CARBOXYPEPT	509	32	44.4	1253	2	T45787	disease resistance
437	32	44.4	468	2	A72619	probable NADH dehy	510	32	44.4	1289	2	AE2217	hypothetical prote
438	32	44.4	472	2	H90563	hypothetical prote	511	32	44.4	1332	1	I48314	homeotic protein C
439	32	44.4	474	2	D84631	probable serine ca	512	32	44.4	1374	2	T30809	plasmidogen relate
440	32	44.4	480	2	G85397	male sterility 2-1	513	32	44.4	1404	2	F86470	probable retroelem
441	32	44.4	480	2	T46047	hypothetical prote	514	32	44.4	1445	2	T15212	hypothetical prote
442	32	44.4	481	2	F86208	protein F22G5.30 [515	32	44.4	1450	2	S78060	probable DNA-direc
443	32	44.4	485	1	ANHU	angiotensin precur	516	32	44.4	1451	2	S42167	190K protein - hum
444	32	44.4	489	2	D87551	hypothetical prote	517	32	44.4	1713	2	A55347	adhesive ligand ep
445	32	44.4	492	2	T30066	hypothetical prote	518	32	44.4	1732	2	T43026	probable DNA-direc
446	32	44.4	498	2	T51430	dolichyl-phosphate	519	32	44.4	1787	2	AG1360	probable tape-meas
447	32	44.4	500	1	ITHUC1	complement C1 inhi	520	32	44.4	1788	2	AH1447	probable tape-meas
448	32	44.4	500	2	AD1625	transporter homolo	521	32	44.4	1794	2	T38459	hypothetical diver
449	32	44.4	501	2	AB1263	transporter homolo	522	32	44.4	1824	2	T07589	disease resistance
450	32	44.4	506	2	S63181	hypothetical prote	523	32	44.4	1895	2	T06609	disease resistance
451	32	44.4	507	1	PMLVA	H+-transporting tw	524	32	44.4	2150	1	GNVYH2	genome polyprotein
452	32	44.4	508	2	T45867	hypothetical prote	525	32	44.4	2195	2	S61103	SEC16 protein - ye
453	32	44.4	508	2	G83977	L-2,4-diaminobuty	526	32	44.4	3511	2	A59295	unconventional myo
454	32	44.4	516	2	A53772	transcription fact	527	32	44.4	4273	2	C69679	polyketide synthas
455	32	44.4	520	2	T16593	hypothetical prote	528	31.5	43.8	153	2	D71556	hypothetical prote
456	32	44.4	536	2	AB1983	hypothetical prote	529	31.5	43.8	249	2	T32566	hypothetical prote
457	32	44.4	541	2	A48717	glutamate formimid	530	31.5	43.8	254	2	E97358	inner membrane pro
458	32	44.4	544	2	E97051	site-specific DNA	531	31.5	43.8	269	2	F70377	shikimate 5-dehydr
459	32	44.4	549	2	D71969	L-lactate permease	532	31.5	43.8	305	2	S44159	hypothetical prote
460	32	44.4	549	2	D64537	L-lactate permease	533	31.5	43.8	306	2	G97457	hypothetical prote
461	32	44.4	552	2	S36786	carboxylesterase (534	31.5	43.8	306	2	AH2675	conserved hypotet
462	32	44.4	556	1	E69589	arginine-tRNA liga	535	31.5	43.8	342	2	S71398	farnesyl-pyrophosp
463	32	44.4	564	2	T09976	H+-transporting tw	536	31.5	43.8	385	2	C82478	probable integrase
464	32	44.4	564	1	S36787	carboxylesterase (537	31.5	43.8	594	2	JT0766	transcription fact
465	32	44.4	566	2	T45626	hypothetical prote	538	31.5	43.8	760	2	S62792	probable lipoprote
466	32	44.4	567	2	T03948	probable glucose-6	539	31.5	43.8	978	2	A70387	conserved hypotet
467	32	44.4	567	2	T02094	glucose-6-phosphat	540	31.5	43.8	1173	2	T08610	major core capsid

541	31.5	43.8	1556	2	F96587	hypothetical prote	614	31	43.1	261	2	T11081	cytochrome-c oxida
542	31.5	43.8	1816	2	E84845	probable ABC trans	615	31	43.1	270	2	G85078	probable transposo
543	31	43.1	39	2	E81540	hypothetical prote	616	31	43.1	273	2	D64201	methyltetrahydryl
544	31	43.1	70	2	G71716	hypothetical prote	617	31	43.1	273	2	AD2409	GDP-D-mannose dehy
545	31	43.1	50	2	AH0428	conserved hypotet	618	31	43.1	273	2	D70428	hypothetical prote
546	31	43.1	76	2	G63584	reverse transcript	619	31	43.1	278	2	T29994	hypothetical prote
547	31	43.1	81	2	T03712	reverse transcript	620	31	43.1	286	2	AE1200	3-hydroxyisobutyra
548	31	43.1	94	2	S13265	heme oxygenase (de	621	31	43.1	286	2	AC1558	3-hydroxyisobutyra
549	31	43.1	99	2	T43600	probable transposo	622	31	43.1	287	2	A64225	thymidylate synth
550	31	43.1	102	2	PH1267	IG heavy chain V r	623	31	43.1	290	2	F89605	protein F18GS.5 (l
551	31	43.1	102	2	G90223	IG heavy chain V r	624	31	43.1	291	2	B11097	hypothetical prote
552	31	43.1	113	2	G90223	DNA-directed RNA p	625	31	43.1	299	2	E83161	hypothetical prote
553	31	43.1	117	2	S19669	IG heavy chain V r	626	31	43.1	302	2	G72553	hypothetical prote
554	31	43.1	119	2	F71011	hypothetical prote	627	31	43.1	306	2	T43597	yop targeting nega
555	31	43.1	123	2	A88065	protein T16Al.5 (l	628	31	43.1	308	2	D83629	probable permease
556	31	43.1	126	2	PH1417	hypothetical prote	629	31	43.1	310	2	D87704	integral membrane
557	31	43.1	126	2	PH1418	IG heavy chain V r	630	31	43.1	313	2	G81173	adhesin mafa - Nei
558	31	43.1	126	2	PH1418	IG heavy chain V r	631	31	43.1	313	2	S73033	probable metalloth
559	31	43.1	131	2	F70920	probable moaB prot	632	31	43.1	317	2	E84434	probable phloem-ap
560	31	43.1	136	2	G90557	hypothetical prote	633	31	43.1	318	2	T41838	BRO-c - Bomby mor
561	31	43.1	137	2	E81355	hypothetical prote	634	31	43.1	320	2	T28992	hypothetical prote
562	31	43.1	138	2	AG1695	PTS mannose-specif	635	31	43.1	322	2	B65024	probable hydrogena
563	31	43.1	142	1	R5BY25	ribosomal protein	636	31	43.1	322	2	E85891	hydrogenase 4 memb
564	31	43.1	142	2	S30000	ribosomal protein	637	31	43.1	322	2	A91047	hydrogenase 4 memb
565	31	43.1	142	2	S29999	ribosomal protein	638	31	43.1	323	2	AD2753	lipoic Acid Synth
566	31	43.1	152	2	B71035	hypothetical prote	639	31	43.1	323	2	B97534	lipoic acid synth
567	31	43.1	153	2	T36799	hypothetical prote	640	31	43.1	325	2	T26260	hypothetical prote
568	31	43.1	156	2	I40704	gene eae ORFU homo	641	31	43.1	326	2	B71681	pyruvate dehydroge
569	31	43.1	156	2	D86045	hypothetical prote	642	31	43.1	327	1	D69751	glutamine homolo
570	31	43.1	156	2	F91198	Cest protein (limpo	643	31	43.1	330	2	G81165	phenylalanyl-tRNA
571	31	43.1	157	2	I41196	Tir chaperone - Es	644	31	43.1	330	2	F81939	probable phenylala
572	31	43.1	157	2	H96993	transcription regu	645	31	43.1	330	2	C69649	transcription repr
573	31	43.1	161	2	A70207	conserved hypotet	646	31	43.1	330	2	B71015	hypothetical prote
574	31	43.1	169	2	T04207	phospholipid-hydro	647	31	43.1	333	2	F90225	alcohol dehydrogen
575	31	43.1	172	2	H72731	hypothetical prote	648	31	43.1	333	2	T40923	pyridoxal reductas
576	31	43.1	172	2	C82129	conserved hypotet	649	31	43.1	338	2	S38030	suppressor protein
577	31	43.1	175	2	G96532	hypothetical prote	650	31	43.1	338	2	F71957	ABC transporter, p
578	31	43.1	176	2	T35459	hypothetical prote	651	31	43.1	341	2	T29598	hypothetical prote
579	31	43.1	177	2	AF3129	hypothetical prote	652	31	43.1	342	2	AD2032	hypothetical prote
580	31	43.1	178	2	S67379	hypothetical prote	653	31	43.1	344	2	T25951	hypothetical prote
581	31	43.1	179	2	B72612	hypothetical prote	654	31	43.1	344	2	A84750	probable mitochond
582	31	43.1	181	2	F70105	ribonuclease H (rn	655	31	43.1	345	2	T44521	polysaccharide bio
583	31	43.1	184	2	F90026	hypothetical prote	656	31	43.1	345	2	T44510	Vi polysaccharide
584	31	43.1	184	2	H84162	hypothetical prote	657	31	43.1	349	2	T41892	BRO-d orf2 - Bomby
585	31	43.1	186	2	C98158	hypothetical prote	658	31	43.1	351	2	T43791	cystathionine beta
586	31	43.1	190	2	A84029	septum formation m	659	31	43.1	360	2	T00882	hypothetical prote
587	31	43.1	193	2	AB3421	hypothetical prote	660	31	43.1	360	2	T29004	hypothetical prote
588	31	43.1	195	2	T32819	hypothetical prote	661	31	43.1	362	1	B70382	chorismate mutase/
589	31	43.1	203	2	D95152	v-type sodium ATP	662	31	43.1	362	2	S74433	GDP-D-mannose dehy
590	31	43.1	214	2	S17807	hypothetical prote	663	31	43.1	370	2	H89971	hypothetical prote
591	31	43.1	219	2	E82825	hypothetical prote	664	31	43.1	371	2	T30762	hypothetical prote
592	31	43.1	220	2	A81959	probable pseudourid	665	31	43.1	374	2	T15940	hypothetical prote
593	31	43.1	223	1	MFVNSV	matrix protein - s	666	31	43.1	377	2	AD3363	queine tRNA-ribos
594	31	43.1	225	2	T28319	ORF MSV158 probabl	667	31	43.1	378	2	G90770	probable third cyt
595	31	43.1	228	2	F89941	hypothetical prote	668	31	43.1	378	2	C85633	probable third cyt
596	31	43.1	228	2	S57697	hypothetical prote	669	31	43.1	378	2	A64839	cytochrome oxidase
597	31	43.1	228	2	G83700	hypothetical prote	670	31	43.1	379	1	B39790	cytochrome d ubiqu
598	31	43.1	230	2	S34645	fibrillar-like p	671	31	43.1	379	1	B28940	cytochrome d ubiqu
599	31	43.1	232	2	A99245	fibrillar-like p	672	31	43.1	379	2	A99725	cytochrome d ubiqu
600	31	43.1	233	2	E85888	hypothetical prote	673	31	43.1	379	2	B85576	cytochrome d ubiqu
601	31	43.1	233	2	B91044	hypothetical prote	674	31	43.1	381	2	F72756	probable multiple
602	31	43.1	233	2	C65021	Ethanolamine utili	675	31	43.1	382	2	S08595	TrfA transcription
603	31	43.1	234	2	T10217	hypothetical prote	676	31	43.1	384	2	C86831	hypothetical prote
604	31	43.1	241	2	S77548	lumQ protein - syn	677	31	43.1	388	2	T10765	patatin-like latex
605	31	43.1	243	2	D84474	hypothetical prote	678	31	43.1	388	2	T10770	patatin-like latex
606	31	43.1	243	2	T46461	hypothetical prote	679	31	43.1	388	2	T10763	patatin-like latex
607	31	43.1	248	2	F84277	uridine kinase (im	680	31	43.1	392	2	D70475	conserved hypotet
608	31	43.1	250	2	F75054	hypothetical prote	681	31	43.1	393	2	S03576	DNA-directed RNA p
609	31	43.1	252	2	F83443	hypothetical prote	682	31	43.1	393	2	AC1472	aminotransferase h
610	31	43.1	259	2	S59988	cytochrome-c oxida	683	31	43.1	394	2	G85829	O antigen polymera
611	31	43.1	259	2	G96673	hypothetical prote	684	31	43.1	394	2	D90984	O antigen polymera
612	31	43.1	261	2	T11028	cytochrome-c oxida	685	31	43.1	395	2	T23402	hypothetical prote
613	31	43.1	261	2	T11186	cytochrome-c oxida	686	31	43.1	397	2	H81744	conserved hypotet

687	31	43.1	398	2	A70520	probable aceAb pro	760	591	2	H86267	probable protein p
688	31	43.1	400	2	B36190	penicillin-binding	761	599	2	T12994	riboflavin biosynt
689	31	43.1	401	2	C83309	conserved hypotet	762	601	2	T38736	hypothetical prote
690	31	43.1	403	2	AF2151	aminotransferase [763	615	2	F64572	arginine decarboxy
691	31	43.1	405	2	S19355	hypothetical prote	764	615	2	C71867	arginine decarboxy
692	31	43.1	406	2	G70410	glutamyl tRNA redu	765	628	2	A84087	hypothetical prote
693	31	43.1	407	2	F64666	glucose/galactose	766	632	1	JC4919	2-oxoacid-ferredox
694	31	43.1	407	2	A71850	glucose/galactose	767	633	2	S61435	metalloproteinase
695	31	43.1	410	2	C84176	oxalate/formate an	768	635	2	T23874	hypothetical prote
696	31	43.1	417	2	S07286	hypothetical prote	769	642	2	H69466	conserved hypotet
697	31	43.1	418	2	F64473	D-alanine transami	770	649	2	S42894	metalloproteinase
698	31	43.1	418	2	T47818	hypothetical prote	771	650	2	T15972	hypothetical prote
699	31	43.1	425	2	F85360	SERINE CARBOXYPEPT	772	651	2	G69177	methionine-tRNA li
700	31	43.1	425	2	C97013	probable non-proce	773	651	2	D72042	conserved hypotet
701	31	43.1	428	2	JH0634	site-specific DNA-	774	651	2	B86581	CHLUPN 76 kDa homol
702	31	43.1	429	2	AB2456	glycosyltransferas	775	658	2	T20042	hypothetical prote
703	31	43.1	429	2	S45459	TOM34 protein - ye	776	660	2	G82672	ATP sulfurylase, l
704	31	43.1	439	2	T49739	related to cyclohe	777	672	2	C69120	conserved hypotet
705	31	43.1	442	2	T03172	helicase homolog 0	778	677	2	T39713	zinc finger protei
706	31	43.1	445	2	H96560	hypothetical prote	779	696	2	T50391	probable anaphase-
707	31	43.1	449	2	S55092	hypothetical prote	780	703	2	T39997	Thalp - fission ye
708	31	43.1	453	2	S58318	SlyA1 protein - ye	781	703	2	B34434	arylphorin beta ch
709	31	43.1	454	2	D75446	oxidoreductase - D	782	704	2	H95850	probable hydantoin
710	31	43.1	454	2	AC0862	conserved hypotet	783	715	2	T15124	hypothetical prote
711	31	43.1	454	2	A85931	hypothetical prote	784	724	2	C49423	semaphorin II prec
712	31	43.1	454	2	G65061	hypothetical prote	785	725	2	AG2547	hypothetical prote
713	31	43.1	454	2	G91085	hypothetical prote	786	730	2	T05345	hypothetical prote
714	31	43.1	456	2	A60090	peripherin - Afric	787	770	2	T04792	hypothetical prote
715	31	43.1	462	2	T47808	allyl alcohol deny	788	777	2	T00208	transposase-like p
716	31	43.1	463	2	T45756	hypothetical prote	789	783	2	S51968	probable membrane
717	31	43.1	464	2	AE2650	glutamine syntheta	790	787	2	T16901	hypothetical prote
718	31	43.1	466	2	E84132	aminopeptidase BH3	791	801	2	B83195	hypothetical prote
719	31	43.1	467	1	MNVUW1	nonstructural prot	792	801	2	G82302	probable cellobios
720	31	43.1	468	2	A37176	glutamate-ammonia	793	802	2	S49252	penicillin amidase
721	31	43.1	469	2	A64411	hypothetical prote	794	802	2	I39665	penicillin amidase
722	31	43.1	476	2	T05269	adenyl cyclase-a	795	825	1	GLHQ	UDP-N-acetylmuram
723	31	43.1	477	2	H75026	oligopeptide abc t	796	833	2	B81737	probable endopepti
724	31	43.1	479	2	D97432	probable glutamine	797	848	2	C70834	disease resistance
725	31	43.1	481	2	T14300	hypothetical prote	798	853	2	T17461	probable endopepti
726	31	43.1	489	2	AF2970	conserved hypotet	799	857	2	E87546	TonB-dependent rec
727	31	43.1	489	2	D98312	hypothetical prote	800	881	2	T31739	hypothetical prote
728	31	43.1	491	2	B81558	conserved hypotet	801	885	1	T04321	endopeptidase la h
729	31	43.1	496	2	AE0305	probable sugar tra	802	892	2	D69393	large helicase-rel
730	31	43.1	502	2	T26256	hypothetical prote	803	900	2	T33482	hypothetical prote
731	31	43.1	506	1	ACRYG1	nicotinic acetylch	804	920	2	T40771	hypothetical prote
732	31	43.1	506	2	T07209	H+-transporting tw	805	926	2	T04679	hypothetical prote
733	31	43.1	506	2	G86509	monooxygenase [imp	806	940	2	AB1744	internalin protein
734	31	43.1	506	2	A72113	monooxygenase - Ch	807	958	2	S73012	polyketide synthas
735	31	43.1	508	2	S51809	phosphoprotein pho	808	968	2	C82452	hypothetical prote
736	31	43.1	510	2	C84718	probable kinesin 1	809	992	2	S04781	excinuclease ABC c
737	31	43.1	512	2	AD0416	probable type II s	810	1018	2	B83099	probable RND efflu
738	31	43.1	514	2	S12394	probable transport	811	1019	1	A45341	major structural c
739	31	43.1	514	2	A71362	probable nitrogen	812	1056	2	S55151	probable membrane
740	31	43.1	519	2	S58155	RNA binding protei	813	1076	2	I39580	nccA protein - Alic
741	31	43.1	530	1	B82271	transglycosylase,	814	1077	2	D90387	peptidase related
742	31	43.1	538	2	BWB5D5	BUD5 protein - yea	815	1079	2	C96772	probable receptor
743	31	43.1	543	2	T37570	WD repeat protein	816	1085	2	S55352	IFH1 protein - yea
744	31	43.1	544	2	F97170	uncharacterized co	817	1088	1	YGBSTB	phenylalanine race
745	31	43.1	549	2	H07074	probable atpA prot	818	1091	2	T48444	hypothetical prote
746	31	43.1	550	2	E72481	hypothetical prote	819	1104	2	A60999	alpha-amylase (EC
747	31	43.1	550	2	T22557	hypothetical prote	820	1104	2	S36773	GPrase-activation f
748	31	43.1	550	2	T32543	hypothetical prote	821	1147	2	T42627	ADP-ribosylation f
749	31	43.1	557	2	AF3091	hypothetical prote	822	1165	2	A48667	peroxisomal assemb
750	31	43.1	557	2	D98195	hypothetical prote	823	1215	2	H84513	probable disease r
751	31	43.1	558	2	T34028	hypothetical prote	824	1235	2	AC1358	ATP-dependent deox
752	31	43.1	559	2	S54358	transcription fact	825	1270	2	T51227	related to verruco
753	31	43.1	563	2	T40705	conserved hypotet	826	1279	2	T41389	rna binding protei
754	31	43.1	566	2	A84562	probable integral	827	1335	2	JQ1258	RNA-directed RNA p
755	31	43.1	568	2	F86224	hypothetical prote	828	1429	2	T13720	gene expanded prot
756	31	43.1	581	2	S49096	penicillin-binding	829	1454	2	S48264	protein kinase vps
757	31	43.1	582	2	S49097	penicillin-binding	830	1474	2	F69009	probable membrane
758	31	43.1	582	2	S49091	penicillin-binding	831	1531	2	T42218	slit-1 protein hom
759	31	43.1	582	2	A36190	penicillin-binding	832	1613	2	D90129	hypothetical prote

833	31	43.1	1871	2	A87204	polyketide synthas	906	30	41.7	206	1	E70197	conserved hypothet
834	31	43.1	2021	2	A22267	serine/threonine k	907	30	41.7	208	2	F97570	GTP cyclohydrolase
835	31	43.1	2114	2	E96505	hypothetical prote	908	30	41.7	208	2	A27291	GTP cyclohydrolase
836	31	43.1	2345	1	A35578	acetyl-CoA carboxy	909	30	41.7	210	2	H82747	ubiquinol cytochro
837	31	43.1	3165	2	S15010	hypothetical prote	910	30	41.7	210	2	T17910	hypothetical prote
838	31	43.1	4092	1	S38128	dynein heavy chain	911	30	41.7	210	2	C97260	probable membrane
839	31	43.1	4196	2	T43274	dynein heavy chain	912	30	41.7	211	2	H69539	SSU ribosomal prot
840	31	43.1	4344	1	A53489	dynein heavy chain	913	30	41.7	213	2	S29924	cyclin 1 - alfalfa
841	31	43.1	4845	2	T31067	BIR repeat contain	914	30	41.7	215	2	F71456	hypothetical prote
842	30.5	42.4	69	2	A05061	hypothetical prote	915	30	41.7	216	2	T45901	GTPase AtRAB8 - Ar
843	30.5	42.4	70	2	T07575	ribosomal protein	916	30	41.7	217	1	WJWSX2	homocyst protein H
844	30.5	42.4	111	2	E64219	ribosomal protein	917	30	41.7	218	1	Q8EC24	probable transcrip
845	30.5	42.4	286	2	S75740	hypothetical prote	918	30	41.7	218	2	AE0749	invasion response-
846	30.5	42.4	368	2	F48864	hypothetical prote	919	30	41.7	218	2	E85808	probable 2-compone
847	30.5	42.4	420	2	F51088	l-SF precursor - J	920	30	41.7	218	2	D90960	probable 2-compone
848	30.5	42.4	447	2	G70030	amino acid permeas	921	30	41.7	220	2	C40818	hypothetical prote
849	30.5	42.4	495	2	T25066	probable farnesyl	922	30	41.7	221	2	T25027	hypothetical prote
850	30.5	42.4	498	2	G70964	probable arsc prot	923	30	41.7	224	2	F81329	probable two-compo
851	30.5	42.4	533	2	E95160	hypothetical prote	924	30	41.7	224	2	F90606	conserved hypothet
852	30.5	42.4	553	2	D98026	hypothetical prote	925	30	41.7	224	2	T32185	hypothetical prote
853	30.5	42.4	611	2	E72114	oligoendopeptidase	926	30	41.7	224	2	S64867	probable membrane
854	30.5	42.4	611	2	H86507	oligoendopeptidase [im	927	30	41.7	231	2	D81283	hypothetical prote
855	30.5	42.4	768	2	G82251	cation transport A	928	30	41.7	235	2	T40009	hypothetical prote
856	30.5	42.4	3712	1	YGC25V	alpha-aminoacyl-	929	30	41.7	235	2	B72369	ABC transporter, A
857	30	41.7	52	2	AF2556	hypothetical prote	930	30	41.7	237	2	T47499	hypothetical prote
858	30	41.7	61	2	S66329	protein kinase AK1	931	30	41.7	242	2	G90104	putative tetramer
859	30	41.7	64	2	F48858	hypothetical prote	932	30	41.7	242	2	E81337	ABC-transporter Ar
860	30	41.7	69	2	A3620	hypothetical prote	933	30	41.7	244	2	F96733	hypothetical prote
861	30	41.7	71	2	P82606	hypothetical prote	934	30	41.7	244	2	H97139	phage related anti
862	30	41.7	76	2	I59567	histone H2A - rat	935	30	41.7	246	2	AH0393	probable exported
863	30	41.7	86	2	S20849	Ig heavy chain V r	936	30	41.7	251	2	C83053	triosephosphate is
864	30	41.7	96	2	H86681	prophage pil prote	937	30	41.7	251	2	G84957	di-trans,poly-cis-
865	30	41.7	101	2	T17689	hypothetical prote	938	30	41.7	252	2	B84097	cyclase hisF (impo
866	30	41.7	111	2	B72476	hypothetical prote	939	30	41.7	252	2	A12523	site-specific DNA-
867	30	41.7	116	2	S56693	glutathione peroxi	940	30	41.7	253	2	G70317	cyclase hisF [imi
868	30	41.7	121	2	C86783	hypothetical prote	941	30	41.7	254	1	G64346	hypothetical prote
869	30	41.7	123	2	T17538	hypothetical prote	942	30	41.7	254	2	E97242	signal peptidase t
870	30	41.7	127	2	PH1421	Ig heavy chain V r	943	30	41.7	256	2	AH3562	triose-phosphate i
871	30	41.7	128	2	S06986	probable nitrogen	944	30	41.7	256	2	I49846	spaz9 protein - Sh
872	30	41.7	129	2	C97182	biotin carboxyl ca	945	30	41.7	256	2	B75079	hypothetical prote
873	30	41.7	132	2	PH1427	Ig heavy chain V r	946	30	41.7	257	2	H95163	hydrolase, haloaci
874	30	41.7	133	2	AP1077	PTS system, fructo	947	30	41.7	257	2	G98029	N-acetyl-glucosami
875	30	41.7	135	2	S34192	cysB protein - Thi	948	30	41.7	259	2	AD3141	hypothetical prote
876	30	41.7	136	2	T22797	hypothetical prote	949	30	41.7	259	2	H98146	probable amino-aci
877	30	41.7	138	2	AE1324	PTS mannose-specif	950	30	41.7	261	2	B97028	probable xylanase/
878	30	41.7	141	2	T40501	60s ribosomal prot	951	30	41.7	262	2	T01562	hypothetical prote
879	30	41.7	142	2	T03074	dual specificity p	952	30	41.7	262	2	B97310	probable amidohedr
880	30	41.7	143	2	T45259	hypothetical prote	953	30	41.7	262	2	F97009	uncharacterized co
881	30	41.7	146	2	G69020	conserved hypothet	954	30	41.7	263	2	S30400	hypothetical prote
882	30	41.7	147	2	B69040	hypothetical prote	955	30	41.7	265	2	H84005	hypothetical prote
883	30	41.7	147	2	AH2948	hypothetical prote	956	30	41.7	265	2	E89891	conserved hypothet
884	30	41.7	147	2	B98334	hypothetical prote	957	30	41.7	266	2	B70132	bacitracin resista
885	30	41.7	150	2	I70163	integrin beta 3 su	958	30	41.7	266	2	AH2467	transcription regu
886	30	41.7	150	2	C86876	hypothetical prote	959	30	41.7	267	2	B71828	phosphatidylserine
887	30	41.7	151	2	E43584	15K cysteine-rich	960	30	41.7	270	2	G90595	conserved hypothet
888	30	41.7	154	2	S17149	rusticyanin - Thio	961	30	41.7	271	2	JN0850	hypothetical 28.3k
889	30	41.7	155	2	S29825	rusticyanin - Thio	962	30	41.7	272	2	F75412	spemidine/putresc
890	30	41.7	158	2	B71190	hypothetical prote	963	30	41.7	275	2	F84088	N-acetylmuramoyl-L
891	30	41.7	161	2	AD2214	hypothetical prote	964	30	41.7	275	2	T24608	hypothetical prote
892	30	41.7	164	2	T20143	hypothetical prote	965	30	41.7	275	2	E90501	hypothetical prote
893	30	41.7	167	1	S33618	glutathione peroxi	966	30	41.7	276	2	S27641	hypothetical prote
894	30	41.7	167	2	H86784	VPS29-like phospho	967	30	41.7	278	2	AC3479	ATP-dependent heli
895	30	41.7	169	2	G83992	cell-cycle regulat	968	30	41.7	279	2	T47942	hypothetical prote
896	30	41.7	169	2	E97775	hypothetical prote	969	30	41.7	279	2	AC3114	hypothetical prote
897	30	41.7	172	2	B95361	protein [imported	970	30	41.7	280	2	T04769	hypothetical prote
898	30	41.7	173	2	T31343	hypothetical prote	971	30	41.7	280	2	E85225	hypothetical prote
899	30	41.7	175	2	S14023	hypothetical prote	972	30	41.7	281	1	S26018	NADH2 dehydrogenas
900	30	41.7	180	2	T12633	glutathione peroxi	973	30	41.7	284	1	S74516	(adenine-N6,N6-)-d
901	30	41.7	184	2	S73532	ribosome releasing	974	30	41.7	284	1	F64338	agmatinase (EC 3.5
902	30	41.7	186	2	T17497	ankyrin repeat pro	975	30	41.7	288	2	H90216	hypothetical prote
903	30	41.7	186	2	S42941	hypothetical prote	976	30	41.7	289	2	S04648	ampr protein - Rho
904	30	41.7	201	2	F72390	viral infectivity	977	30	41.7	290	2	B69772	conserved hypothet
905	30	41.7	203	2	T23282	hypothetical prote	978	30	41.7	293	2	D90153	cobalamin biosynth

979 30 41.7 294 2 S44080 beta-lactamase (BC
980 30 41.7 294 2 AD2387 hypothetical prote
981 30 41.7 298 1 C42902 3-hydroxyisobutyra
982 30 41.7 298 2 C55223 minor tail protein
983 30 41.7 299 1 RPSCGP glycerol-3-phospha
984 30 41.7 300 2 A69351 heterodisulfide re
985 30 41.7 301 2 D90224 spermidine synthas
986 30 41.7 301 2 T24993 hypothetical prote
987 30 41.7 302 2 S61836 cher protein - Rhi
988 30 41.7 302 2 B98173 hypothetical prote
989 30 41.7 305 2 AC25010 pectinesterase (BC
990 30 41.7 308 2 C84072 UDP-glucose 4-epim
991 30 41.7 309 2 F72368 hypothetical prote
992 30 41.7 309 2 AH3122 IS3 family transpo
993 30 41.7 309 2 G98164 IS3 family orfB pr
994 30 41.7 310 2 AC2035 phytoene synthase
995 30 41.7 311 2 F72487 hypothetical prote
996 30 41.7 312 2 F86044 secreted protein E
997 30 41.7 312 2 B91198 EspB protein (limp
998 30 41.7 313 2 AC1101 L-lactate dehydrog
999 30 41.7 313 2 AC1463 L-lactate dehydrog
1000 30 41.7 313 2 T30139 hypothetical prote

ALIGNMENTS

RESULT 1
B48089 growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: B48089
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: B48089
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:41-92/Domain: Gla domain homology #status atypical <GLA>
F:120-153/Domain: EGF homology <EG1>
F:160-195/Domain: EGF homology <EG2>
F:201-236/Domain: EGF homology <EG3>
F:242-277/Domain: EGF homology <EG4>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 284 VPFSVAKSVKSLYL 298

RESULT 2
A48089 growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: A48089; S37437
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: A48089

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 95.8%; Score 69; DB 2; Length 673;
Best Local Similarity 93.3%; Pred. No. 8.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSVAKSVKSLYL 295

RESULT 3
I55476 growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55476
R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.;
J. Biol. Chem. 270, 5702-5705, 1995
A:Title: Vascular smooth muscle cell-derived, Gla-containing growth-potentiating factor f
A:Reference number: I55476; MUID:95197586; PMID:7890695

A:Accession: I55476
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-674 <RES>
A:C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:29-89/Domain: Gla domain homology <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 95.8%; Score 69; DB 2; Length 674;
Best Local Similarity 93.3%; Pred. No. 8.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSVAKSVKSLYL 295

RESULT 4
S28285 hypothetical protein C38C10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S28285
R:Thomas, K.
Submitted to the EMBL Data Library, December 1992

A:Reference number: S28285
A:Accession: S28285
A:Molecule type: DNA
A:Residues: 1-374 <THO>
A:C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

A:Reference number: S28285
A:Accession: S28285
A:Molecule type: DNA
A:Residues: 1-374 <THO>
A:C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

C:Accession: S48877; S64008
R:Cunningham, K.W.; Fink, G.R.
J. Cell Biol. 124, 351-363, 1994
A:Title: Calceinurin-dependent growth control in *Saccharomyces cerevisiae* mutants lacking
A:Reference number: S48877; MUID:94124630; PMID:7507493
A:Accession: S48877
A:Molecule type: DNA
A:Residues: 1-1173 <CUN>
A:Cross-references: UNIPROT:P38929; EMBL:U03060; NID:G454002; PIDN:AAC48919.1; PID:G45400
R:Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64003
A:Accession: S64008
A:Molecule type: DNA
A:Residues: 1-1173 <HEB>
A:Cross-references: EMBL:Z72528; NID:G1322456; PIDN:CAA96706.1; PID:G1322457; MIPS:YGL00
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PMCL
A:Cross-references: SGD:S0002974; MIPS:YGL006W
A:Map position: 7L
A:Function:
A:Description: pumps Ca2+ into the vacuole; participates in the control of the cytosolic
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: calcium transport; hydrolase; transmembrane protein; yeast vacuole
F:119-135/Domain: transmembrane #status predicted <TM1>
F:157-173/Domain: transmembrane #status predicted <TM2>
F:344-360/Domain: transmembrane #status predicted <TM3>
F:386-402/Domain: transmembrane #status predicted <TM4>
F:732-907/Domain: ATPase nucleotide-binding domain homology <ATN>
F:904-920/Domain: transmembrane #status predicted <TM5>
F:933-949/Domain: transmembrane #status predicted <TM6>
F:978-994/Domain: transmembrane #status predicted <TM7>
F:1068-1084/Domain: transmembrane #status predicted <TM8>
F:1101-1117/Domain: transmembrane #status predicted <TM9>

Query Match 56.9%; Score 41; DB 2; Length 1173;
Best Local Similarity 46.2%; Pred. No. 34;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
DB 1089 PFSIARQTKSMWI 1101
|||:|: |||:
|||:|: |||:

RESULT 10
VGUVRF
M polyprotein - Rift Valley fever virus (strain ZH-548M12)
N:Contains: glycoprotein G1; glycoprotein G2; nonstructural protein NS-M
C:Species: Rift Valley fever virus
A:Notes: host (mosquito); Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: A30183
R:Takehara, K.; Min, M.K.; Battles, J.K.; Sugiyama, K.; Emery, V.C.; Dalrymple, J.M.; Bi
Virology 169, 452-457, 1989
A:Title: Identification of mutations in the M RNA of a candidate vaccine strain of Rift
A:Reference number: A30183; MUID:89204917; PMID:2705307
A:Accession: A30183
A:Molecule type: Genomic RNA
A:Residues: 1-1197 <TAK>
A:Cross-references: UNIPROT:P21401; GB:M25276; NID:G538444; PIDN:AAA47449.1; PID:G538445
C:Genetics:
A:Map position: segment M
C:Superfamily: phlebovirus M polyprotein
C:Keywords: glycoprotein; nonstructural protein; polyprotein
F:1-153/Product: nonstructural protein NS-M #status predicted <NSM>
F:154-690/Product: glycoprotein G1 #status predicted <GG1>
F:691-1197/Product: glycoprotein G2 #status predicted <GG2>
F:88,438,794,829,1035,1077/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 41; DB 1; Length 1197;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 343 VPFAVFKNSKKVYL 356
|||:|: |||:
|||:|: |||:

RESULT 11
VGUVRF
M polyprotein - Rift Valley fever virus (strain ZH-501)
N:Contains: glycoprotein G1; glycoprotein G2; nonstructural protein NS-M
C:Species: Rift Valley fever virus
A:Note: host (mosquito); Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C:Accession: A04110
R:Collett, M.S.; Purchio, A.F.; Keegan, K.; Frazier, S.; Hays, W.; Anderson, D.K.; Parker
Virology 144, 228-245, 1985
A:Title: Complete nucleotide sequence of the M RNA segment of Rift valley fever virus.
A:Reference number: A04110; MUID:86045943; PMID:2998042
A:Accession: A04110
A:Molecule type: genomic RNA
A:Residues: 1-1206 <COL>
A:Cross-references: UNIPROT:P03518
C:Genetics:
A:Map position: segment M
C:Superfamily: phlebovirus M polyprotein
C:Keywords: glycoprotein; nonstructural protein; polyprotein
F:1-153/Product: nonstructural protein NS-M #status predicted <NSM>
F:154-690/Product: glycoprotein G1 #status predicted <GG1>
F:691-1206/Product: glycoprotein G2 #status predicted <GG2>
F:88,794,1035,1077/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 41; DB 1; Length 1206;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 343 VPFAVFKNSKKVYL 356
|||:|: |||:
|||:|: |||:

RESULT 12
D70335
hypothetical protein aq_391 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: D70335
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: D70335
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-250 <AQF>
A:Cross-references: UNIPROT:O66712; GB:AE000688; NID:G2983063; PIDN:AAC06677.1; PID:G2983
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_391
C:Superfamily: Aquifex aeolicus hypothetical protein aq_391
Query Match 55.6%; Score 40; DB 2; Length 250;
Best Local Similarity 53.8%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 13
DB 181 IPFDVGKSVKTAW 193
|||:|: |||:
|||:|: |||:

RESULT 13
A48359
glutamyl-tRNA reductase (EC 1.2.1.1-) Hema - Chlorobium vibrioforme

C;Species: Chlorobium vibrioforme
 C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A48359; S27546
 R;Majumdar, D.; Avisar, Y.J.; Wyche, J.H.; Beale, S.I.
 Arch. Microbiol. 156, 281-289, 1991
 A;Title: Structure and expression of the Chlorobium vibrioforme hema gene.
 A;Reference number: A48359; MUID:92171712; PMID:1793335
 A;Accession: A48359
 A;Molecule type: DNA
 A;Residues: 1-415 <MAJ>
 A;Cross-references: UNIPROT:P28462; EMBL:M59194; NID:g144474; PID:g144475
 A;Note: submitted to the EMBL Data Library, July 1991
 A;Note: sequence extracted from NCBI backbone (NCBIN:86184, NCBI:P:86186)
 C;Function:
 A;Description: catalyzes the reduction of glutamyl-tRNA (GLU) by NADPH to glutamic acid
 A;Pathway: aminolevulinate biosynthesis; porphyrin biosynthesis
 C;Superfamily: glutamyl-tRNA reductase
 C;Keywords: aminolevulinate biosynthesis; NADP; oxidoreductase; porphyrin biosynthesis

Query Match 55.8%; Score 40; DB 1; Length 415;
 Best Local Similarity 80.0%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRSVAKSVKS 11
 ||||| ||:
 Db 145 PFSVAKVKVT 154

RESULT 14
 T08268
 conserved hypothetical protein H0581 - Halobacterium sp. (strain NRC-1) plasmid pNRC100
 N;Alternate names: hypothetical protein H1776
 C;Species: Halobacterium sp.
 A;Variety: strain NRC-1
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T08375
 R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bungarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
 Genome Res. 8, 1131-1141, 1998
 A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or
 A;Reference number: Z16408; MUID:99063795; PMID:9847077
 A;Accession: T08268
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-421 <NGW>
 A;Cross-references: UNIPROT:O54630; EMBL:AF016485; NID:g2822278; PID:g2822329; HALOSP:H0
 A;Experimental source: strain NRC-1
 A;Genetics: COP1
 A;Accession: T08375
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-421 <DAS>
 A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822436; HALOSP:H1776
 A;Experimental source: strain NRC-1
 A;Genetics: COP2
 C;Genetics: <COP1>
 A;Gene: HALOSP:H0581
 A;Genome: plasmid pNRC100
 C;Genetics: <COP2>
 A;Gene: HALOSP:H1776
 A;Genome: plasmid pNRC100
 C;Superfamily: hypothetical protein b2322

Query Match 54.2%; Score 39; DB 2; Length 421;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 ||: ||: ||:
 Db 60 VSFGIVKSIILNLYAG 74

RESULT 15
 T48015
 conserved hypothetical protein T23F1.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T25168
 R;Wilkinson, J.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z19990
 A;Accession: T25168
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1362 <WIL>
 A;Cross-references: UNIPROT:O18117; EMBL:Z81129; PIDN:CAB03404.1; GSPDB:GN00023; CESP:T2;
 A;Experimental source: clone T23F1
 C;Genetics:
 A;Gene: CESP:T23F1.5
 A;Map position: 5
 A;Introns: 49/3; 201/1; 505/3; 609/3; 909/1; 944/2; 1025/2; 1079/1; 1168/3; 1225/1

Query Match 54.2%; Score 39; DB 2; Length 1262;
 Best Local Similarity 42.9%; Pred. No. 87;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 15
 ||: ||: ||:
 Db 363 PFNDLKTIRPIYL 376

RESULT 17
 S60949
 probable phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein O5064; protein YOR222w; protein YOR50-12
 C;Species: Saccharomyces cerevisiae
 C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S60949; S67115; B37984; S71724
 R;Gallison, F.; Dujon, B.
 submitted to the EMBL Data Library, October 1995
 A;Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosome
 A;Reference number: S60938
 A;Accession: S60949
 A;Molecule type: DNA
 A;Residues: 1-307 <GAL>
 A;Cross-references: UNIPROT:Q99297; EMBL:X92441; NID:g1050762; PID:g1050774
 R;Boyer, J.; Fairhead, C.; Gaillon, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon, B.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S67104

hypothetical protein T17J13.190 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: T48015
 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, T.
 submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24482
 A;Accession: T48015
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-461 <RIE>
 A;Cross-references: UNIPROT:O9M101; EMBL:AL138651
 A;Experimental source: cultivar Columbia; BAC clone T17J13
 C;Genetics:
 A;Map position: 3
 A;Note: T17J13.190

Query Match 54.2%; Score 39; DB 2; Length 461;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
 : ||: ||: ||:
 Db 111 IEFVSKNVKHLFL 124

RESULT 16
 T25168
 hypothetical protein T23F1.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T25168
 R;Wilkinson, J.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z19990
 A;Accession: T25168
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1362 <WIL>
 A;Cross-references: UNIPROT:O18117; EMBL:Z81129; PIDN:CAB03404.1; GSPDB:GN00023; CESP:T2;
 A;Experimental source: clone T23F1
 C;Genetics:
 A;Gene: CESP:T23F1.5
 A;Map position: 5
 A;Introns: 49/3; 201/1; 505/3; 609/3; 909/1; 944/2; 1025/2; 1079/1; 1168/3; 1225/1

Query Match 54.2%; Score 39; DB 2; Length 1262;
 Best Local Similarity 42.9%; Pred. No. 87;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 15
 ||: ||: ||:
 Db 363 PFNDLKTIRPIYL 376

RESULT 17
 S60949
 probable phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein O5064; protein YOR222w; protein YOR50-12
 C;Species: Saccharomyces cerevisiae
 C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S60949; S67115; B37984; S71724
 R;Gallison, F.; Dujon, B.
 submitted to the EMBL Data Library, October 1995
 A;Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosome
 A;Reference number: S60938
 A;Accession: S60949
 A;Molecule type: DNA
 A;Residues: 1-307 <GAL>
 A;Cross-references: UNIPROT:Q99297; EMBL:X92441; NID:g1050762; PID:g1050774
 R;Boyer, J.; Fairhead, C.; Gaillon, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon, B.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S67104

C:Accession: S67115
A:Molecule type: DNA
A:Residues: 1-307 <BOY>
A:Cross-references: EMBL:Z75130; NID:g1420513; PID:g1420514; MIPS:YOR222w
A:Experimental source: strain S288C
R:Guerin, B.; Bukusoglu, C.; Rakotomanana, F.; Wohlrab, H.
J. Biol. Chem. 265, 19736-19741, 1990
A:Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity correlates with
A:Reference number: A37984; MUID:91060585; PMID:2246257
A:Accession: B37984
A:Molecule type: protein
A:Residues: 30,'X',32,'I',34-39 <GUE>
R:Galisson, P.; Dujon, B.
Yeast 12, 877-885, 1996
A:Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of
A:Reference number: S71713; MUID:96437977; PMID:8840505
A:Accession: S71724
A:Molecule type: DNA
A:Residues: 1-307 <GAW>
A:Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63185.1; PID:g1050774
C:Genetics:
A:Gene: SGD:ODC2
A:Cross-references: SGD:S0005748
A:Map position: 15R
A:Note: YOR222w
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:9-107/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:115-201/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:208-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>
Query Match 52.8%; Score 38; DB 2; Length 307;
Best Local Similarity 52.6%; Pred. No. 30;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 VPFSVAK----SVKSLYL 15
|||:| ||| |||
DB 137 VPFEIKIRMQDVKSYL 155
|||:| ||| |||
RESULT 18
C75012
hypothetical protein PAB1275 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75012
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: C75012
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <KAW>
A:Cross-references: UNIPROT:Q9UY75; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5053
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1275
Query Match 52.8%; Score 38; DB 2; Length 317;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 14
|||:| ||| |||
DB 27 VPFGLENSIKSLVI 40
|||:| ||| |||
RESULT 19
B83902
transcription repressor (beta-galactosidase gene) lacR [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: B83902
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83902
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <STO>
A:Cross-references: UNIPROT:Q9KBB0; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB0573
A:Experimental source: strain C-125
C:Genetics:
A:Gene: lacR
C:Superfamily: lac repressor
Query Match 52.8%; Score 38; DB 2; Length 330;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 7 KSVKSLYL 15
|||:| ||| |||
DB 312 KSVKTLYL 320
|||:| ||| |||
RESULT 20
S59308
probable membrane protein YMR315w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YM924.07
C:Species: Saccharomyces cerevisiae
C:Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: S59308
R:Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A:Reference number: S59302
A:Accession: S59308
A:Molecule type: DNA
A:Residues: 1-349 <CHU>
A:Cross-references: UNIPROT:Q04869; EMBL:Z54141; NID:g1072408; PID:g984688; GSPDB:GN00013
A:Experimental source: strain AB972
C:Genetics:
A:Gene: MIPS:YMR315w
A:Cross-references: SGD:S0004932
A:Map position: 13R
C:Superfamily: Streptomyces griseus strI protein
C:Keywords: transmembrane protein
F:189-205/Domain: transmembrane #status predicted <TMM>
Query Match 52.8%; Score 38; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 15
|||:| ||| |||
DB 307 AVSKKDSLYL 318
|||:| ||| |||
RESULT 21
T03841
patatin homolog - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
R:Accession: T03841
R:Drews, G.N.; Beals, T.P.; Bui, A.Q.; Goldberg, R.B.
Plant Cell 4, 1383-1404, 1992
A:Title: Regional and cell-specific gene expression patterns during petal development.
A:Reference number: Z15112; MUID:93120883; PMID:1477554
A:Accession: T03841
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-390 <DRE>
A:Cross-references: UNIPROT:O24152; EMBL:U68484; NID:g1546816; PIDN:AAB08428.1; PID:g1546
C:Superfamily: patatin

Query Match 52.8%; Score 38; DB 2; Length 390;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
DB 95 PFSAAKDIVSFY 106
|||||:|:|

RESULT 22
T51407
proline-rich protein - Arabidopsis thaliana
N;Alternate names: protein F14P8_160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51407
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A;Reference number: 225394
A;Accession: T51407
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <SAT>
A;Cross-references: UNIPROT:Q9LFU8; EMBL:AL391144
A;Experimental source: cultivar Columbia; BAC clone F14P8
C;Genetics:
A;Map position: 5
A;Introns: 66/1
A;Note: F14P8_160

Query Match 52.8%; Score 38; DB 2; Length 401;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
DB 98 LPFSVSKHVKKI 109
:||||:|:|

RESULT 23
PWKWA
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - Chlamydomonas reinhardtii
N;Alternate names: adenosinetriphosphatase
C;Species: chloroplast Chlamydomonas reinhardtii
C;Date: 31-Mar-1992 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: S20503; A05002; S17093; S68388
R;Leu, S.; Schlesinger, J.; Michaels, A.; Shavit, N.
Plant Mol. Biol. 18, 613-616, 1992
A;Title: Complete DNA sequence of the Chlamydomonas reinhardtii chloroplast atpA gene.
A;Reference number: S20503; MUID:92163030; PMID:1531617
A;Accession: S20503
A;Molecule type: DNA
A;Residues: 1-508 <LEU>
A;Cross-references: UNIPROT:P26526; GB:X60298; NID:g11427
R;Dron, M.; Rahire, M.; Rochaix, J.D.
J. Mol. Biol. 162, 775-793, 1982
A;Title: Sequence of the chloroplast DNA region of Chlamydomonas reinhardtii containing
A;Reference number: A92892; MUID:83189072; PMID:6302265
A;Accession: A05002
A;Molecule type: DNA
A;Residues: 1-112 <DRO>
A;Cross-references: GB:J01399; NID:g336683
R;Leu, S.; Schlesinger, J.; Michaels, A.; Shavit, N.
submitted to the EMBL Data Library, September 1991
A;Reference number: S17093
A;Accession: S17093
A;Molecule type: DNA
A;Residues: 55-112, 'A', 114-508 <LEW>
A;Cross-references: EMBL:X60298; NID:g11427; PIDN:CAA42840.1; PID:g1334356
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A;Title: Isolation of CF(O)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal
A;Reference number: S68388; MUID:96128220; PMID:8543042

A;Accession: S68388
A;Molecule type: protein
A;Residues: 2-9, 'XX', 12-13 <FIE>
A;Experimental source: strain CW15
C;Genetics:
A;Gene: atpA
A;Genome: Chloroplast
C;Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase alpha chain
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucleotide
F;170-177/Region: nucleotide-binding motif A (P-loop)
F;195-367/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
F;258-263/Region: nucleotide-binding motif B #status atypical
F;176/Binding site: ATP (Lys) #status predicted
F;366/Active site: Arg #status predicted

Query Match 52.8%; Score 38; DB 1; Length 508;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLG 15
DB 428 PLSVERQVASLYAG 441
|||||:|:|

RESULT 24
T29550
hypothetical protein ZK377.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29550
R;Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid ZK377.
A;Reference number: Z20639
A;Accession: T29550
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-615 <NHA>
A;Cross-references: UNIPROT:P91573; EMBL:U88183; PIDN:AAB52656.1; GSPDB:GN00028; CESP:ZK377
A;Experimental source: strain Bristol N2; clone ZK377
C;Genetics:
A;Gene: CESP:ZK377.1
A;Map position: X
A;Introns: 46/1; 70/3; 157/2; 176/1; 245/2; 314/3; 402/3; 499/2

Query Match 52.8%; Score 38; DB 2; Length 615;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYLG 15
DB 112 SDAKTIKSIFLG 123
|||||:|:|

RESULT 25
I56258
RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56258
R;Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A;Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a member
A;Reference number: I56258; MUID:95204928; PMID:7897216
A;Accession: I56258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-661 <RES>
A;Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761712

Query Match 52.8%; Score 38; DB 2; Length 661;
Best Local Similarity 46.7%; Pred. No. 68;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
:| | | | | | | | | |
Db 143 IPLNQKLTLESYL 157

RESULT 26
G70446
hypothetical protein aq_1695 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: G70446
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: G70446
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-296 <AQF>
A:Cross-references: UNIPROT:O67600; GB:AE000751; NID:g2984013; PIDN:AAC07562.1; PID:g298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_1695

Query Match 52.1%; Score 37.5; DB 2; Length 296;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 VPFSVAKS-VKSLYL 14
:| | | | | | | | | |
Db 234 IFFERAKSLVKMYL 248

RESULT 27
OYECHF
imidazoleglycerol-phosphate synthase (EC 4.3.2.-) cyclase chain hisF [validated] - Esche
N:Alternate names: cyclase
C:Species: Escherichia coli
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: JS0134; I76779; H64967
R:Carlomagno, M.S.; Chiarottili, L.; Alifano, P.; Nappo, A.G.; Bruni, C.B.
J. Mol. Biol. 203, 585-606, 1988
A:Title: Structure and function of the Salmonella typhimurium and Escherichia coli K-12
A:Reference number: JS0131; MUID:89094829; PMID:3062174
A:Accession: JS0134
A:Molecule type: DNA
A:Residues: 1-258 <CAR>
A:Cross-references: UNIPROT:P60664; GB:X13462; NID:g41706; PIDN:CAA31817.1; PID:g41714
A:Experimental source: strain K12
R:Sugiyama, T.; Kido, N.; Komatsu, T.; Ohta, M.; Jann, K.; Jann, B.; Saeki, A.; Kato, N.
Microbiology 140, 59-71, 1994
A:Title: Genetic analysis of Escherichia coli O9 rfb: identification and DNA sequence of
A:Reference number: I57096; MUID:94214678; PMID:8162191
A:Accession: I76779
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 109-258 <RES>
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:197426617; PMID:9278503
A:Accession: H64967
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-258 <BLAT>
A:Cross-references: GB:AE000293; NID:u00096; NID:g2367127; PIDN:AAC75086.1; PID:g1788336;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: hisF

A:Map position: 44 min
C:Function:
A:Description: catalyzes the cyclization reaction that produces D-erythro-imidazole glyce
A:Pathway: histidine biosynthesis
A>Note: hisH and hisF gene products form a dimer that constitutes imidazole glycerol pho
C:Superfamily: cyclase hisF
C:Keywords: amidine-lyase; carbon-nitrogen lyase; histidine biosynthesis

Query Match 51.4%; Score 37; DB 1; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
:| | | | | | | | | |
Db 75 IFFCVAGGIKSL 86

RESULT 28
B90982
imidazoleglycerol-phosphate synthase (EC 4.3.2.-) cyclase chain hisF [similarity] - Esche
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B90982
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B90982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <HAY>
A:Cross-references: UNIPROT:P60665; GB:BA000007; PIDN:BA836249.1; PID:g13362294; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIND 0509952
C:Genetics:
A:Gene: ECS2826
C:Superfamily: cyclase hisF
C:Keywords: amidine-lyase; carbon-nitrogen lyase

Query Match 51.4%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
:| | | | | | | | | |
Db 75 IFFCVAGGIKSL 86

RESULT 29
H85827
imidazoleglycerol-phosphate synthase (EC 4.3.2.-) cyclase chain hisF [similarity] - Esche
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85827
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85827
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <STO>
A:Cross-references: UNIPROT:P60665; GB:AE005174; NID:g12516206; PIDN:AAG57084.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: hisF
C:Superfamily: cyclase hisF
C:Keywords: amidine-lyase; carbon-nitrogen lyase

Query Match 51.4%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
: || || : ||
Db 75 IPFCVAGGIKSL 86

RESULT 30
B54052
cyclase hisF - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B54052
R:Bieder, G.; Merrick, M.J.; Castorff, H.; Kleiner, D.
J. Biol. Chem. 269, 14386-14390, 1994
A:Title: Function of hisF and hisH gene products in histidine biosynthesis.
A:Reference number: A54052; MUID:94237842; PMID:8182043
A:Accession: B54052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <RIE>
A:Cross-references: UNIPROT:P45603; GB:X56607; NID:G530021; PIDN:CAA3944.1; PID:G530022
A:Experimental source: M5a1
C:Note: sequence extracted from NCBI backbone (NCBIN:148607, NCBIP:148609)
C:Genetics:
A:Gene: hisF
C:Superfamily: cyclase hisF
C:Keywords: histidine biosynthesis

Query Match 51.4%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
: || || : ||
Db 75 IPFCVAGGIKSL 86

RESULT 31
T37185
probable gntR-family transcription regulator - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37185
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T37185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-259 <SEE>
A:Cross-references: UNIPROT:Q9X9TG; EMBL:AL096823; PIDN:CAB46970.1; GSPDB:GN000070; SCOP
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SQ11.15C
C:Superfamily: korA protein

Query Match 51.4%; Score 37; DB 2; Length 259;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
: || || : ||
Db 154 IPFEVAESVPAL 165

RESULT 32
S47620
beta-lactamase - Proteus vulgaris
C:Species: Proteus vulgaris
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S47620
R:Peduzzi, J.; Reynaud, A.; Baron, P.; Barthelemy, M.; Labia, R.
Biochim. Biophys. Acta 1207, 31-39, 1994

QY 1 VPFSVAKSVKSL 12
: || || : ||
Db 159 PIAMAKSLQALTIG 172

RESULT 33
S51044
beta-lactamase - Proteus vulgaris
C:Species: Proteus vulgaris
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51044
R:Datz, M.; Joris, B.; Azab, E.A.M.; Galleni, M.; van Beeumen, J.; Frere, J.M.; Martin, F.
Eur. J. Biochem. 226, 149-157, 1994
A:Title: A common system controls the induction of very different genes. The class-A beta-lactamase
A:Reference number: S51044; MUID:95045583; PMID:7957242
A:Accession: S51044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <DAT>
A:Cross-references: UNIPROT:P52664; EMBL:X80128; NID:G511055; PIDN:CAA56427.1; PID:G511055
C:Superfamily: beta-lactamase I

Query Match 51.4%; Score 37; DB 2; Length 300;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYIG 15
: : || || : : ||
Db 188 PIAMAKSLQALTIG 201

RESULT 34
A55792
beta-lactamase (EC 3.5.2.6) precursor - Proteus vulgaris
C:Species: Proteus vulgaris
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-2004
C:Accession: A55792
R:Tamaki, M.; Nukaga, M.; Sawai, T.
Biochemistry 33, 10200-10206, 1994
A:Title: Replacement of serine 237 in class A beta-lactamase of Proteus vulgaris modifies
A:Reference number: A55792; MUID:94339110; PMID:8060386
A:Accession: A55792
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <TAM>
A:Cross-references: UNIPROT:O52615; GB:D29982; NID:G484056; PIDN:BAA06252.1; PID:G599572
C:Superfamily: Beta-lactamase I
C:Keywords: hydrolase
F:46/Active site: Ser #status predicted

Query Match 51.4%; Score 37; DB 2; Length 300;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYIG 15
: : || || : : ||
Db 188 PIAMAKSLQALTIG 201

RESULT 35

A:Title: Chromosomally encoded cephalosporin-hydrolyzing beta-lactamase of Proteus vulgaris
A:Reference number: S47620; MUID:94318667; PMID:8043607
A:Accession: S47620
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-271 <PED>
A:Cross-references: UNIPROT:P80298
C:Superfamily: beta-lactamase I

SS3908
 hypothetical protein YNL072w - yeast (*Saccharomyces cerevisiae*)
 A:Alternate names: hypothetical protein N2369
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S53908; S63004; S63937
 R:Poehlmann, R.; Philippsen, P.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: S53896
 A:Accession: S53908
 A:Molecule type: DNA
 A:Residues: 1-307 <POE>
 A:Cross-references: UNIPROT:P53942; EMBL:X86470; NID:g791101; PID:g791114
 R:Poehlmann, R.; Philippsen, P.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62997
 A:Accession: S63004
 A:Molecule type: DNA
 A:Residues: 1-307 <POW>
 A:Cross-references: EMBL:X71348; NID:g1301956; PID:e239686; PID:g1301957; MIPS:YNL072w
 A:Experimental source: strain S288C
 R:Poehlmann, R.; Philippsen, P.
 yeast 12, 391-402, 1996
 A:Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12
 A:Reference number: S63937
 A:Accession: S63937
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-307 <POF>
 A:Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60188.1; PID:g791114
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C:Genetics:
 A:Gene: SGD:RNH35
 A:Cross-references: SGD:S0005016; MIPS:YNL072w
 A:Map position: 14L

Query Match 51.4%; Score 37; DB 2; Length 307;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VFPSVAKSVKSLYL 13
 | : | | | | |
 Db 174 VRFTVAKKADSLY 186
 RESULT 36
 A53120
 intracellular coagulation inhibitor LICI precursor - horseshoe crab (*Tachyplesus tridentatus*)
 C:Species: *Tachyplesus tridentatus*
 C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C:Accession: A53120
 R:Mura, Y.; Kawabata, S.; Iwanaga, S.
 J. Biol. Chem. 269, 542-547, 1994
 A:Title: A Limulus intracellular coagulation inhibitor with characteristics of the serpin
 A:Reference number: A53120; MUID:94103268; PMID:8276848
 A:Accession: A53120
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <MIU>
 A:Cross-references: UNIPROT:Q27085; GB:D14483; NID:G441213; PIDN:BAA03374.1; PID:G441214
 C:Superfamily: intracellular coagulation inhibitor LICI
 C:Keywords: serine proteinase inhibitor
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-418/Product: intracellular coagulation inhibitor LICI #status experimental <MAT>

Query Match 51.4%; Score 37; DB 2; Length 418;
 Best Local Similarity 50.0%; Pred. No. 64;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PFSVAKSVKSLYL 15
 | : | | : | | |
 Db 72 PYSLASVAMLYLG 85

RESULT 37
 AG1028
 prepilin [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A:Note: this species has also been called *Salmonella typhi*
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AG1028
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AG1028
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-435 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD09328.1; PID:g16505328; GSPDB:GN00176
 C:Genetics:
 A:Gene: pilV
 C:Superfamily: shufflon
 Query Match 51.4%; Score 37; DB 2; Length 435;
 Best Local Similarity 46.2%; Pred. No. 67;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 3 FSVAKSVKSLYL 15
 | : | : | : | : |
 Db 366 FNVGKNVQYIG 378
 RESULT 38
 G31090
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - *Anabaena* sp.
 C:Species: *Anabaena* sp.
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C:Accession: G31090
 R:McCarn, D.F.; Whitaker, R.A.; Alam, J.; Vrba, J.M.; Curtis, S.E.
 J. Bacteriol. 170, 3448-3458, 1988
 A:Title: Genes encoding the alpha, gamma, delta, and four P-0 subunits of ATP synthase cc
 A:Reference number: A91875; MUID:88298650; PMID:2900236
 A:Accession: G31090
 A:Molecule type: mRNA
 A:Residues: 1-506 <MCC>
 A:Cross-references: UNIPROT:P12405; GB:M21659; NID:g141996; PIDN:AAA21991.1; PID:g142003
 A:Experimental source: PCC 7120
 C:Genetics:
 A:Gene: atpA
 C:Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding;
 F:171-178/Region: nucleotide-binding motif A (P-loop)
 F:196-368/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
 Query Match 51.4%; Score 37; DB 2; Length 506;
 Best Local Similarity 57.1%; Pred. No. 79;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 PFSVAKSVKSLYL 15
 | | | : | | | |
 Db 429 FLSVAEQVAILVAG 442
 RESULT 39
 AE1807
 ATP synthase chain alpha [imported] - *Nostoc* sp. (strain PCC 7120)
 C:Species: *Nostoc* sp. PCC 7120
 A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AE1807
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:2159285; PMID:11759840
A;Accession: AE1807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <KUR>
A;Cross-references: UNIPROT: P12405; GB:BA0000019; PIDN: BAB7529.1; PID: gl7134983; GSPDB: G12405
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: atpA
C;Superfamily: H⁺-transporting ATP synthase alpha chain; H⁺-transporting ATP synthase alpha chain

Query Match 51.4%; Score 37; DB 2; Length 506;
Best Local Similarity 57.4%; Pred. No. 79;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLG 15
|||:|:|:|
Db 429 PLSVAQVAILYAG 442

RESULT 40
C86897
hypothetical protein ywfF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86897
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich, S.; Artigues, C.; et al.
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86897
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-513 <STO>
A;Cross-references: UNIPROT: Q9CDP0; GB:AE005176; PID: gl2725241; PIDN: AAK06277.1; GSPDB: G12725241
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ywfF

Query Match 51.4%; Score 37; DB 2; Length 513;
Best Local Similarity 53.8%; Pred. No. 80;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
:|:|:|:|:|:|
Db 344 IGFVAKVKVSVH 356

RESULT 41
E97854
H⁺-transporting two-sector ATPase (EC 3.6.3.14) - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 03-Jun-2002
C;Accession: E97854
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; et al.
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97854
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <KUR>
A;Cross-references: GB:AE006914; PIDN: AAL03775.1; PID: gl5620371; GSPDB: GN00173
C;Genetics:
A;Gene: atpA
C;Superfamily: H⁺-transporting ATP synthase alpha chain; H⁺-transporting ATP synthase alpha chain
C;Keywords: hydrolase

Query Match 51.4%; Score 37; DB 2; Length 533;
Best Local Similarity 42.9%; Pred. No. 83;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLG 15
|||:|:|:|
Db 458 PPFVEQIVSIYVG 471

RESULT 42

S42459
DNA-directed DNA polymerase (EC 2.7.7.7) Vent, interin containing precursor - Thermococcus
N;Contains: DNA endonuclease (EC 3.1.1.-) PI-I; DNA endonuclease (EC 3.1.1.-) PI-II; DNA
C;Species: Thermococcus litoralis
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S42459; S42451; S42450; S42458
R;Perlier, F.B.; Comb, D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, R.B.; Benner, J.J.
submitted to the EMBL Data Library, September 1992
A;Reference number: S42458
A;Accession: S42459
A;Molecule type: DNA
A;Residues: 1-1702 <PERI>
A;Cross-references: UNIPROT: P30317; EMBL: M74198; NID: gl54685; PIDN: AAA72100.1; PID: gl54685
R;Perlier, F.B.; Comb, D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, R.B.; Benner, J.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 5577-5581, 1992
A;Title: Intervening sequences in an Archaea DNA polymerase gene.
A;Reference number: S42450; MUID: 92302285; PMID: 1508969
A;Accession: S42451

A;Molecule type: DNA

A;Residues: 181-222; 387-425; 452-476; 483-524; 1021-1062; 1076-1099; 1466-1489; 1533-1547 <PERI>
A;Cross-references: EMBL: M74198

R;Hodges, R.A.; Perlier, F.B.; Noren, C.J.; Jack, W.E.

Nucleic Acids Res. 20, 6153-6157, 1992

A;Title: Protein splicing removes intervening sequences in an archaea DNA polymerase.

A;Reference number: S40788; MUID: 93117083; PMID: 1475179

C;Contents: annotation

C;Function: <VENT>

A;Description: nucleotidyltransferase

A;Note: DNA-directed DNA polymerase Vent

C;Function: <END1>

A;Description: endonuclease; hydrolase

A;Note: DNA endonuclease PI-Tlii

C;Function: <END2>

A;Description: endonuclease; hydrolase

A;Note: DNA endonuclease PI-Tlii

C;Superfamily: Thermococcus litoralis DNA-directed DNA polymerase Vent

C;Keywords: DNA binding; endonuclease; hydrolase; nucleotidyltransferase; protein splicing

F;1-494/Domain: DNA-directed DNA polymerase Vent extein 1 #status predicted <XT1>

F;495-1032/Product: DNA endonuclease PI-II (pol Vent extein 1) #status predicted <XT2>

F;1033-1081/Domain: DNA-directed DNA polymerase Vent extein 2 #status predicted <XT2>

F;1082-1471/Product: DNA endonuclease PI-I (pol Vent extein 2) #status predicted <XT3>

F;1472-1702/Domain: DNA-directed DNA polymerase Vent extein 3 #status predicted <XT3>

F;494-1033/Cross-link: peptide (Asn-Ser) #status predicted

F;1081-1472/Cross-link: peptide (Asp-Thr) #status predicted

Query Match 51.4%; Score 37; DB 2; Length 1702;
Best Local Similarity 63.6%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSL 12
|||:|:|:|

Db 1195 PPELGKAVKSL 1205

RESULT 43

T00127

hypothetical protein 5 - Leptospira interrogans

C;Species: Leptospira interrogans

C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004

C;Accession: T00127

R;Takahashi, Y.; Akase, K.; Hirano, H.; Fukunaga, M.

Gene 215, 37-45, 1998

A;Title: Physical and genetic maps of the Leptospira interrogans serovar icterohaemorrhagiae

A;Reference number: Z14115; MUID: 98332717; PMID: 9666070

A:Accession: T00127
 A:Status: preliminary; translated from GB/EMBL/DBDJB
 A:Molecule type: DNA
 A:Residues: 1-437 <YAK>

A:Cross-references: UNIPROT:P97044; EMBL:AB010203; NID:g2780763; PIDN:BAA24374.1; PID:g2780763; strain Ictero No.1; substrain icterohaemorrhagiae
 A:Experimental source: strain Ictero No.1; substrain icterohaemorrhagiae
 C:Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 50.7%; Score 36.5; DB 2; Length 437;
 Best Local Similarity 50.0%; Pred. No. 84; Mismatches 2; Indels 1; Gaps 1;
 Matches 8; Conservative 5;

QY 1 VPFSVAKSVKS-LYLIG 15
 :|: ||||:|:|:|
 Db 304 IPRVAKVRSDLIMG 319

RESULT 44

C91278
 hypothetical protein ECs5195 [imported] - Escherichia coli (strain O157:H7, substrain R1)
 C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: C91278

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: C91278
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-81 <HAY>
 A:Cross-references: UNIPROT:Q8XCG4; GB:BA000007; PIDN:BAE38618.1; PID:g13364672; GSPDB:C91278

A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: ECs5195

Query Match 50.0%; Score 36; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 17; Mismatches 1; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 2 PFSVAKSVKSLYLIG 15
 :|: ||||:|:|:|
 Db 22 PLQVAKYVKILFRG 35

RESULT 45

C86119
 hypothetical protein ytfk [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
 C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C86119

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C86119
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-81 <STO>
 A:Cross-references: UNIPROT:Q8XCG4; GB:AE005174; NID:g12519216; PIDN:AAG59415.1; GSPDB:C86119

A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ytfk

Query Match 50.0%; Score 36; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 17; Mismatches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 2 PFSVAKSVKSLYLIG 15
 :|: ||||:|:|:|
 Db 22 PLQVAKYVKILFRG 35

RESULT 46

D65233

hypothetical 9.6 kD protein in cysg-mara intergenic region - Escherichia coli (strain K-12)

A:Alternate names: hypothetical protein o81
 C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: D65233; S56442

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: D65233

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-81 <BLAT>
 A:Cross-references: UNIPROT:Q8XCG4; GB:AE000493; GB:U00096; NID:g2367360; PIDN:AAC77174.1

A:Experimental source: strain K-12, substrain MG1655
 R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.

Nucleic Acids Res. 23, 2105-2119, 1995
 A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8

A:Reference number: S56314; MUID:95334362; PMID:7610040
 A:Accession: S56442

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 'V', 2-81 <BUR>
 A:Cross-references: EMBL:U14003

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 C:Genetics:
 A:Gene: ytfk

A:Start codon: GTG

Query Match 50.0%; Score 36; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 17; Mismatches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 2 PFSVAKSVKSLYLIG 15
 :|: ||||:|:|:|
 Db 22 PLQVAKYVKILFRG 35

RESULT 47

AH1054

conserved hypothetical protein ytfk [imported] - Salmonella enterica subsp. enterica sero

C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AH1054

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AH1054

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-90 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD06885.1; PID:g16505533; GSPDB:GN00176

C:Genetics:
 A:Gene: ytfk

Query Match 50.0%; Score 36; DB 2; Length 90;
 Best Local Similarity 57.1%; Pred. No. 19; Mismatches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 2 PFSVAKSVKSLYLIG 15
 :|: ||||:|:|:|
 Db 31 PLQVAKYVKILFRG 44

RESULT 48

C90217
hypotheical protein SSO0693 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: C90217
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90217
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <KUR>
A:Cross-references: UNIPROT:Q9UX82; GB:AE006641; NID:gl13813862; PIDN:AAK40994.1; GSPDB:C
C:Genetics:
A:Gene: SSO0693

Query Match 50.0%; Score 36; DB 2; Length 149;
Best Local Similarity 42.9%; Pred. No. 33;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
|: ||| :||
Db 108 IPLYTAKSSSNMYL 121

RESULT 49

AB2147
hypotheical protein alr2729 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AB2147
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2147
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <KUR>
A:Cross-references: UNIPROT:Q8YTI8; GB:BA000019; PIDN:BA874428.1; PID:gl17131822; GSPDB:C
C:Genetics:
A:Experimental source: strain PCC 7120
A:Gene: alr2729

Query Match 50.0%; Score 36; DB 2; Length 166;
Best Local Similarity 58.3%; Pred. No. 37;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
|: ||||| :|
Db 80 PYEVAKSVLNLH 91

RESULT 50

A64209
ribosomal protein L1 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: A64209
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: A64209

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-226 <TIGR>

A:Cross-references: UNIPROT:P47328; GB:U39688; GB:L43967; NID:gl045753; PID:gl045759; TIC

A:Experimental source: strain G-37

C:Genetics:

A:Genetic code: SGC3

C:Superfamily: ribosomal protein L1p/L10e

Query Match 50.0%; Score 36; DB 2; Length 226;

Best Local Similarity 54.5%; Pred. No. 52;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSL 12

Db 66 PFSIGKSIRIL 76

Search completed: July 7, 2005, 09:37:15

Job time : 34.0385 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:31:46 ; Search time 26.044 Seconds
(without alignments)
222.507 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYLIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_5/ptodata/1/pubaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubaa/US10E_PUBCOMB.pep.*

18: /cgn2_6/ptodata/1/pubaa/US10F_PUBCOMB.pep.*

19: /cgn2_6/ptodata/1/pubaa/US11A_PUBCOMB.pep.*

20: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	72	100.0	510	16	US-10-367-094-34	Sequence 34, Appl
2	72	100.0	678	16	US-10-671-054-3	Sequence 3, Appl
3	72	100.0	678	17	US-10-696-909A-41	Sequence 41, Appl
4	72	100.0	686	16	US-10-671-054-1	Sequence 1, Appl
5	69	95.8	673	14	US-10-223-085-48	Sequence 48, Appl
6	69	95.8	673	14	US-10-223-084-48	Sequence 48, Appl
7	69	95.8	673	14	US-10-223-088-48	Sequence 48, Appl
8	69	95.8	673	14	US-10-223-090-48	Sequence 48, Appl
9	69	95.8	673	14	US-10-223-087-48	Sequence 48, Appl
10	69	95.8	673	14	US-10-223-083-48	Sequence 48, Appl
11	69	95.8	673	14	US-10-223-089-48	Sequence 48, Appl

85	36	50.0	900	13	US-10-060-230-15	Sequence 15, Appl	158	35	48.6	421	14	US-10-142-423-302	Sequence 302, App
86	36	50.0	900	13	US-10-060-230-16	Sequence 16, Appl	159	35	48.6	421	14	US-10-121-050-302	Sequence 302, App
87	36	50.0	900	13	US-10-060-230-17	Sequence 17, Appl	160	35	48.6	421	14	US-10-141-755-302	Sequence 302, App
88	36	50.0	900	13	US-10-060-230-18	Sequence 18, Appl	161	35	48.6	421	14	US-10-143-032-302	Sequence 302, App
89	36	50.0	900	15	US-10-369-493-22269	Sequence 22269, A	162	35	48.6	421	14	US-10-123-108-302	Sequence 302, App
90	36	50.0	900	15	US-10-447-515-2	Sequence 2, Appl1	163	35	48.6	421	14	US-10-123-236-302	Sequence 302, App
91	36	50.0	931	14	US-10-198-070-91	Sequence 91, Appl	164	35	48.6	421	14	US-10-123-261-302	Sequence 302, App
92	36	50.0	931	15	US-10-391-399-6	Sequence 6, Appl1	165	35	48.6	421	14	US-10-140-921-302	Sequence 302, App
93	36	50.0	1086	15	US-10-369-493-5963	Sequence 5963, Ap	166	35	48.6	421	14	US-10-140-928-302	Sequence 302, App
94	36	50.0	1098	16	US-10-437-963-188638	Sequence 188638, A	167	35	48.6	421	14	US-10-121-045-302	Sequence 302, App
95	36	50.0	2396	16	US-10-437-963-122555	Sequence 122555, S	168	35	48.6	421	14	US-10-123-292-302	Sequence 302, App
96	35.5	49.3	95	16	US-10-425-115-335678	Sequence 335678, A	169	35	48.6	421	14	US-10-123-903-302	Sequence 302, App
97	35.5	49.3	119	11	US-09-864-408A-5200	Sequence 5200, Ap	170	35	48.6	421	14	US-10-124-819-302	Sequence 302, App
98	35.5	49.3	267	15	US-10-369-493-21906	Sequence 21906, A	171	35	48.6	421	14	US-10-124-822-302	Sequence 302, App
99	35.5	49.3	382	9	US-09-801-368-210	Sequence 210, App	172	35	48.6	421	14	US-10-140-925-302	Sequence 302, App
100	35.5	49.3	681	16	US-10-425-115-197585	Sequence 197585, S	173	35	48.6	421	14	US-10-160-498-302	Sequence 302, App
101	35.5	49.3	704	16	US-10-425-115-197587	Sequence 197587, S	174	35	48.6	421	14	US-10-124-824-302	Sequence 302, App
102	35.5	49.3	713	15	US-10-425-114-68803	Sequence 68803, A	175	35	48.6	421	14	US-10-127-825A-302	Sequence 302, App
103	35.5	49.3	1065	16	US-10-437-963-109994	Sequence 109994, S	176	35	48.6	421	14	US-10-127-829A-302	Sequence 302, App
104	35	48.6	33	15	US-10-424-599-183107	Sequence 183107, S	177	35	48.6	421	14	US-10-127-835A-302	Sequence 302, App
105	35	48.6	48	16	US-10-424-599-204734	Sequence 204734, S	178	35	48.6	421	14	US-10-127-839A-302	Sequence 302, App
106	35	48.6	49	15	US-10-425-115-204734	Sequence 204734, S	179	35	48.6	421	14	US-10-127-901A-302	Sequence 302, App
107	35	48.6	50	14	US-10-424-599-168973	Sequence 168973, S	180	35	48.6	421	14	US-10-128-693A-302	Sequence 302, App
108	35	48.6	52	16	US-10-029-386-29686	Sequence 29686, A	181	35	48.6	421	14	US-10-128-693A-302	Sequence 302, App
109	35	48.6	55	15	US-10-437-963-119218	Sequence 119218, S	182	35	48.6	421	14	US-10-131-813A-302	Sequence 302, App
110	35	48.6	72	16	US-10-425-114-44607	Sequence 44607, A	183	35	48.6	421	14	US-10-131-818A-302	Sequence 302, App
111	35	48.6	77	16	US-10-437-963-168065	Sequence 168065, S	184	35	48.6	421	14	US-10-131-823A-302	Sequence 302, App
112	35	48.6	89	16	US-10-425-115-232780	Sequence 232780, S	185	35	48.6	421	14	US-10-131-824A-302	Sequence 302, App
113	35	48.6	116	16	US-10-425-115-348576	Sequence 348576, S	186	35	48.6	421	14	US-10-131-830A-302	Sequence 302, App
114	35	48.6	118	16	US-10-437-963-113299	Sequence 113299, S	187	35	48.6	421	14	US-10-131-837A-302	Sequence 302, App
115	35	48.6	196	15	US-10-424-599-277729	Sequence 277729, S	188	35	48.6	421	14	US-10-137-872A-302	Sequence 302, App
116	35	48.6	210	16	US-10-767-701-51202	Sequence 51202, A	189	35	48.6	421	14	US-10-147-500-302	Sequence 302, App
117	35	48.6	243	16	US-10-739-930-7168	Sequence 7168, Ap	190	35	48.6	421	14	US-10-147-502-302	Sequence 302, App
118	35	48.6	291	16	US-10-437-963-143303	Sequence 143303, S	191	35	48.6	421	14	US-10-147-515-302	Sequence 302, App
119	35	48.6	362	15	US-10-336-603A-28	Sequence 28, Appl	192	35	48.6	421	14	US-10-147-526-302	Sequence 302, App
120	35	48.6	363	16	US-10-437-963-187230	Sequence 187230, S	193	35	48.6	421	14	US-10-147-527-302	Sequence 302, App
121	35	48.6	366	15	US-10-369-493-19321	Sequence 19321, A	194	35	48.6	421	14	US-10-121-041-302	Sequence 302, App
122	35	48.6	367	14	US-10-238-075-323	Sequence 323, App	195	35	48.6	421	14	US-10-121-043-302	Sequence 302, App
123	35	48.6	379	14	US-10-094-944-9	Sequence 9, Appl1	196	35	48.6	421	14	US-10-121-047-302	Sequence 302, App
124	35	48.6	379	15	US-10-336-603A-30	Sequence 30, Appl	197	35	48.6	421	14	US-10-123-215-302	Sequence 302, App
125	35	48.6	379	16	US-10-408-765A-1561	Sequence 1561, Ap	198	35	48.6	421	14	US-10-123-502-302	Sequence 302, App
126	35	48.6	379	16	US-10-782-401-3	Sequence 3, Appl1	199	35	48.6	421	14	US-10-123-908-302	Sequence 302, App
127	35	48.6	379	16	US-10-733-969A-77	Sequence 77, Appl	200	35	48.6	421	14	US-10-123-909-302	Sequence 302, App
128	35	48.6	379	17	US-10-971-461-14	Sequence 14, Appl	201	35	48.6	421	14	US-10-123-910-302	Sequence 302, App
129	35	48.6	382	15	US-10-369-493-8378	Sequence 8378, Ap	202	35	48.6	421	14	US-10-124-813-302	Sequence 302, App
130	35	48.6	391	15	US-10-628-088-396	Sequence 396, App	203	35	48.6	421	14	US-10-124-817-302	Sequence 302, App
131	35	48.6	391	15	US-10-628-088-397	Sequence 397, App	204	35	48.6	421	14	US-10-125-922-302	Sequence 302, App
132	35	48.6	391	16	US-10-432-234A-557	Sequence 557, App	205	35	48.6	421	14	US-10-125-924-302	Sequence 302, App
133	35	48.6	391	16	US-10-811-508-4	Sequence 4, Appl1	206	35	48.6	421	14	US-10-140-860-302	Sequence 302, App
134	35	48.6	391	17	US-10-722-045-5	Sequence 5, Appl1	207	35	48.6	421	14	US-10-142-417-302	Sequence 302, App
135	35	48.6	391	17	US-10-722-045-6	Sequence 6, Appl1	208	35	48.6	421	14	US-10-147-519-302	Sequence 302, App
136	35	48.6	391	17	US-10-722-045-42	Sequence 42, Appl	209	35	48.6	421	14	US-10-157-782-302	Sequence 302, App
137	35	48.6	391	17	US-10-466-811-4	Sequence 4, Appl1	210	35	48.6	421	14	US-10-152-395-302	Sequence 302, App
138	35	48.6	391	17	US-10-466-811-5	Sequence 5, Appl1	211	35	48.6	421	14	US-10-125-926A-302	Sequence 302, App
139	35	48.6	393	17	US-10-722-045-7	Sequence 7, Appl1	212	35	48.6	421	14	US-10-125-930A-302	Sequence 302, App
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141	35	48.6	396	15	US-10-424-599-167860	Sequence 167860, S	214	35	48.6	421	14	US-10-137-846A-302	Sequence 302, App
142	35	48.6	396	16	US-10-836-673-5	Sequence 5, Appl1	215	35	48.6	421	14	US-10-137-838B-302	Sequence 302, App
143	35	48.6	410	15	US-10-282-122A-68579	Sequence 68579, A	216	35	48.6	421	14	US-10-127-842A-302	Sequence 302, App
144	35	48.6	421	14	US-10-028-072-302	Sequence 302, App	217	35	48.6	421	14	US-10-127-843A-302	Sequence 302, App
145	35	48.6	421	14	US-10-140-808-302	Sequence 302, App	218	35	48.6	421	14	US-10-127-845A-302	Sequence 302, App
146	35	48.6	421	14	US-10-121-049-302	Sequence 302, App	219	35	48.6	421	14	US-10-127-846A-302	Sequence 302, App
147	35	48.6	421	14	US-10-123-904-302	Sequence 302, App	220	35	48.6	421	14	US-10-137-848A-302	Sequence 302, App
148	35	48.6	421	14	US-10-140-470-302	Sequence 302, App	221	35	48.6	421	14	US-10-127-849A-302	Sequence 302, App
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151	35	48.6	421	14	US-10-137-865-302	Sequence 302, App	224	35	48.6	421	14	US-10-128-684A-302	Sequence 302, App
152	35	48.6	421	14	US-10-137-865-302	Sequence 302, App	225	35	48.6	421	14	US-10-128-686A-302	Sequence 302, App
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156	35	48.6	421	14	US-10-143-419-302	Sequence 302, App	229	35	48.6	421	14	US-10-131-829A-302	Sequence 302, App
157	35	48.6	421	14	US-10-123-262-302	Sequence 302, App	230	35	48.6	421	14	US-10-131-836A-302	Sequence 302, App

231	35	48.6	421	14	US-10-146-729-302	Sequence 302, App	304	35	48.6	421	14	US-10-145-748-302	Sequence 302, App
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233	35	48.6	421	14	US-10-147-484-302	Sequence 302, App	306	35	48.6	421	14	US-10-145-826-302	Sequence 302, App
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239	35	48.6	421	14	US-10-121-061-302	Sequence 302, App	312	35	48.6	421	14	US-10-146-725-302	Sequence 302, App
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243	35	48.6	421	14	US-10-147-832-302	Sequence 302, App	316	35	48.6	421	14	US-10-147-506-302	Sequence 302, App
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245	35	48.6	421	14	US-10-123-905-302	Sequence 302, App	318	35	48.6	421	14	US-10-147-510-302	Sequence 302, App
246	35	48.6	421	14	US-10-123-907-302	Sequence 302, App	319	35	48.6	421	14	US-10-147-511-302	Sequence 302, App
247	35	48.6	421	14	US-10-124-815-302	Sequence 302, App	320	35	48.6	421	14	US-10-147-529-302	Sequence 302, App
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249	35	48.6	421	14	US-10-125-928A-302	Sequence 302, App	322	35	48.6	421	14	US-10-153-586-302	Sequence 302, App
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251	35	48.6	421	14	US-10-127-822A-302	Sequence 302, App	324	35	48.6	421	14	US-10-137-870-302	Sequence 302, App
252	35	48.6	421	14	US-10-127-824A-302	Sequence 302, App	325	35	48.6	421	14	US-10-137-870-302	Sequence 302, App
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254	35	48.6	421	14	US-10-127-827A-302	Sequence 302, App	327	35	48.6	421	14	US-10-140-021-302	Sequence 302, App
255	35	48.6	421	14	US-10-127-828A-302	Sequence 302, App	328	35	48.6	421	14	US-10-140-471-302	Sequence 302, App
256	35	48.6	421	14	US-10-127-830A-302	Sequence 302, App	329	35	48.6	421	14	US-10-140-923-302	Sequence 302, App
257	35	48.6	421	14	US-10-127-832A-302	Sequence 302, App	330	35	48.6	421	14	US-10-145-631-302	Sequence 302, App
258	35	48.6	421	14	US-10-127-833A-302	Sequence 302, App	331	35</					

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379	35	48.6	421	14	US-10-158-792-302	Sequence 302, App	452	35	48.6	421	14	US-10-124-814-302	Sequence 302, App
380	35	48.6	421	14	US-10-158-463-302	Sequence 302, App	453	35	48.6	421	14	US-10-124-816-302	Sequence 302, App
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384	35	48.6	421	14	US-10-145-824-302	Sequence 302, App	457	35	48.6	421	14	US-10-142-889-302	Sequence 302, App
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404	35	48.6	421	14	US-10-152-406-302	Sequence 302, App	477	35	48.6				

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527	35	48.6	421	15	US-10-145-632-302	Sequence 302, App	600	35	48.6	715	15	US-10-282-122A-68039	Sequence 68039, A
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537	35	48.6	421	15	US-10-152-376-302	Sequence 302, App	610	35	48.6	775	14	US-10-140-470-120	Sequence 120, App
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564	35	48.6	421	15	US-10-152-405-302	Sequence 302, App	637	35	48.6	775	14	US-10-127-825A-120	Sequence 120, App
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572	35	48.6	421	15	US-10-144-993-302	Sequence 302, App	645	35	48.6	775	14	US-10-131-823A-120	Sequence 120, App
573	35	48.6	421	15	US-10-158-787-302	Sequence 302, App	646	35	48.6	775	14	US-10-131-824A-120	Sequence 120, App
574	35	48.6	421	15	US-10-140-024-302	Sequence 302, App	647	35	48.6	775	14	US-10-131-830A-120	Sequence 120, App
575	35	48.6	421	15	US-10-147-536-302	Sequence 302, App	648	35	48.6	775	14	US-10-131-837A-120	Sequence 120, App
576	35	48.6	421	16	US-10-152-372-302	Sequence 302, App	649	35	48.6	775	14	US-10-137-872A-120	Sequence 120, App
577	35	48.6	421	16	US-10-125-793-302	Sequence 302, App	650	35	48.6	775	14	US-10-147-500-120	Sequence 120, App
578	35	48.6	421	16	US-10-145-626-302	Sequence 302, App	651	35	48.6	775	14	US-10-147-515-120	Sequence 120, App
579	35	48.6	421	16	US-10-145-819-302	Sequence 302, App	652	35	48.6	775	14	US-10-147-515-120	Sequence 120, App
580	35	48.6	421	16	US-10-145-825-302	Sequence 302, App	653	35	48.6	775	14	US-10-147-517-120	Sequence 120, App
581	35	48.6	421	16	US-10-147-513-302	Sequence 302, App	654	35	48.6	775	14	US-10-147-526-120	Sequence 120, App
582	35	48.6	421	16	US-10-147-518-302	Sequence 302, App	655	35	48.6	775	14	US-10-147-527-120	Sequence 120, App
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584	35	48.6	421	16	US-10-723-860-1403	Sequence 1403, App	657	35	48.6	775	14	US-10-121-043-120	Sequence 120, App
585	35	48.6	421	16	US-10-147-488-302	Sequence 302, App	658	35	48.6	775	14	US-10-121-047-120	Sequence 120, App
586	35	48.6	421	16	US-10-147-531-302	Sequence 302, App	659	35	48.6	775	14	US-10-123-215-120	Sequence 120, App
587	35	48.6	421	17	US-10-931-886-302	Sequence 302, App	660	35	48.6	775	14	US-10-123-908-120	Sequence 120, App
588	35	48.6	421	17	US-10-158-788-302	Sequence 302, App	661	35	48.6	775	14	US-10-123-908-120	Sequence 120, App
589	35	48.6	421	20	US-11-019-829-19	Sequence 19, App1	662	35	48.6	775	14	US-10-123-910-120	Sequence 120, App
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591	35	48.6	452	15	US-10-282-122A-74654	Sequence 74654, A	664	35	48.6	775	14	US-10-124-813-120	Sequence 120, App
592	35	48.6	469	16	US-10-451-467A-220	Sequence 220, App	665	35	48.6	775	14	US-10-124-817-120	Sequence 120, App
593	35	48.6	517	16	US-10-686-947-230	Sequence 230, App	666	35	48.6	775	14	US-10-125-922-120	Sequence 120, App
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670	35	48.6	775	14	US-10-147-519-120	Sequence 120, App	743	35	48.6	775	14	US-10-123-912-120	Sequence 120, App
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682	35	48.6	775	14	US-10-127-848A-120	Sequence 120, App	755	35	48.6	775	14	US-10-140-926-120	Sequence 120, App
683	35	48.6	775	14	US-10-127-849A-120	Sequence 120, App	756	35	48.6	775	14	US-10-141-698-120	Sequence 120, App
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685	35	48.6	775	14	US-10-127-851A-120	Sequence 120, App	758	35	48.6	775	14	US-10-141-704-120	Sequence 120, App
686	35	48.6	775	14	US-10-128-684A-120	Sequence 120, App	759	35	48.6	775	14	US-10-142-421-120	Sequence 120, App
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689	35	48.6	775	14	US-10-128-691A-120	Sequence 120, App	762	35	48.6	775	14	US-10-143-033-120	Sequence 120, App
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692	35	48.6	775	14	US-10-131-836A-120	Sequence 120, App	765	35	48.6	775	14	US-10-145-748-120	Sequence 120, App
693	35	48.6	775	14	US-10-146-729-120	Sequence 120, App	766	35	48.6	775	14	US-10-145-748-120	Sequence 120, App
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695	35	48.6	775	14	US-10-147-484-120	Sequence 120, App	768	35	48.6	775	14	US-10-145-826-120	Sequence 120, App
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961 35 48.6 775 14 US-10-124-823-120 Sequence 120, App
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967 35 48.6 775 15 US-10-131-820A-120 Sequence 120, App
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969 35 48.6 775 15 US-10-146-728-120 Sequence 120, App
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999 35 48.6 775 15 US-10-147-537-120 Sequence 120, App
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ALIGNMENTS

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RESULT 1
US-10-367-094-34
; Sequence 34, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-34
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Query Match 100.0%; Score 72; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYL 15
Db 122 VPFSVAKSVKSLYL 136
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RESULT 2
US-10-671-054-3
; Sequence 3, Application US/10671054
; Publication No. US20040157774A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; TITLE OF INVENTION: EPITOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: CEN-5015USNP
; CURRENT APPLICATION NUMBER: US/10/671,054
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/413157
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-3
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Query Match 100.0%; Score 72; DB 16; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298
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RESULT 3
US-10-696-909A-41
; Sequence 41, Application US/10696909A
; Publication No. US20050118604A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Atchison, Robert E.
; APPLICANT: Frieria, Anabella
; APPLICANT: Holland, Sacha
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
; FILE REFERENCE: 021044-005820US
; CURRENT APPLICATION NUMBER: US/10/696,909A
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/512,251
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/421,989
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: growth arrest-specific 6 (GAS6), AXL stimulatory
; OTHER INFORMATION: factor
US-10-696-909A-41
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Query Match 100.0%; Score 72; DB 17; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298
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RESULT 4
US-10-671-054-1
; Sequence 1, Application US/10671054
; Publication No. US20040157774A1
; GENERAL INFORMATION:
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; APPLICANT: Johnson & Johnson
; TITLE OF INVENTION: EPITOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6
; FILE REFERENCE: CEN-5015USNP
; CURRENT APPLICATION NUMBER: US/10/671,054
; PRIOR FILING DATE: 2003-09-24
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-671-054-1

Query Match      100.0%; Score 72; DB 16; Length 686;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLYLIG 15
Db      284 VPFSVAKSVKSLYLIG 298
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RESULT 5
US-10-223-085-48
; Sequence 48, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PC10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-084-48

Query Match      95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLYLIG 15
Db      281 VPFSMAKSVKSLYLIG 295
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RESULT 6
US-10-223-084-48
; Sequence 48, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PC15
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-084-48

Query Match      95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLYLIG 15
Db      281 VPFSMAKSVKSLYLIG 295
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QY

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Db      281 VPFSMAKSVKSLYLG 295

RESULT 7
US-10-223-088-48
; Sequence 48, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC6
; CURRENT APPLICATION NUMBER: US/10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-088-48

Query Match      95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 1;

Qy      1 VPFSMAKSVKSLYLG 15
Db      281 VPFSMAKSVKSLYLG 295

RESULT 9
US-10-223-087-48
; Sequence 48, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
```

1	APPLICANT: Ye, Weilan	2
2	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND	3
3	FILE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS AND	4
4	FILE REFERENCE: P3235P1C4	5
5	CURRENT APPLICATION NUMBER: US/10/223,087	6
6	CURRENT FILING DATE: 2002-08-15	7
7	PRIOR APPLICATION NUMBER: US 10/081,056	8
8	PRIOR FILING DATE: 2002-02-20	9
9	PRIOR APPLICATION NUMBER: US 60/213,637	10
10	PRIOR FILING DATE: 2000-06-23	11
11	PRIOR APPLICATION NUMBER: US 60/219,556	12
12	PRIOR FILING DATE: 2000-07-20	13
13	PRIOR APPLICATION NUMBER: US 60/220,624	14
14	PRIOR FILING DATE: 2000-07-25	15
15	PRIOR APPLICATION NUMBER: US 60/220,664	16
16	PRIOR FILING DATE: 2000-07-25	17
17	PRIOR APPLICATION NUMBER: PCT/US00/20710	18
18	PRIOR FILING DATE: 2000-07-28	19
19	PRIOR APPLICATION NUMBER: US 60/222,695	20
20	PRIOR FILING DATE: 2000-08-02	21
21	PRIOR APPLICATION NUMBER: US 09/643,657	22
22	PRIOR FILING DATE: 2000-08-17	23
23	PRIOR APPLICATION NUMBER: PCT/US00/23522	24
24	PRIOR FILING DATE: 2000-08-23	25
25	PRIOR APPLICATION NUMBER: PCT/US00/23328	26
26	PRIOR FILING DATE: 2000-08-24	27
27	PRIOR APPLICATION NUMBER: US 60/230,978	28
28	PRIOR FILING DATE: 2000-09-07	29
29	PRIOR APPLICATION NUMBER: US 60/232,887	30
30	PRIOR FILING DATE: 2000-09-15	31
31	PRIOR APPLICATION NUMBER: US 09/664,610	32
32	PRIOR FILING DATE: 2000-09-18	33
33	PRIOR APPLICATION NUMBER: US 09/665,350	34
34	PRIOR FILING DATE: 2000-09-18	35
35	PRIOR APPLICATION NUMBER: US 60/242,922	36
36	PRIOR FILING DATE: 2000-10-24	37
37	PRIOR APPLICATION NUMBER: US 09/709,238	38
38	PRIOR FILING DATE: 2000-11-08	39
39	PRIOR APPLICATION NUMBER: PCT/US00/30952	40
40	PRIOR FILING DATE: 2000-11-08	41
41	PRIOR APPLICATION NUMBER: PCT/US00/30873	42
42	PRIOR FILING DATE: 2000-11-10	43
43	PRIOR APPLICATION NUMBER: PCT/US00/32678	44
44	PRIOR FILING DATE: 2000-12-01	45
45	PRIOR APPLICATION NUMBER: US 09/747,259	46
46	PRIOR FILING DATE: 2000-12-20	47
47	PRIOR APPLICATION NUMBER: PCT/US00/34956	48
48	PRIOR FILING DATE: 2000-12-20	49
49	PRIOR APPLICATION NUMBER: US 09/767,609	50
50	PRIOR FILING DATE: 2001-01-22	51
51	PRIOR APPLICATION NUMBER: US 09/796,498	52
52	PRIOR FILING DATE: 2001-02-28	53
53	PRIOR APPLICATION NUMBER: PCT/US01/06520	54
54	PRIOR FILING DATE: 2001-02-28	55
55	PRIOR APPLICATION NUMBER: PCT/US01/06666	56
56	PRIOR FILING DATE: 2001-03-01	57
57	PRIOR APPLICATION NUMBER: US 09/802,706	58
58	PRIOR FILING DATE: 2001-03-09	59
59	PRIOR APPLICATION NUMBER: US 09/808,689	60
60	PRIOR FILING DATE: 2001-03-14	61
61	PRIOR APPLICATION NUMBER: US 09/816,744	62
62	PRIOR FILING DATE: 2001-03-22	63
63	PRIOR APPLICATION NUMBER: US 09/828,366	64
64	PRIOR FILING DATE: 2001-04-05	65
65	PRIOR APPLICATION NUMBER: US 09/854,208	66
66	PRIOR FILING DATE: 2001-05-10	67
67	PRIOR APPLICATION NUMBER: US 09/854,280	68
68	PRIOR FILING DATE: 2001-05-10	69
69	PRIOR APPLICATION NUMBER: US 09/866,028	70
70	PRIOR FILING DATE: 2001-05-25	71
71	PRIOR APPLICATION NUMBER: US 09/866,034	72
72	PRIOR FILING DATE: 2001-05-25	73
73	PRIOR APPLICATION NUMBER: PCT/US01/17092	74

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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-087-48

Query Match          95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0;

Qy      1  VPFSAKSVKSLYLG 15
        |||:|||||
Db      281  VPFSAKSVKSLYLG 295

RESULT 10
US-10-223-083-48
; Sequence 48, Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITL OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328

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; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-083-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
||||:|||||||
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 11
US-10-223-089-48
; Sequence 48, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC9
; CURRENT APPLICATION NUMBER: US/10/223,089
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-089-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYLIG 15
||||:|||||||
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 12
US-10-223-081-48
; Sequence 48, Application US/10223081
; Publication No. US20030186866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC7
; CURRENT APPLICATION NUMBER: US/10/223,081
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-081-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
||||:|||||||
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 13
US-10-223-082-48
; Sequence 48, Application US/10223082
; Publication No. US20030191059A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C3
CURRENT APPLICATION NUMBER: US/10/223,082
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-223-082-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 14
US-10-305-654-48
Sequence 48, Application US/10305654
Publication No. US20030224984A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hans-Peter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, J.

APPLICANT: Paoni, N. F.
APPLICANT: Stephan, J-P F.
APPLICANT: Watanabe, C.K.
APPLICANT: Wood, W.I.
APPLICANT: Williams, P.M.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235R1C1
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-305-654-48

Query Match 95.8%; Score 69; DB 15; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 15
US-10-081-056-48
Sequence 48, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07

US-10-081-056-48

Query Match 95.8%; Score 69; DB 15; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSMAKSVKSLYL 295

RESULT 16

US-10-367-094-31

Query Match 95.8%; Score 69; DB 16; Length 697;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 314 VPFSMAKSVKSLYL 328

RESULT 17

US-10-369-493-5833

Query Match 95.8%; Score 69; DB 16; Length 697;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 314 VPFSMAKSVKSLYL 328

RESULT 18

US-10-437-963-128669

Query Match 61.1%; Score 44; DB 15; Length 374;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 13
DB 142 LPFAIAASVNSLY 154

US-10-367-094-31

Sequence 31, Application US/10367094
Publication No. US20040170982A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001500
CURRENT APPLICATION NUMBER: US/10/367,094
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 697
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(697)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-367-094-31

Query Match 95.8%; Score 69; DB 16; Length 697;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 314 VPFSMAKSVKSLYL 328

RESULT 17

US-10-369-493-5833

Sequence 5833, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5833
LENGTH: 374
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5833

Query Match 61.1%; Score 44; DB 15; Length 374;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 13
DB 142 LPFAIAASVNSLY 154

RESULT 18

US-10-437-963-128669

Sequence 128669, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei


```
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128669
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31000C.1.pep
US-10-437-963-128669

Query Match          59.7%; Score 43; DB 16; Length 606;
Best Local Similarity 61.5%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLY 13
DB      323 LPFSVVWVWVMIY 335

RESULT 19
US-10-425-115-203276
; Sequence 203276, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 203276
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116975C.1.pep
US-10-425-115-203276

Query Match          59.0%; Score 42.5; DB 16; Length 72;
Best Local Similarity 73.3%; Pred. No. 5.8;
Matches 11; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY      2 PFSV---AKSVKSLY 13
DB      40 PPSVLFSVSVKSLY 54

RESULT 20
US-10-062-188-1
; Sequence 1, Application US/10062188
; Publication No. US20040096826A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Methods For Creating Recombination
; TITLE OF INVENTION: Products Between Nucleotide Sequences
; FILE REFERENCE: P-EA 5008
; CURRENT APPLICATION NUMBER: US/10/062,188
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; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-062-188-1

Query Match          58.3%; Score 42; DB 15; Length 291;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 PFSVAKSVKSLYLG 15
DB      184 PAAVAKSLKTLALG 197

RESULT 21
US-09-801-368-332
; Sequence 332, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match          58.3%; Score 42; DB 9; Length 1220;
Best Local Similarity 81.8%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKS 11
DB      955 VKFSVAKSIRKS 965

RESULT 22
US-10-369-493-22082
; Sequence 22082, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
```

```
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22082
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22082

Query Match          58.3%; Score 42; DB 15; Length 1220;
Best Local Similarity 81.8%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKS 11
   |||||:|
Db 955 VKFSVAKSIKS 965

RESULT 23
US-10-425-115-268339
; Sequence 268339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 268339
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(283)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_176326C.1.ppep
US-10-425-115-268339

Query Match          56.9%; Score 41; DB 16; Length 283;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
   ||:||||:|
Db 146 PFNGAKSVRDLY 157

RESULT 24
US-10-425-115-256726
; Sequence 256726, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```

```
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256726
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165723C.1.ppep
US-10-425-115-256726

Query Match          56.9%; Score 41; DB 16; Length 323;
Best Local Similarity 53.8%; Pred. No. 62;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
   |||||:|:|
Db 292 LPFSVVKMQTIY 304

RESULT 25
US-10-739-930-9784
; Sequence 9784, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 9784
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C176_291.p
US-10-739-930-9784

Query Match          56.9%; Score 41; DB 16; Length 366;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
   ||:||||:|
Db 146 PFNGAKSVRDLY 157

RESULT 26
US-10-369-493-21954
; Sequence 21954, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21954
; LENGTH: 1173
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-21954

Query Match          56.9%; Score 41; DB 15; Length 1173;
Best Local Similarity 46.2%; Pred. No. 2.7e+02;
```

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|: |||:|:
Db 1089 PFSIARQTKSMWI 1101

RESULT 27
US-10-741-849-7057
; Sequence 7057, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7057
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-741-849-7057

Query Match 56.9%; Score 41; DB 17; Length 1235;
Best Local Similarity 53.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|: |||:|:
Db 52 PFNVKSLQTIYL 64

RESULT 28
US-10-424-599-201272
; Sequence 201272, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201272
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(132)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23774C.1.pap
US-10-424-599-201272

Query Match 55.6%; Score 40; DB 15; Length 132;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 15
|||:|: |||:|:
Db 9 YSIMRTTRSLYL 21

Db 115 FSVCRSFGSLYL 127

RESULT 29
US-10-032-585-7469
; Sequence 7469, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7469
; LENGTH: 969
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7469

Query Match 55.6%; Score 40; DB 14; Length 969;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
|||:|: |||:|:
Db 792 LPFGVAKSKSKELG 806

RESULT 30
US-10-425-115-190887
; Sequence 190887, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 190887
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_105668C.1.pap
US-10-425-115-190887

Query Match 54.2%; Score 39; DB 16; Length 70;
Best Local Similarity 46.2%; Pred. No. 25;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 15
|||:|: |||:|:
Db 9 YSIMRTTRSLYL 21

RESULT 31
US-10-328-675A-74
; Sequence 74, Application US/10328675A
; Publication No. US20030159171A1
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael

```

; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: 30857USNPDI.V1
; CURRENT APPLICATION NUMBER: US/10/328,675A
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/519,232
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/219,338
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-328-675A-74

```

Query Match	54.2%	Score 39	DB 14	Length 369
Best Local Similarity	53.8%	Pred. No. 1.7e+02		
Matches	7	Conservative	4	Mismatches 2
				Indels 0
				Gaps 0

Qy 1 VPFSVAKSVKSLY 13
||| ||::|| |:
Db 237 VPFEVAENTIKLLW 249

RESULT 32
US-10-437-963-171845
; Sequence 171845, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

Query Match	54.2%	Score 39;	DB 16;	Length 484;
Best Local Similarity	58.3%;	Pred. No. 2.3e+02;		
Matches	7;	Conservative	3;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy 2 PFSVAKSVKSLY 13
|||:||||::
Db 406 PFVLAKSVKXIF 417

RESULT 33
US-10-437-963-126646
; Sequence 126646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126646
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(829)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29172C.1.pap
; US-10-437-963-126646

```

Query Match	54.2%	Score 39	DB 16	Length 829
Best Local Similarity	72.7%	Pred. No. 4.3e+02		
Matches	8	Conservative	1	Mismatches 2
				Indels 0
				Gaps 0

Qy 3 FSVAKSVKSLY 13
| | | | | | | |
Db 77 FRVAKSTKSVY 87

```

RESULT 34
US-10-437-963-171836
; Sequence 171836, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Mol
; TITLE OF INVENTION: Plants and Uses Ther
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171836
; LENGTH: 1256
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT4530
US-10-437-963-171836

```

Query Match 54.2%; Score 39; DB 16; Length 1256;
Best Local Similarity 58.3%; Pred. No. 6.9e+02;
Matches 7; Conservative 3; Mismatches 2; Indels

Qy 2 PFSVAKSVKSLY 13
|||:||||::
Db 502 PFVLAKSVKQIF 513

RESULT 35
US-10-425-115-302429
; Sequence 302429, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 302429
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_38890C.1.pep
US-10-425-115-302429

Query Match 52.8%; Score 38; DB 16; Length 38;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
DB 22 PFSISKSVTLII 34
|||:||||:|:
|||:||||:|:

RESULT 36
US-10-437-963-188870
; Sequence 188870, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuc, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 188870
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85433C.1.pep
US-10-437-963-188870

Query Match 52.8%; Score 38; DB 16; Length 78;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSVAKSVKS 11
DB 8 PFSIAQSIKN 17
|||:||||:|:
|||:||||:|:

RESULT 37
US-10-363-616-335
; Sequence 335, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 335
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-335

Query Match 52.8%; Score 38; DB 15; Length 133;
Best Local Similarity 34.8%; Pred. No. 79;
Matches 8; Conservative 5; Mismatches 2; Indels 8; Gaps 1;

QY 1 VPFSVAKS-----VKSLYL 15
DB 73 IPFEVSKGEPQPKDNLIRSLFLG 95
:||||:|:
:||||:|:

RESULT 38
US-10-425-115-331872
; Sequence 331872, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 331872
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_65774C.1.pep
US-10-425-115-331872

Query Match 52.8%; Score 38; DB 16; Length 260;
Best Local Similarity 56.2%; Pred. No. 17e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 VPFSVAK--SVKSLYL 14
DB 177 IPFSVGEMTSLKSLWL 192
:||||:|:
:||||:|:

RESULT 39
US-10-369-493-22398
; Sequence 22398, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22398
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22398

Query Match 52.8%; Score 38; DB 15; Length 307;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 VPFSVAK-----SVKSLYL 15
DB 137 VPFELIKIRMQVKSSYL 155

RESULT 40
US-10-425-115-318065
; Sequence 318065, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 318065
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(399)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_53150C.1.pep
US-10-425-115-318065

Query Match 52.8%; Score 38; DB 16; Length 399;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
DB 338 PXCVAKKVKDLY 349

RESULT 41
US-10-092-771-10
; Sequence 10, Application US/10092771
; Publication No. US20030064381A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
; TITLE OF INVENTION: HGPRTMY26, EXPRESSED HIGHLY IN TESTIS AND GASTROINTESTINAL TISSU
; FILE REFERENCE: D0128NP
; CURRENT APPLICATION NUMBER: US/10/092,771
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/273,963
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/278,927
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 418
; TYPE: PRT
; ORGANISM: SUS SCROFA
US-10-092-771-10

Query Match 52.8%; Score 38; DB 14; Length 418;
Best Local Similarity 46.2%; Pred. No. 2.9e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
DB 198 PVATASSIVSVYL 210

RESULT 42
US-10-437-963-120006
; Sequence 120006, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120006
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23167C.1.pep
US-10-437-963-120006

Query Match 52.8%; Score 38; DB 16; Length 441;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
DB 161 LPFVSQVMVKFY 173

RESULT 43
US-10-424-599-183414
; Sequence 183414, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 183414
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136636C.1.pep
US-10-424-599-183414

Query Match 52.8%; Score 38; DB 15; Length 632;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 3 VPFSVAAAPASLYVG 17

RESULT 44

US-10-425-114-37208
; Sequence 37208, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37208
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-110-D8_FLI.pbp
US-10-425-114-37208

Query Match 52.8%; Score 38; DB 15; Length 637;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15

Db 8 VPFSVAAAPASLYVG 22

RESULT 45

US-10-437-963-132886
; Sequence 132886, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132886
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34810C.1.pbp
US-10-437-963-132886

Query Match 52.8%; Score 38; DB 16; Length 645;
Best Local Similarity 53.3%; Pred. No. 4.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15

Db 240 VFESMFQKLLFLG 254

RESULT 46

US-10-038-854-135
; Sequence 135, Application US/10038854

Publication No. US20040022781A1

; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-038-854-135

Query Match 52.8%; Score 38; DB 15; Length 661;
Best Local Similarity 46.7%; Pred. No. 5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15

Db 143 IPLHNQKTLESYLG 157

RESULT 47

US-10-037-417-107

; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsodrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 107
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-107

Query Match 52.8%; Score 38; DB 15; Length 661;
Best Local Similarity 46.7%; Pred. No. 5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 143 IPLHQKLTLESYL 157

RESULT 48
US-10-437-963-193517
; Sequence 193517, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 193517
; LENGTH: 1870
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_89649C.1.pep
US-10-437-963-193517

Query Match 52.8%; Score 38; DB 16; Length 1870;
Best Local Similarity 69.2%; Pred. No. 1.7e+03;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 15
DB 1482 FPGTSTNKSLLYL 1494

RESULT 49
US-10-425-115-254685
; Sequence 254685, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 254685
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_163853C.1.pep
US-10-425-115-254685

Query Match 51.4%; Score 37; DB 16; Length 54;
Best Local Similarity 61.5%; Pred. No. 42;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
DB 13 PVSFAKSTKQLHL 25

RESULT 50
US-09-864-761-36016
; Sequence 36016, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36016
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008053.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.97
; OTHER INFORMATION: EST HUMAN HIT: BE176836.1, EVALUE 1.00e-30
; OTHER INFORMATION: SWISSPROT HIT: P79400, EVALUE 3.40e+00
US-09-864-761-36016

Query Match 51.4%; Score 37; DB 9; Length 62;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13
Db 30 IPYSITFSMSLY 42

Search completed: July 7, 2005, 10:29:31
Job time : 41.044 secs

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OM protein.- protein search, using sw model

Run on: July 7, 2005, 08:51:19 ; Search time 20.0687 Seconds
(without alignments)
382.745 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72
Sequence: 1 VPFSVAKSVKSLYLIG 15

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	72	100.0	721	1 GAS66 HUMAN
2	69	95.8	674	1 GAS66 MOUSE
3	69	95.8	674	1 GAS66 RAT
4	69	95.8	674	1 GAS66 RAT
5	46	63.9	668	2 O6PAE0
6	44	61.1	374	1 YLD1 CAEL
7	44	61.1	571	1 UVRC MYCAA
8	43	59.7	417	2 Q624E5
9	43	59.7	606	2 Q624E7
10	43	59.7	669	2 Q6DPA5
11	42	58.3	252	2 Q9V984
12	42	58.3	292	1 BLAN ENTCL
13	42	58.3	292	2 Q46991
14	42	58.3	344	2 Q6AMY9
15	42	58.3	1220	1 SLN1 YEAST
16	42	58.3	4345	2 Q9VLA0
17	42	58.3	4374	2 Q7KTG2
18	41	56.9	218	2 Q9QXB0
19	41	56.9	242	2 Q9QXB1
20	41	56.9	242	2 Q9QXB2
21	41	56.9	242	2 Q9QXB3
22	41	56.9	242	2 Q9QXB4
23	41	56.9	243	2 Q8JUF8
24	41	56.9	243	2 Q9QKC6
25	41	56.9	244	2 Q9QXB5
26	41	56.9	244	2 Q9QXB8
27	41	56.9	244	2 Q9QXB9
28	41	56.9	245	2 Q9QKC1
29	41	56.9	245	2 Q9QKC4
30	41	56.9	246	2 Q9QXB6
31	41	56.9	246	2 Q9QXB7

32	41	56.9	246	2	Q9QKC0	Q9qkc0 rift valley
33	41	56.9	246	2	Q9QKC2	Q9qkc2 rift valley
34	41	56.9	246	2	Q9QKC3	Q9qkc3 rift valley
35	41	56.9	246	2	Q9QKC5	Q9qkc5 rift valley
36	41	56.9	354	1	Y419 METUA	Q57862 methanococ
37	41	56.9	355	2	Q7N4C9	Q7n4c9 photorhabd
38	41	56.9	377	2	Q8JU22	Q8ju22 lumpy skin
39	41	56.9	381	1	VQ3JL_CAPVK	Q86917 capripoxvir
40	41	56.9	381	2	Q8JTY0	Q8jty0 lumpy skin
41	41	56.9	381	2	Q91MZ3	Q91mz3 lumpy skin
42	41	56.9	381	2	Q91T39	Q91t39 lumpy skin
43	41	56.9	1173	1	ATC2_YEAST	P38929 saccharomyc
44	41	56.9	1197	1	VGLM_RVFPVZ	P21401 rift valley
45	41	56.9	1206	1	VGLM_RVFPV	P03518 rift valley
46	41	56.9	3457	2	Q6EEL1	Q6eel1 maize chlor
47	40	55.6	250	2	Q66712	Q66712 aquifex aeo
48	40	55.6	405	2	Q93CR3	Q93cr3 shigella bo
49	40	55.6	413	2	Q9U7C8	Q9u7c8 dictyosteli
50	40	55.6	424	1	HEM1_CHLVI	P28462 chlorobium
51	40	55.6	471	2	Q70LJ0	Q70lj0 legioneella
52	40	55.6	587	2	Q7WBV0	Q7wbv0 bordetella
53	40	55.6	587	2	Q7WPU6	Q7wpu6 bordetella
54	40	55.6	630	2	Q6BK57	Q6bk57 debaryomyce
55	40	55.6	722	2	Q86J22	Q86j22 dictyosteli
56	40	55.6	945	2	Q6L465	Q6l465 solanum dem
57	40	55.6	1721	2	Q6L450	Q6l450 solanum dem
58	40	55.6	2573	2	Q6L432	Q6l432 solanum dem
59	39	54.2	256	2	Q6MBS9	Q6mbs9 parachlamyd
60	39	54.2	310	2	Q9L106	Q9l106 streptomyce
61	39	54.2	341	2	Q94AA9	Q94aa9 arabidopsis
62	39	54.2	406	2	Q6LY56	Q6ly56 methanococ
63	39	54.2	407	2	Q6LY57	Q6ly57 methanococ
64	39	54.2	421	2	Q54630	Q54630 halobacteri
65	39	54.2	440	2	Q7XGJ4	Q7xgj4 oryza sativ
66	39	54.2	461	2	Q9MIQ1	Q9miq1 arabidopsis
67	39	54.2	465	2	Q7SA07	Q7sa07 neurospora
68	39	54.2	507	2	Q7UFB7	Q7urb7 rhodospirell
69	39	54.2	522	2	Q86J22	Q86j22 dictyosteli
70	39	54.2	588	2	Q6QUG9	Q6gue9 nicotiana t
71	39	54.2	588	2	Q8L4N8	Q8l4n8 oryza sativ
72	39	54.2	1256	2	Q8L4N8	Q8l4n8 oryza sativ
73	39	54.2	1262	2	Q18117	Q18117 caenorhabdi
74	39	54.2	1826	1	BGS3_SCHPO	Q9p377 schizosacch
75	38	52.8	91	2	Q91FX1	Q91fx1 chilo iride
76	38	52.8	95	2	Q9DKL6	Q9dkl6 spodoptera
77	38	52.8	180	2	Q9U7D2	Q9u7d2 caenorhabdi
78	38	52.8	199	2	Q8EWV4	Q8ewv4 mycoplasma
79	38	52.8	263	2	Q7DMC7	Q7dmc7 nicotiana t
80	38	52.8	275	2	Q9BFX0	Q9bfx0 okapia john
81	38	52.8	275	2	Q9BFX1	Q9bfx1 sus scrofa
82	38	52.8	275	2	Q9BFX2	Q9bfx2 tragelaphus
83	38	52.8	275	2	Q9BFX4	Q9bfx4 hippopotamu
84	38	52.8	275	2	Q9BP04	Q9bp04 muscardinus
85	38	52.8	277	2	Q71BQ3	Q71bq3 cynocephalu
86	38	52.8	277	2	Q9BFX7	Q9bfx7 cynocephalu
87	38	52.8	291	2	Q7W8M4	Q7w8m4 bordetella
88	38	52.8	305	1	NAA2_ECOL6	Q8fd27 escherichia
89	38	52.8	305	2	Q6KD26	Q6kd26 escherichia
90	38	52.8	306	1	MTSA_STRMU	Q9ki13 streptococc
91	38	52.8	307	1	ODC2_YEAST	Q99297 saccharomyc
92	38	52.8	317	2	Q9U775	Q9uy75 pyrococcus
93	38	52.8	330	1	Q9KBB0	Q9kbb0 bacillus ha
94	38	52.8	333	1	Y282_BUCAP	Q8k9n9 buchnera ap
95	38	52.8	349	1	YM94_YEAST	Q04869 saccharomyc
96	38	52.8	369	2	Q6FPH7	Q6fph7 candida gla
97	38	52.8	382	2	Q8VHP7	Q8vhp7 mus musculu
98	38	52.8	390	2	Q4152	Q24152 nicotiana t
99	38	52.8	401	2	Q9LUF8	Q9luf8 arabidopsis
100	38	52.8	408	2	Q6FFN2	Q6ffn2 arabidopsis
101	38	52.8	409	2	Q6GN71	Q6gn71 xenopus lae
102	38	52.8	409	2	Q6P614	Q6p614 xenopus tro
103	38	52.8	418	1	B2AR_BOVIN	Q28044 bos taurus
104	38	52.8	418	1	B2AR_FIG	Q28997 sus scrofa

105	38	52.8	418	2	Q6QTF6	Q6qtf6 sus scrofa	178	37	51.4	700	2	Q823V4	Q823v4 chlamydomphi
106	38	52.8	430	2	Q8A5C0	Q8a5c0 bacteroides	179	37	51.4	711	2	Q6MV61	Q6mv61 neurospora
107	38	52.8	441	2	Q7XSW2	Q7xsw2 oryza sativ	180	37	51.4	947	2	Q7RK48	Q7rk48 plasmodium
108	38	52.8	507	1	ATPA_CHLRE	P28526 chlamydomon	181	37	51.4	1018	2	Q63L89	Q63l89 burkholderi
109	38	52.8	526	2	Q73EB1	Q73eb1 bacillus ce	182	37	51.4	1033	2	Q62C67	Q62c67 burkholderi
110	38	52.8	556	2	Q61V04	Q61v04 photobacter	183	37	51.4	1140	2	Q7XTR3	Q7xtr3 oryza sativ
111	38	52.8	565	2	Q8GA94	Q8ga94 dictyosteli	184	37	51.4	1356	2	Q8WRE2	Q8wre2 anopheles g
112	38	52.8	581	2	Q8GUF2	Q8guf2 lycopersico	185	37	51.4	1664	2	Q8JIF9	Q8jif9 acanthogobi
113	38	52.8	593	2	P91573	P91573 caenorhabdi	186	37	51.4	1702	1	DPOL_THELI	P30317 thermococu
114	38	52.8	602	2	Q7RHH6	Q7rhh6 plasmodium	187	37	51.4	6199	2	Q6JANO	Q6jano brachydanio
115	38	52.8	661	1	C180_MOUSE	Q62192 mus musculu	188	36.5	50.7	773	2	Q824T3	Q824t3 chlamydomphi
116	38	52.8	661	1	Q8C251	Q8c251 mus musculu	189	36.5	50.7	437	2	P97044	P97044 leptospira
117	38	52.8	781	1	TL22_CHICK	Q9gb6 gallus gall	190	36.5	50.7	437	2	Q72VY5	Q72vy5 leptospira
118	38	52.8	793	1	TL21_CHICK	Q9dd78 gallus gall	191	36.5	50.7	783	2	Q8C8A8	Q8c8a8 mus musculu
119	38	52.8	822	2	Q7XQT9	Q7xqt9 oryza sativ	192	36.5	50.7	853	2	Q8T4K1	Q8t4k1 dictyosteli
120	38	52.8	942	2	Q938A0	Q938a0 mycobacteri	193	36.5	50.7	973	1	TRP5_HUMAN	Q9ul62 homo sapien
121	38	52.8	2607	2	Q6L4J5	Q6l4j5 solanum dem	194	36.5	50.7	974	1	TRP5_RABIT	Q82852 oryctolagus
122	38	52.8	4466	2	Q81LS4	Q81ls4 plasmodium	195	36.5	50.7	974	2	Q8VD38	Q8vd38 rattus norv
123	37.5	52.1	251	2	Q73B70	Q73b70 bacillus ce	196	36.5	50.7	975	1	TRP5_MOUSE	Q9qx29 mus musculu
124	37.5	52.1	296	2	Q67600	Q67600 aquifex ao	197	36	50.0	47	2	Q727A1	Q727a1 desulfovibr
125	37.5	52.1	4055	2	Q8R1L8	Q8r1l8 human group	198	36	50.0	66	2	Q87SW7	Q87sw7 vibrio para
126	37.5	52.1	6724	2	Q6R1L9	Q6r1l9 human group	199	36	50.0	68	1	YIFK_ECOLI	P93318 escherichia
127	37.5	52.1	6729	2	Q6Q1S3	Q6qls3 human coron	200	36	50.0	81	2	Q7UANI	Q7uani shigella fl
128	37	51.4	68	2	Q6D149	Q6d149 erwinia car	201	36	50.0	81	2	Q8XCG4	Q8xcg4 escherichia
129	37	51.4	73	2	Q7PHY0	Q7phy0 anopheles g	202	36	50.0	90	2	Q8Z151	Q8z151 salmonella
130	37	51.4	134	2	Q6TK41	Q6tk41 drosophila	203	36	50.0	90	2	Q8ZK72	Q8zk72 salmonella
131	37	51.4	180	2	Q6BFB7	Q6bfb7 drosophila	204	36	50.0	114	2	Q8DF41	Q8df41 vibrio vuln
132	37	51.4	207	2	Q6ZMB4	Q6zmb4 homo sapien	205	36	50.0	123	2	Q8CB92	Q8cb92 mus musculu
133	37	51.4	258	1	HIS6_ECO57	P60665 escherichia	206	36	50.0	149	2	Q9UX82	Q9ux82 sulfolobus
134	37	51.4	258	1	HIS6_ECOL6	Q8fg48 escherichia	207	36	50.0	160	2	Q6V4U3	Q6v4u3 enterococcu
135	37	51.4	258	1	HIS6_ECOLI	P60664 escherichia	208	36	50.0	166	2	Q8YTI8	Q8yti8 anabaena sp
136	37	51.4	258	1	HIS6_KLEOX	P45603 klebsiella	209	36	50.0	198	2	Q6LMM9	Q6lmn9 photobacter
137	37	51.4	258	1	HIS6_SHIFL	Q83r03 shigella fl	210	36	50.0	200	2	Q8G9L7	Q8g9l7 rhodococcus
138	37	51.4	259	2	Q9X9T6	Q9x9t6 streptomyce	211	36	50.0	202	2	Q9LHW4	Q9lhw4 mycobacteri
139	37	51.4	271	1	BLAC_PROVU	P80298 proteus vul	212	36	50.0	217	2	Q6BW74	Q6bw74 debaryomyce
140	37	51.4	292	2	Q52I31	Q52i31 enterococcu	213	36	50.0	226	1	Q6CXV0	Q6cxv0 kluyveromyca
141	37	51.4	295	2	Q93PQ0	Q93pq0 citrobacter	214	36	50.0	258	1	R1L1_MYCGE	P47328 mycoplasma
142	37	51.4	295	2	Q9RI06	Q9riq6 serratia fo	215	36	50.0	261	1	HIS6_CANBF	Q7vqw5 candidatus
143	37	51.4	295	2	Q9RIR0	Q9rir0 serratia fo	216	36	50.0	278	2	Q7QLZ1	Q7qlz1 anopheles g
144	37	51.4	295	2	Q9RIR1	Q9rir1 serratia fo	217	36	50.0	282	2	Q7RHB3	Q7rhb3 plasmodium
145	37	51.4	295	2	Q9RIR2	Q9rir2 serratia fo	218	36	50.0	297	1	Q6LMM9	Q6lmw9 methanococc
146	37	51.4	295	2	Q9RIR3	Q9rir3 serratia fo	219	36	50.0	307	2	MURB_AQUAE	Q66805 aquifex ao
147	37	51.4	295	2	Q9XE09	Q9xe09 enterobacte	220	36	50.0	314	2	P95426	Q6fmn9 candida gla
148	37	51.4	298	2	Q8VNT0	Q8vnt0 proteus pen	221	36	50.0	352	2	Q6K948	P95426 pseudomonas
149	37	51.4	300	1	BLAB_PROVU	P52664 proteus vul	222	36	50.0	352	2	Q91ZS2	Q6k948 oryza sativ
150	37	51.4	300	2	Q52615	Q52615 proteus vul	223	36	50.0	356	2	Q622B9	Q91zsz zea mogaic
151	37	51.4	303	2	Q743Y6	Q743y6 mycobacteri	224	36	50.0	365	2	Q622B9	Q82269 caenorhabdi
152	37	51.4	307	1	RNHL_YEAST	P53942 saccharomyc	225	36	50.0	365	2	Q7QW39	Q7qw39 giardia lam
153	37	51.4	308	2	Q9R7H7	Q9r7h7 thermococ	226	36	50.0	366	2	Q97E26	Q97e26 clostridium
154	37	51.4	309	2	Q92FP2	Q9zfp2 enterococcu	227	36	50.0	381	2	Q6FA36	Q6fa36 acinetobact
155	37	51.4	328	2	Q6EQX0	Q6eqx0 oryza sativ	228	36	50.0	390	2	Q86JF6	Q86jfe dictyosteli
156	37	51.4	357	2	Q6LIF80	Q6ly80 methanococc	229	36	50.0	397	2	Q99XC4	Q99xc4 staphylococ
157	37	51.4	397	2	Q812M0	Q812m0 plasmodium	230	36	50.0	397	2	Q7A200	Q7a200 staphylococ
158	37	51.4	418	2	Q27085	Q27085 tachypleus	231	36	50.0	397	2	Q7A894	Q7a894 staphylococ
159	37	51.4	420	2	Q8BY99	Q8byy9 mus musculu	232	36	50.0	399	2	Q6GD39	Q6gd39 bordetella
160	37	51.4	422	1	QMD_BOVIN	Q77742 bos taurus	233	36	50.0	406	2	Q7W0H7	Q7w0h7 bordetella
161	37	51.4	435	2	Q51801	Q51801 salmonella	234	36	50.0	406	2	Q7W3N0	Q7w3n0 bordetella
162	37	51.4	440	1	HEN1_HELHP	Q7vff1 helicobacte	235	36	50.0	406	2	Q7WF06	Q7wf06 bordetella
163	37	51.4	442	2	Q7SHQ3	Q7shq3 neurospora	236	36	50.0	406	2	Q7MHL7	Q7mhl7 vibrio vuln
164	37	51.4	456	2	Q9H6D2	Q9h6d2 homo sapien	237	36	50.0	409	2	Q8DC94	Q8dc94 vibrio vuln
165	37	51.4	471	2	Q899G0	Q899g0 clostridium	238	36	50.0	409	2	Q8EIH7	Q8eih7 shewanella
166	37	51.4	476	2	Q8PZZ4	Q8pzz4 methanosarc	239	36	50.0	409	2	Q9KP92	Q9kp92 vibrio chol
167	37	51.4	498	2	Q87Q32	Q87q32 vibrio para	240	36	50.0	409	2	Q8KP92	Q8kp92 haemophilus
168	37	51.4	506	1	ATPA_ANASP	P12405 anabaena sp	241	36	50.0	410	1	SERA_HAEIN	Q85r10 mannheimia
169	37	51.4	510	1	ATPA_RICCN	Q92g86 rickettsia	242	36	50.0	410	2	Q85RR0	Q87r18 vibrio para
170	37	51.4	510	2	Q7P9Y0	Q7p9y0 rickettsia	243	36	50.0	410	2	Q87LL8	Q9ckf1 pasteurella
171	37	51.4	513	1	YWFF_LACLA	Q9cdp0 lactococcus	244	36	50.0	416	2	Q9CKE1	Q83d50 coxiella bu
172	37	51.4	545	2	Q6AJU1	Q6aju1 desulfotale	245	36	50.0	432	1	HEM1_CAMJE	Q9phx2 campylobact
173	37	51.4	571	1	UVRG_MYCBV	Q84898 mycoplasma	246	36	50.0	437	2	Q7NIH9	Q7nih9 gloeobacter
174	37	51.4	601	2	Q825X1	Q825x1 streptomyce	247	36	50.0	454	2	Q8A7Y7	Q8a7y7 bacteroides
175	37	51.4	601	2	Q6AME9	Q6ame9 desulfotale	248	36	50.0	455	2	Q8A7Y7	Q8a7y7 bacteroides
176	37	51.4	623	2	Q71AZ7	Q71az7 homo sapien	249	36	50.0	455	2	Q794W0	Q794w0 bacillus su
177	37	51.4	699	2	Q7TP87	Q7tp87 rattus norv	250	36	50.0	458	2	Q45613	Q45613 bacillus su

251	36	50.0	479	2	Q7PR59	Q7px59 anopheles g	324	35	48.6	230	2	Q9E8D6	Q9e8d6 bovine resp
252	36	50.0	480	2	Q9L072	Q9l072 streptomyc	325	35	48.6	230	2	Q9E8D7	Q9e8d7 bovine resp
253	36	50.0	486	1	YD97 METJA	Q58792 methanococ	326	35	48.6	230	2	Q9E8D8	Q9e8d8 bovine resp
254	36	50.0	501	1	ATPA NEPOL	Q9t116 nephroselm	327	35	48.6	230	2	Q9E8D9	Q9e8d9 bovine resp
255	36	50.0	501	1	AGG29	Q9gg29 valliseria	328	35	48.6	230	2	Q9E8E0	Q9e8e0 bovine resp
256	36	50.0	505	2	Q9S0U1	Q9s0u1 hyaloraphid	329	35	48.6	230	2	Q9E8E1	Q9e8e1 bovine resp
257	36	50.0	506	2	ATPA EUGGR	P30392 euglena gra	330	35	48.6	230	2	Q9E8E2	Q9e8e2 bovine resp
258	36	50.0	506	2	Q7R344	Q7r344 giardia lam	331	35	48.6	230	2	Q9E8E3	Q9e8e3 bovine resp
259	36	50.0	520	2	Q6W099	Q6wm99 bdellovibri	332	35	48.6	230	2	Q9E8E4	Q9e8e4 bovine resp
260	36	50.0	529	2	Q92F60	Q92f60 listeria in	333	35	48.6	230	2	Q9E8E5	Q9e8e5 bovine resp
261	36	50.0	529	2	Q9KPC7	Q9kpc7 vibrio chol	334	35	48.6	230	2	Q9E8E6	Q9e8e6 bovine resp
262	36	50.0	542	2	Q81TD6	Q81td6 bacillus an	335	35	48.6	230	2	Q9E8E7	Q9e8e7 bovine resp
263	36	50.0	547	1	SYM_THEAC	Q9hj12 thermoplasm	336	35	48.6	230	2	Q9E8E8	Q9e8e8 bovine resp
264	36	50.0	551	2	Q8W4E1	Q8w4e1 arabisdopsis	337	35	48.6	230	2	Q9E8E9	Q9e8e9 bovine resp
265	36	50.0	551	2	Q9LN70	Q9ln70 arabisdopsis	338	35	48.6	230	2	Q9E8F0	Q9e8f0 bovine resp
266	36	50.0	589	2	Q8EWS6	Q8ews6 mycoplasma	339	35	48.6	230	2	Q9QAB1	Q9qab1 bovine resp
267	36	50.0	594	2	Q7QHB1	Q7qhb1 anopheles g	340	35	48.6	234	2	Q9QNM3	Q9qnm3 leishmania
268	36	50.0	604	2	Q7NHI7	Q7nhi7 gloebacter	341	35	48.6	236	1	PYRF_BUCAP	Q8k9q1 buchnera ap
269	36	50.0	605	2	Q8Y9L3	Q8y9l3 listeria mo	342	35	48.6	243	2	Q73R80	Q73r80 treponema d
270	36	50.0	609	2	Q723D6	Q723d6 listeria mo	343	35	48.6	250	2	Q8QMHO	Q8qmho tomatato chlo
271	36	50.0	611	2	Q92EE6	Q92ee6 listeria in	344	35	48.6	251	1	HIS6_HELHP	Q7vgz1 helicobacte
272	36	50.0	639	2	Q6UDM4	Q6udm4 psittacid h	345	35	48.6	255	2	Q9RTC8	Q9rtc8 deinococcus
273	36	50.0	703	2	Q6CJ78	Q6cj78 kluyveromyc	346	35	48.6	281	2	Q7TEK3	Q7tek3 human respi
274	36	50.0	705	2	Q73BH4	Q73bh4 bacillus ce	347	35	48.6	281	2	Q7TEK4	Q7tek4 human respi
275	36	50.0	757	2	Q8G337	Q8g337 tropheryma	348	35	48.6	281	2	Q7TEK5	Q7tek5 human respi
276	36	50.0	765	2	Q6HLL6	Q6hll6 bacillus th	349	35	48.6	281	2	Q7TEK6	Q7tek6 human respi
277	36	50.0	772	2	Q63E41	Q63e41 bacillus ce	350	35	48.6	281	2	Q7TEK7	Q7tek7 human respi
278	36	50.0	814	2	Q6L2C3	Q6l2c3 picrophilus	351	35	48.6	281	2	Q7TEK8	Q7tek8 human respi
279	36	50.0	816	2	Q44872	Q44872 caenorhabdi	352	35	48.6	281	2	Q7TEK9	Q7tek9 human respi
280	36	50.0	871	2	Q7JEX5	Q7jex5 rhodopirell	353	35	48.6	281	2	Q7TELO	Q7tel0 human respi
281	36	50.0	878	2	Q9V6U4	Q9v6u4 drosophila	354	35	48.6	281	2	Q7TELO	Q7tel0 human respi
282	36	50.0	886	2	Q816Y9	Q816y9 caenorhabdi	355	35	48.6	281	2	Q7TELO	Q7tel0 human respi
283	36	50.0	900	1	FOX2 YEAST	Q02207 saccharomyc	356	35	48.6	281	2	Q7TELO	Q7tel0 human respi
284	36	50.0	931	1	TRP6_HUMAN	Q9y210 homo sapien	357	35	48.6	281	2	Q7TELO	Q7tel0 human respi
285	36	50.0	1053	2	Q6FWA6	Q6fwa6 candida gla	358	35	48.6	281	2	Q7TELO	Q7tel0 human respi
286	36	50.0	1086	2	Q9TYN3	Q9tyn3 caenorhabdi	359	35	48.6	281	2	Q7TELO	Q7tel0 human respi
287	36	50.0	1122	2	Q6FXU4	Q6fxu4 candida gla	360	35	48.6	284	2	Q9GL33	Q9gl33 bos taurus
288	36	50.0	1232	1	ADDA_BACSU	P23478 bacillus su	361	35	48.6	284	2	Q6MKY1	Q6mkyl bdellovibri
289	36	50.0	1257	2	Q8EA09	Q8ea09 shewanella	362	35	48.6	293	2	Q8PZW6	Q8pzw6 methanosarc
290	36	50.0	1437	2	Q7VYG8	Q7vyg8 cryptospori	363	35	48.6	293	2	Q8TL92	Q8tl92 methanosarc
291	36	50.0	1585	2	Q9F8Q4	Q9f8q4 streptococ	364	35	48.6	298	1	YK23_ARCFU	Q28256 archaeoglob
292	36	50.0	2195	2	Q6WV07	Q6wv07 neurospora	365	35	48.6	299	2	Q7WZT6	Q7wzt6 citrobacter
293	36	50.0	2209	2	Q7SH44	Q7sh44 neurospora	366	35	48.6	300	2	Q8EGC2	Q8egc2 shewanella
294	36	50.0	3064	2	Q782Q8	Q782q8 gallid herp	367	35	48.6	302	2	Q8EH91	Q8eh91 shewanella
295	36	50.0	3064	2	Q9WSX7	Q9wex7 marek's dis	368	35	48.6	304	2	Q8Z015	Q8z015 anabaena sp
296	36	50.0	15281	2	Q916A7	Q916a7 tolypoclad	369	35	48.6	305	2	Q02677	Q02677 podospora a
297	35.5	49.3	107	2	Q88GP1	Q88gp1 pseudomonas	370	35	48.6	320	2	Q7VT37	Q7vt37 bordetella
298	35.5	49.3	239	2	Q8SHC8	Q8shc8 arabisdopsis	371	35	48.6	320	2	Q7WFI0	Q7wfi0 bordetella
299	35.5	49.3	382	1	MIG2 YEAST	P53035 saccharomyc	372	35	48.6	330	2	Q62NE5	Q62ne5 bacillus li
300	35.5	49.3	419	2	Q8F535	Q8f535 leptospira	373	35	48.6	330	2	Q65CX0	Q65cx0 bacillus li
301	35.5	49.3	420	2	Q72QS1	Q72qsl1 leptospira	374	35	48.6	345	2	Q97FV6	Q97fv6 clostridium
302	35.5	49.3	496	2	Q9U4W2	Q9u4w2 aedes aegy	375	35	48.6	355	2	Q8GZ19	Q8gz19 arabisdopsis
303	35.5	49.3	1065	2	Q9LGI5	Q9lg15 oryza sativ	376	35	48.6	358	2	Q64862	Q64862 arabisdopsis
304	35.5	49.3	2183	2	Q89ZD7	Q89zd7 bacteroides	377	35	48.6	361	2	Q8DDC5	Q8ddc5 vibrio vuln
305	35	48.6	71	2	Q7RBI4	Q7rb14 plasmodium	378	35	48.6	368	2	Q7WQH0	Q7wqh0 vibrio vuln
306	35	48.6	115	2	Q9B339	Q9b339 coturnix ch	379	35	48.6	372	2	Q7QL57	Q7ql57 anopheles g
307	35	48.6	118	2	Q6ZX06	Q6zx06 oryza sativ	380	35	48.6	374	2	Q8FPB2	Q8fbb2 escherichia
308	35	48.6	141	2	Q8BBE9	Q8bbe9 pseudomonas	381	35	48.6	379	1	ILEU_HUMAN	P30740 homo sapien
309	35	48.6	169	2	Q8ZW60	Q8zw60 pyrobaculum	382	35	48.6	382	2	O53311	O53311 mycobacteri
310	35	48.6	194	2	Q8SRB8	Q8srb8 mannheimia	383	35	48.6	382	2	Q7TX50	Q7tx50 mycobacteri
311	35	48.6	195	2	Q8XVB8	Q8xvb8 ralstonia s	384	35	48.6	388	2	Q9WZ90	Q9wz90 thermotoga
312	35	48.6	195	2	Q72WN6	Q72wn6 desulfovibr	385	35	48.6	391	1	NCAP_BRSV3	P32677 bovine resp
313	35	48.6	201	2	Q7QPY7	Q7qpy7 giardia lam	386	35	48.6	391	1	NCAP_BRSV3	P32677 bovine resp
314	35	48.6	210	2	Q6PTG6	Q6ptg6 saccollossu	387	35	48.6	391	1	NCAP_BRSV1	Q65708 bovine resp
315	35	48.6	218	2	Q6NGY7	Q6ngy7 corynebacte	388	35	48.6	391	1	NCAP_HRSV1	P24566 human respi
316	35	48.6	230	2	Q9E8C8	Q9e8c8 bovine resp	389	35	48.6	391	1	NCAP_HRSV1	P03418 human respi
317	35	48.6	230	2	Q9E8C9	Q9e8c9 bovine resp	390	35	48.6	391	1	NCAP_ORSVW	Q83957 ovine respi
318	35	48.6	230	2	Q9E8D0	Q9e8d0 bovine resp	391	35	48.6	391	2	O12395	O12395 human respi
319	35	48.6	230	2	Q9E8D1	Q9e8d1 bovine resp	392	35	48.6	391	2	O42053	O42053 human respi
320	35	48.6	230	2	Q9E8D2	Q9e8d2 bovine resp	393	35	48.6	391	2	O6V2F2	O6v2f2 human respi
321	35	48.6	230	2	Q9E8D3	Q9e8d3 bovine resp	394	35	48.6	391	2	Q76TL0	Q76tl0 respiratory
322	35	48.6	230	2	Q9E8D4	Q9e8d4 bovine resp	395	35	48.6	391	2	Q77L02	Q77l02 bovine resp
323	35	48.6	230	2	Q9E8D5	Q9e8d5 bovine resp	396	35	48.6	391	2	Q77X51	Q77x51 bovine resp

397	35	48.6	393	1	NCAP_PVM	P26589 pneumonia v	470	35	48.6	793	2	O7XFR8	O7xfr8 oryza sativ
398	35	48.6	395	2	Q6DCG0	O6dcg0 xenopus lae	471	35	48.6	796	2	O75D27	O75d27 ashbya goss
399	35	48.6	398	2	Q97Z54	O97z54 sulfobolus	472	35	48.6	802	2	O87LX1	O87lx1 vibrio para
400	35	48.6	400	2	Q86LAS	Q86las dictyosteli	473	35	48.6	811	2	O7FZR1	O7fzr1 arabidopsis
401	35	48.6	408	2	Q8KVB5	Q8kvw5 ruegeria sp	474	35	48.6	828	2	O6MB95	O6mb95 parachlamyd
402	35	48.6	414	2	Q8HT32	Q8ht32 pseudomonas	475	35	48.6	851	2	O6CRTL	O6crt1 kluyveromyc
403	35	48.6	416	1	MTPL_PSYTA	O33481 psychrobact	476	35	48.6	902	2	O6WSR4	O6wsr4 triticum ae
404	35	48.6	421	1	OMD_HUMAN	O99983 homo sapien	477	35	48.6	906	2	O83517	O83517 enterococcu
405	35	48.6	423	1	OMD_MOUSE	O35103 mus musculu	478	35	48.6	907	2	O947C7	O947c7 triticum mo
406	35	48.6	423	1	OMD_RAT	O921s7 rattus norv	479	35	48.6	915	2	O93538	O93538 caenorhabdi
407	35	48.6	425	2	Q96VU0	Q96vu0 amanita mus	480	35	48.6	921	2	O6WSR5	O6wsr5 triticum ae
408	35	48.6	426	2	Q886T1	Q886t1 pseudomonas	481	35	48.6	936	1	CDGA_HUMAN	O9y5h3 homo sapien
409	35	48.6	432	2	O14452	O14452 schizosacch	482	35	48.6	956	2	O759B4	O759b4 ashbya goss
410	35	48.6	444	2	Q924S8	Q924s8 mus musculu	483	35	48.6	965	2	O84VT3	O84vt3 phalaenopsi
411	35	48.6	446	2	Q9HW32	Q9hw32 pseudomonas	484	35	48.6	965	2	O84VT4	O84vt4 phalaenopsi
412	35	48.6	450	2	Q7O6S9	Q7o6s9 anopheles g	485	35	48.6	984	2	O6MQ52	O6mq52 bdellovibri
413	35	48.6	452	1	MURD_STRP3	Q7d6s9 anopheles g	486	35	48.6	990	2	O7PAW0	O7paw0 rickettsia
414	35	48.6	452	1	MURD_STRP8	Q879a1 streptococc	487	35	48.6	1003	2	O9TXJ6	O9txj6 leishmania
415	35	48.6	452	1	MURD_STRP5	Q8p063 streptococc	488	35	48.6	1004	2	O9LGN1	O9lgn1 oryza sativ
416	35	48.6	460	2	Q9V5S1	P61418 streptococc	489	35	48.6	1008	2	O92J58	O92j58 rickettsia
417	35	48.6	469	1	SE33_YEAST	Q9v5s1 drosophila	490	35	48.6	1067	2	O01419	O01419 bombyx mori
418	35	48.6	470	2	Q75CF2	P40510 saccharomyc	491	35	48.6	1075	2	O7NNM9	O7nm9 gloeobacter
419	35	48.6	471	2	Q93FR8	Q75cf2 ashbya goss	492	35	48.6	1089	2	O7NFA7	O7nia7 gloeobacter
420	35	48.6	473	2	Q97AZ9	Q97fr8 ashbya rum	493	35	48.6	1145	2	O7V5E6	O7v5e6 prochloroco
421	35	48.6	476	2	Q91242	Q97az9 thermoplasm	494	35	48.6	1167	2	O74ZT2	O74zt2 ashbya goss
422	35	48.6	478	2	O8TL51	Q91242 pseudomonas	495	35	48.6	1358	2	O63NV1	O63nv1 burkholderi
423	35	48.6	489	2	Q9S0T1	O8tl51 methanosarc	496	35	48.6	1602	2	O9XY00	O9xy00 entameba h
424	35	48.6	489	2	Q7AJR3	Q9s0t1 bacillus le	497	35	48.6	1685	2	O04142	O04142 porphyra ye
425	35	48.6	499	1	SYFA_PYRFO	Q7ajr3 bacillus ha	498	35	48.6	1953	2	O98HJ2	O98hj2 rhizobium l
426	35	48.6	499	1	SYFA_PYRHO	Q8u261 pyrococcus	499	35	48.6	1989	2	O94M34	O94m34 streptococc
427	35	48.6	503	1	ATPA_ODOSI	O58391 pyrococcus	500	35	48.6	2020	2	O8ST27	O8st27 dictyosteli
428	35	48.6	516	2	Q9C8M8	Q00820 odontella s	501	35	48.6	3127	2	O7PTD4	O7ptd4 anopheles g
429	35	48.6	524	2	Q9ZIM2	Q9c8m8 arabidopsi	502	35	48.6	4773	2	O7QTR6	O7qtr6 giardia lam
430	35	48.6	529	2	Q8YAC9	Q9zim2 listeria mo	503	34.5	47.9	217	2	O6F8H8	O6f8h8 acinetobact
431	35	48.6	529	2	Q724J8	Q8yac9 listeria mo	504	34.5	47.9	223	1	EBP_ARATH	O8962 arabidopsis
432	35	48.6	545	1	CMC1_YEAST	Q724j8 listeria mo	505	34.5	47.9	223	1	O8LDC3	O8ldc3 arabidopsis
433	35	48.6	545	2	Q6GUS1	P48233 saccharomyc	506	34.5	47.9	251	2	O81FY5	O81fy5 bacillus ce
434	35	48.6	547	1	GSPA_AERHY	O96us1 saccharomyc	507	34.5	47.9	305	2	O6D788	O6d788 erwinia car
435	35	48.6	549	2	Q66V87	P45754 aeromonas h	508	34.5	47.9	330	2	O9UG89	O9ug89 homo sapien
436	35	48.6	559	2	Q7VHD7	Q65v87 nonomuraea	509	34.5	47.9	332	2	O6T7F5	O6t7f5 homo sapien
437	35	48.6	563	2	Q98R54	Q7vhd7 helicobacte	510	34.5	47.9	344	1	TA10_RAT	O9233x9 rattus norv
438	35	48.6	564	2	Q98R54	Q98r54 mycoplasma	511	34.5	47.9	344	1	TA11_RAT	O9233y9 rattus norv
439	35	48.6	573	1	INA1_TRIHA	O9ckz5 pasteurella	512	34.5	47.9	344	1	TAR7_RAT	O923v3 rattus norv
440	35	48.6	594	2	P918Z3	P34054 trichoderma	513	34.5	47.9	344	1	TAR4_RAT	O923y5 rattus norv
441	35	48.6	599	2	Q89379	P918z3 caenorhabdi	514	34.5	47.9	345	1	TAR2_RAT	O923y7 rattus norv
442	35	48.6	603	2	Q6MK30	Q89379 paramecium	515	34.5	47.9	347	1	TAR3_HUMAN	O96r19 homo sapien
443	35	48.6	605	1	NU5M_CHICK	Q6mk30 bdellovibri	516	34.5	47.9	348	1	O8NBP3	O8nbp3 homo sapien
444	35	48.6	605	2	Q76L08	P18940 gallus gall	517	34.5	47.9	350	2	O8NG15	O8ng15 homo sapien
445	35	48.6	605	2	Q85A52	Q76l08 gallus gall	518	34.5	47.9	350	2	O9CYN9	O9cyn9 m mus muscu
446	35	48.6	605	2	Q9MPA6	Q85a52 gallus gall	519	34.5	47.9	350	2	O9C7M1	O9c7m1 arabidopsis
447	35	48.6	613	2	Q69NK8	O9mpa6 gallus gall	520	34.5	47.9	422	2	O9C7M1	O9c7m1 arabidopsis
448	35	48.6	628	2	Q7PXV0	Q69nk8 oryza sativ	521	34.5	47.9	583	2	O73MA9	O73ma9 treponema d
449	35	48.6	630	2	Q82QU7	Q7pxv0 anopheles g	522	34.5	47.9	600	2	O8ZVZ4	O8zvz4 pyrobaculum
450	35	48.6	648	2	Q7T3H4	Q82qu7 streptomyce	523	34.5	47.9	627	2	O9N3S2	O9n3s2 caenorhabdi
451	35	48.6	654	2	O81PP3	Q7t3h4 brachydanio	524	34.5	47.9	887	2	O6XDS6	O6xd56 gallus gall
452	35	48.6	663	2	O9M1Z6	Q81pp3 drosophila	525	34.5	47.9	1602	2	O7R391	O7r391 giardia lam
453	35	48.6	698	2	Q8BTU9	O9m1z6 arabidopsis	526	34.5	47.9	1955	1	BGS4_SCHPO	O74475 schizosacch
454	35	48.6	717	2	Q8BM46	Q8btu9 debaryomyce	527	34.5	47.9	1995	2	O86ADA	O86ada dictyosteli
455	35	48.6	719	2	Q9C8M9	Q8bm46 pseudomonas	528	34.5	47.9	2163	2	O9LFF8	O9lfv8 arabidopsis
456	35	48.6	735	2	Q79VU0	Q9c8m9 arabidopsis	529	34.5	47.9	75	1	X1R4_YEAST	O436p2 enterococcu
457	35	48.6	745	2	Q9WN95	Q9hu63 pseudomonas	530	34.5	47.9	76	1	YGZE_YEAST	P53056 saccharomyc
458	35	48.6	745	2	Q9W4C1	Q79vu0 salmonella	531	34.5	47.9	82	2	O62ZQ2	O62zq2 bacillus li
459	35	48.6	759	1	Y363_METUA	O9w95 plasmid r64	532	34.5	47.9	83	2	O85PB3	O85pb3 bacillus li
460	35	48.6	760	2	O81G77	Q9z4c1 plasmid col	533	34.5	47.9	101	1	YBK8_YEAST	P38161 saccharomyc
461	35	48.6	763	2	Q8S603	Q81g77 bacillus ce	534	34.5	47.9	106	2	O7U7W4	O7u7w4 synechococc
462	35	48.6	775	2	Q6UW86	Q8s603 oryza sativ	535	34	47.2	110	1	Y1W0_YEAST	P40584 saccharomyc
463	35	48.6	775	2	O9VB49	O6uw86 homo sapien	536	34	47.2				
464	35	48.6	775	2	Q9V8A9	Q9vb49 drosophila	537	34	47.2				
465	35	48.6	776	1	CME3_BACSU	P39695 bacillus su	538	34	47.2				
466	35	48.6	787	1	VATA_THEVO	Q97cq0 thermoplasm	539	34	47.2				
467	35	48.6	793	2	O891A4	Q891a4 clostridium	540	34	47.2				
468	35	48.6	793	2	Q869L4	Q869l4 dictyosteli	541	34	47.2				
469	35	48.6	793	2	Q85774	Q85774 oryza sativ	542	34	47.2				

543	34	47.2	110	1	YKX3_YEAST	P36031	saccharomyc	616	34	47.2	313	2	Q9J5W0	Q9J5W0	neisseria m
544	34	47.2	110	2	Q9K374	Q9K374	proteus mir	617	34	47.2	317	2	Q7KSQ0	Q7KSQ0	drosophila
545	34	47.2	118	2	O52397	O52397	edwardsiell	618	34	47.2	318	2	Q8INK4	Q8INK4	drosophila
546	34	47.2	119	2	Q95TA0	Q95TA0	drosophila	619	34	47.2	321	2	O22810	O22810	arabidopsis
547	34	47.2	127	2	Q9TTG5	Q9TTG5	ateles belz	620	34	47.2	321	2	O6PBV3	O6PBV3	brachydanio
548	34	47.2	145	2	O6R320	O6R320	escherichia	621	34	47.2	323	2	O8K4V1	O8K4V1	mesocricetu
549	34	47.2	154	2	O7QJW8	O7QJW8	anopheles g	622	34	47.2	329	2	O9HJG1	O9HJG1	halobacteri
550	34	47.2	156	2	O7U3L6	O7U3L6	synecococc	623	34	47.2	329	2	O9SPJ8	O9SPJ8	caenorhabdi
551	34	47.2	166	2	O6XCA0	O6XCA0	mustelus ma	624	34	47.2	331	1	Y274_BUCBP	Y274_BUCBP	buchnera ap
552	34	47.2	171	2	O8RBS9	O8RBS9	thermoanaer	625	34	47.2	331	2	O88JW6	O88JW6	pseudomonas
553	34	47.2	174	2	O6M1L4	O6M1L4	bdellovibri	626	34	47.2	333	2	O8U4J6	O8U4J6	pyrococcus
554	34	47.2	178	1	RM13_DROME	RM13_DROME	drosophila	627	34	47.2	336	2	O7XUS3	O7XUS3	oryza sativ
555	34	47.2	184	2	O8TRB5	O8TRB5	anabaena sp	628	34	47.2	337	2	O6D701	O6D701	erwinia car
556	34	47.2	188	2	O8EWZ1	O8EWZ1	mycoplasma	629	34	47.2	339	1	BMPA_BORAF	BMPA_BORAF	borrelia af
557	34	47.2	190	1	TTT2_CAEEL	TTT2_CAEEL	caenorhabdi	630	34	47.2	342	2	O73UB6	O73UB6	mycobacteri
558	34	47.2	198	2	O970Z5	O970Z5	sulfolobus	631	34	47.2	351	2	O65VV0	O65VV0	mannheimia
559	34	47.2	198	2	O6B8P7	O6B8P7	gracilaria	632	34	47.2	351	2	O74C15	O74C15	geobacter s
560	34	47.2	200	2	O8ZXI8	O8ZXI8	pyrobaculum	633	34	47.2	353	2	O8LEZ0	O8LEZ0	arabidopsis
561	34	47.2	206	2	O6FOZ0	O6FOZ0	mesoplasma	634	34	47.2	353	2	O8LFN7	O8LFN7	arabidopsis
562	34	47.2	224	2	O9YHA8	O9YHA8	myxine glut	635	34	47.2	353	2	O9FKC9	O9FKC9	arabidopsis
563	34	47.2	226	2	O6F162	O6F162	mesoplasma	636	34	47.2	353	2	O9FKD2	O9FKD2	arabidopsis
564	34	47.2	239	2	O9HKL9	O9HKL9	thermoplasma	637	34	47.2	353	2	O9LTB4	O9LTB4	arabidopsis
565	34	47.2	245	2	O8C871	O8C871	mus musculus	638	34	47.2	356	2	O72NK1	O72NK1	leptospi
566	34	47.2	250	2	O6RAW2	O6RAW2	bacterioph	639	34	47.2	356	2	O6GP92	O6GP92	xenopus lae
567	34	47.2	250	2	Q9E004	Q9E004	tomato rugo	640	34	47.2	359	1	CHAD_HUMAN	CHAD_HUMAN	homo sapien
568	34	47.2	251	1	Y116_MYCGE	Y116_MYCGE	mycoplasma	641	34	47.2	359	2	O9D8K8	O9D8K8	mus muscu
569	34	47.2	251	2	O8YIE2	O8YIE2	brucella me	642	34	47.2	359	2	O7SXW0	O7SXW0	brachydanio
570	34	47.2	252	2	O9NV77	O9NV77	homo sapien	643	34	47.2	363	2	O9N4W7	O9N4W7	caenorhabdi
571	34	47.2	256	1	HIS6_PASMU	HIS6_PASMU	pasteurella	644	34	47.2	364	1	MTNA_LEPIC	MTNA_LEPIC	leptospi
572	34	47.2	256	2	O7QWQ3	O7QWQ3	anopheles g	645	34	47.2	364	1	MTNA_LEPIN	MTNA_LEPIN	leptospi
573	34	47.2	257	1	HIS6_PHOPR	HIS6_PHOPR	photobacter	646	34	47.2	369	2	O53623	O53623	sulfolobus
574	34	47.2	258	1	HIS6_BUCAI	HIS6_BUCAI	buchnera ap	647	34	47.2	370	2	O83605	O83605	treponema p
575	34	47.2	258	1	HIS6_BUCAP	HIS6_BUCAP	buchnera ap	648	34	47.2	371	2	O97QS4	O97QS4	streptococ
576	34	47.2	258	1	HIS6_YERPE	HIS6_YERPE	yersinia pe	649	34	47.2	371	2	O6XCC5	O6XCC5	brachydanio
577	34	47.2	258	2	O6GC54	O6GC54	yersinia ps	650	34	47.2	374	2	O8P804	O8P804	leptospi
578	34	47.2	258	2	O6D406	O6D406	erwinia car	651	34	47.2	374	2	O88800	O88800	mus musculu
579	34	47.2	259	2	O6N8Z8	O6N8Z8	rhodospseudo	652	34	47.2	375	2	O8DP51	O8DP51	streptococ
580	34	47.2	261	2	O6UA39	O6UA39	buchnera ap	653	34	47.2	379	2	O26606	O26606	schistosoma
581	34	47.2	261	2	Q9XDR0	Q9XDR0	actinobacil	654	34	47.2	384	2	O7D2Y0	O7D2Y0	agrobacteri
582	34	47.2	276	2	O8VQ11	O8VQ11	acineto	655	34	47.2	386	2	O73860	O73860	meleagris g
583	34	47.2	284	2	O94071	O94071	canida alb	656	34	47.2	390	2	O8LB78	O8LB78	arabidopsi
584	34	47.2	286	2	O8UJ12	O8UJ12	agrobacteri	657	34	47.2	391	2	P88810	P88810	human respi
585	34	47.2	291	1	BLC2_SALTY	BLC2_SALTY	salmonella	658	34	47.2	392	2	O6L1L5	O6L1L5	picophilus
586	34	47.2	291	1	BLC3_SALTY	BLC3_SALTY	salmonella	659	34	47.2	392	2	O96621	O96621	dictyostell
587	34	47.2	291	1	BLC5_SALTY	BLC5_SALTY	salmonella	660	34	47.2	392	2	O9FWK0	O9FWK0	arabidopsi
588	34	47.2	291	1	BLC6_SALTY	BLC6_SALTY	salmonella	661	34	47.2	397	2	O8MMH9	O8MMH9	heliobact
589	34	47.2	291	1	BLR1_ECOLI	BLR1_ECOLI	escherichia	662	34	47.2	397	2	O9SYF6	O9SYF6	arabidopsi
590	34	47.2	291	2	O34177	O34177	salmonella	663	34	47.2	402	2	O62H50	O62H50	burkholderi
591	34	47.2	291	2	O8RKB1	O8RKB1	kluyvera as	664	34	47.2	402	2	O63R34	O63R34	burkholderi
592	34	47.2	291	2	O8VKT5	O8VKT5	kluyvera as	665	34	47.2	402	2	O63R34	O63R34	burkholderi
593	34	47.2	291	2	O8VN22	O8VN22	kluyvera as	666	34	47.2	403	2	O6J2H1	O6J2H1	pseudomonas
594	34	47.2	291	2	O8VN23	O8VN23	kluyvera as	667	34	47.2	403	2	O7N8Z2	O7N8Z2	photorhabd
595	34	47.2	291	2	O8VN24	O8VN24	kluyvera as	668	34	47.2	407	2	O6HA07	O6HA07	branchiost
596	34	47.2	291	2	O8VN25	O8VN25	kluyvera as	669	34	47.2	407	2	O6MMES	O6MMES	bdellovibri
597	34	47.2	291	2	O936V5	O936V5	kluyvera as	670	34	47.2	409	1	SERA_ECOLI	SERA_ECOLI	escherichia
598	34	47.2	291	2	O6BCQ3	O6BCQ3	acineto	671	34	47.2	410	2	O8Z3W3	O8Z3W3	salmonella
599	34	47.2	291	2	O7Q4F7	O7Q4F7	morganela	672	34	47.2	410	2	O8ZM69	O8ZM69	salmonella
600	34	47.2	291	2	O79RM2	O79RM2	proteus mir	673	34	47.2	412	2	O8YB76	O8YB76	brucella me
601	34	47.2	291	2	O7AYD2	O7AYD2	kluyvera as	674	34	47.2	412	2	O8YBS3	O8YBS3	brucella me
602	34	47.2	291	2	O7B0V4	O7B0V4	kluyvera as	675	34	47.2	412	2	O8FMJ9	O8FMJ9	brucella su
603	34	47.2	291	2	O7X209	O7X209	escherichia	676	34	47.2	413	2	O666Q8	O666Q8	yersinia ps
604	34	47.2	291	2	O7X210	O7X210	providencia	677	34	47.2	413	2	O8ZHH9	O8ZHH9	yersinia pe
605	34	47.2	291	2	O9RLX4	O9RLX4	kluyvera as	678	34	47.2	414	2	O7KWM2	O7KWM2	dictyostell
606	34	47.2	291	2	O7WN88	O7WN88	borde	679	34	47.2	421	1	MTTA_THEAQ	MTTA_THEAQ	thermus aqu
607	34	47.2	294	1	BLAC_CITDI	BLAC_CITDI	citrobacter	680	34	47.2	421	2	O5E3B2	O5E3B2	uncultured
608	34	47.2	294	2	O460Z9	O460Z9	citrobacter	681	34	47.2	422	2	O5EL48	O5EL48	caenorhabdi
609	34	47.2	297	2	O7W5Q7	O7W5Q7	borde	682	34	47.2	422	2	O7L670	O7L670	arabidopsi
610	34	47.2	297	2	O7WD93	O7WD93	borde	683	34	47.2	427	2	O9SAF1	O9SAF1	arabidopsi
611	34	47.2	298	2	O64P14	O64P14	bacteroides	684	34	47.2	427	2	O8FX68	O8FX68	brucella su
612	34	47.2	304	2	O73KS1	O73KS1	treponema d	685	34	47.2	432	2	O752N1	O752N1	ashbya gos
613	34	47.2	307	1	YL72_ARCFU	YL72_ARCFU	archaeoglob	686	34	47.2	432	2	O9C333	O9C333	bradyrhizob
614	34	47.2	308	2	O72W81	O72W81	leptospi	687	34	47.2	435	1	HEM1_DESYM	HEM1_DESYM	desulfovibr
615	34	47.2	308	2	O8F9X4	O8F9X4	leptospi	688	34	47.2	443	2	Q93ZH3	Q93ZH3	arabidopsi

689	34	47.2	443	2	Q88PD7	Q88pd7 pseudomonas	762	34	47.2	658	2	Q8L364	Q8L364 xanthomonas
690	34	47.2	445	1	MURD_RICPR	Q9zdc2 rickettsia	763	34	47.2	682	1	Q6FK44	Q6fk44 candida gla
691	34	47.2	445	2	Q96I15	Q96i15 homo sapien	764	34	47.2	683	1	DP19_CABEL	DP1913 caenorhabdi
692	34	47.2	447	2	Q8HPQ2	Q8hpq2 halobacteri	765	34	47.2	684	2	Q9VJ39	Q9vj39 drosophila
693	34	47.2	447	2	Q8CZW0	Q8czw0 yersinia pe	766	34	47.2	685	1	CRPI_PERAM	CRPI11 periplaneta
694	34	47.2	450	1	MURD_STRPN	Q97ru8 streptococc	767	34	47.2	686	2	Q7QYB4	Q7qy84 giardia lam
695	34	47.2	450	1	MURD_STRR6	Q8dqm2 streptococc	768	34	47.2	692	2	Q8SY02	Q8sy02 drosophila
696	34	47.2	450	2	Q9ZHB0	Q9zhb0 streptococc	769	34	47.2	693	2	Q9KT38	Q9kt38 vibrio chol
697	34	47.2	450	2	Q9NL17	Q9nl17 rhodopseudo	770	34	47.2	697	2	Q8PP07	Q8ppq7 xanthomonas
698	34	47.2	451	1	MURD_BACSU	Q03522 bacillus su	771	34	47.2	716	2	Q8EK39	Q8ekr9 shewanella
699	34	47.2	451	1	Y613_STRA3	Q86f15 streptococc	772	34	47.2	718	2	Q7MNX3	Q7mzx3 vibrio vuln
700	34	47.2	451	1	Y633_STRAS	Q86t07 streptococc	773	34	47.2	718	2	Q8DEG9	Q8deg9 vibrio vuln
701	34	47.2	451	2	P97039	Q8e0t7 streptococc	774	34	47.2	724	2	Q7RNX2	Q7rnx2 plasmodium
702	34	47.2	451	2	Q9R6Q2	P97039 lactobacill	775	34	47.2	724	2	Q7RNX2	Q7rnx2 plasmodium
703	34	47.2	451	2	Q74LX6	P97039 lactobacill	776	34	47.2	727	2	Q7Z8N7	Q7z8n7 bipolaris s
704	34	47.2	451	2	Q6D8F5	Q74lx6 lactobacill	777	34	47.2	743	2	Q6PLM7	Q6plm7 homo sapien
705	34	47.2	454	2	Q6D8F5	Q6d8f5 erwinia car	778	34	47.2	756	2	Q8XUW5	Q8xuw5 ralstonia s
706	34	47.2	456	1	MURD_ENTFA	Q07108 enterococc	779	34	47.2	757	2	Q9BGH1	Q9bgh1 cryptocogus
707	34	47.2	463	2	Q9LJ48	Q07108 enterococc	780	34	47.2	757	2	Q9BGH1	Q9bgh1 cryptocogus
708	34	47.2	473	2	Q6AHL8	Q91j48 arabidopsis	781	34	47.2	759	2	Q7Z8P1	Q7z8p1 cochiobolu
709	34	47.2	474	2	Q7N5B1	Q6ahl8 leifsonia x	782	34	47.2	763	2	Q7Y208	Q7y208 arabidopsis
710	34	47.2	478	2	Q6AVE3	Q7n5b1 photorhabdu	783	34	47.2	763	2	Q8YAE7	Q8yae7 listeria mo
711	34	47.2	480	2	Q9RV87	Q6ave3 oryza sativ	784	34	47.2	764	1	DRA_HUMAN	DRA079 homo sapien
712	34	47.2	486	1	ANGT_CALJA	Q9rv87 deinococcus	785	34	47.2	782	2	Q8SSN0	Q8asn0 dictyosteli
713	34	47.2	486	2	Q96700	Q9tse20 callithrix	786	34	47.2	794	2	Q91XZ8	Q91xz8 mus musculu
714	34	47.2	496	1	GTR3_HUMAN	Q96700 ilyanassa o	787	34	47.2	794	2	Q925L0	Q925l0 mus musculu
715	34	47.2	496	2	O8I3I4	P11169 homo sapien	788	34	47.2	794	2	Q8C8Z3	Q8c8z3 mus musculu
716	34	47.2	500	1	SVFA_PYRAB	Q8i3i4 plasmodium	789	34	47.2	798	2	Q6CYA2	Q6cya2 kluyveromyc
717	34	47.2	500	2	Q8RGE0	Q8i3i4 plasmodium	790	34	47.2	805	1	KIP3_YEAST	KIP306 saccharomyc
718	34	47.2	505	2	Q8C472	Q8rge0 fusobacteri	791	34	47.2	814	2	Q7XQU2	Q7xqu2 oryza sativ
719	34	47.2	508	2	Q8TL59	Q8c472 mus musculu	792	34	47.2	820	2	Q7Z8N8	Q7z8n8 stemphylium
720	34	47.2	508	2	Q99W99	Q8tl59 methanosarc	793	34	47.2	820	2	Q7Z8N9	Q7z8n9 setosphaeri
721	34	47.2	508	2	Q7A1S3	Q99w99 staphylococ	794	34	47.2	821	2	Q7Z8N5	Q7z8n5 cochiobolu
722	34	47.2	508	2	Q7A7B1	Q7a1s3 staphylococ	795	34	47.2	825	2	Q8LL11	Q8ll11 oryza sativ
723	34	47.2	508	2	Q6GBY4	Q7a7b1 staphylococ	796	34	47.2	827	2	Q9VKL9	Q9vkl9 drosophila
724	34	47.2	508	2	Q6GJG7	Q6gby4 staphylococ	797	34	47.2	827	2	Q7XQU0	Q7xqu0 oryza sativ
725	34	47.2	509	2	Q7B206	Q6gjt7 staphylococ	798	34	47.2	831	2	Q7RJ03	Q7rj03 plasmodium
726	34	47.2	514	2	GLYM_SOLTU	Q9t252 phytoptthor	799	34	47.2	834	2	Q75ET4	Q75et4 ashbya goes
727	34	47.2	518	1	Q9KIE2	Q97b06 thermoplas	800	34	47.2	855	2	Q8L3Y5	Q8l3y5 glycine max
728	34	47.2	523	2	Q6CUN3	P50433 solanum tub	801	34	47.2	858	2	Q7QX1	Q7qxi1 giardia lam
729	34	47.2	534	2	Q8U3K6	Q9kif2 streptomyc	802	34	47.2	868	2	Q9M9X0	Q9m9x0 arabidopsis
730	34	47.2	537	2	Q74A36	Q6cun3 kluyveromyc	803	34	47.2	873	2	Q6FV4	Q6fvt4 candida gla
731	34	47.2	543	1	Y932_STRR6	Q8u3k6 pyrococcus	804	34	47.2	878	2	Q7QAL3	Q7qal3 anopheles g
732	34	47.2	543	1	Y932_STRR6	Q8dp77 streptococc	805	34	47.2	900	2	Q6EQM5	Q6eqm5 oryza sativ
733	34	47.2	544	1	C3B9_CANAL	Q97r12 streptococc	806	34	47.2	902	2	Q73FX1	Q73fx1 wolbachia p
734	34	47.2	548	2	Q753G1	O42779 candida alb	807	34	47.2	986	2	Q6BNF2	Q6bnf2 lotus japon
735	34	47.2	553	2	Q7S874	Q753g1 ashbya goes	808	34	47.2	1012	2	Q8BNF2	Q8bnf2 debaryomyce
736	34	47.2	553	2	Q6FE47	Q7b874 neurospora	809	34	47.2	1012	2	Q8BNF2	Q8bnf2 debaryomyce
737	34	47.2	555	2	Q6CG37	Q6fe47 acinetobact	810	34	47.2	1027	2	Q65VE8	Q65ve8 mannheimia
738	34	47.2	561	2	Q9SIC1	Q6cg37 yarrowia li	811	34	47.2	1051	2	Q753A0	Q753a0 ashbya goes
739	34	47.2	578	1	HPCL_HUMAN	Q9sic1 arabidopsis	812	34	47.2	1052	2	Q9S1S3	Q9s1s3 streptomyce
740	34	47.2	579	2	Q8Y3W4	Q9uj83 homo sapien	813	34	47.2	1057	2	Q6CES9	Q6ces9 yarrowia li
741	34	47.2	579	2	Q927C6	Q8y3w4 listeria mo	814	34	47.2	1062	2	Q8E0P9	Q8e0p9 streptococc
742	34	47.2	579	2	Q71W56	Q927c6 listeria in	815	34	47.2	1070	2	Q8IPB2	Q8ipb2 drosophila
743	34	47.2	581	1	HPCL_MOUSE	Q927c6 listeria in	816	34	47.2	1080	2	Q9SDC1	Q9sdc1 oryza sativ
744	34	47.2	581	2	Q8CHM7	Q9qxe0 mus musculu	817	34	47.2	1091	2	Q8EFP6	Q8efp6 shewanella
745	34	47.2	582	2	Q73JW2	Q8chm7 rattus norv	818	34	47.2	1114	2	Q7YYT9	Q7yyt9 cryptospori
746	34	47.2	586	2	Q74IP7	Q73jw2 treponema d	819	34	47.2	1137	2	Q8CZU0	Q8czu0 yersinia pe
747	34	47.2	595	2	Q8T4N1	Q74ip7 lactobacill	820	34	47.2	1230	2	Q6SLJ9	Q6slj9 bacillus li
748	34	47.2	596	2	Q875G7	Q8t4n1 trichoplusi	821	34	47.2	1280	2	Q95Y17	Q95y17 asterina pe
749	34	47.2	597	2	Q7R0F7	Q875g7 candida gla	822	34	47.2	1289	2	Q93IR7	Q93ir7 salmonella
750	34	47.2	598	2	Q6FK45	Q7r0f7 giardia lam	823	34	47.2	1289	2	Q8ZRL2	Q8zrl2 salmonella
751	34	47.2	598	2	Q95U43	Q6fk45 candida gla	824	34	47.2	1316	2	Q96968	Q96968 bombyx mori
752	34	47.2	598	2	Q6UP04	Q95u43 drosophila	825	34	47.2	1325	1	YAE6_SCHPO	YAE609 streptococc
753	34	47.2	598	2	Q7NFS2	Q6up04 lactobacill	826	34	47.2	1341	2	Q88304	Q88304 sandfly fev
754	34	47.2	600	2	Q869T6	Q7nfs2 gloeobacter	827	34	47.2	1374	2	Q8E0M9	Q8e0m9 streptococc
755	34	47.2	603	2	Q9U3F4	Q869t6 dictyosteli	828	34	47.2	1419	2	Q6D375	Q6d375 erwinia car
756	34	47.2	620	2	Q895H3	Q9u3f4 caenorhabdi	829	34	47.2	1512	2	Q812I3	Q812i3 plasmodium
757	34	47.2	630	2	Q973J8	Q895h3 clostridium	830	34	47.2	1516	2	Q9Y752	Q9y752 candida alb
758	34	47.2	632	2	Q73VP5	Q973j8 sulfolobus	831	34	47.2	1583	1	MY3A_HUMAN	MY3A04 plasmodium
759	34	47.2	648	2	Q6CSM4	Q73vp5 corynebacte	832	34	47.2	1616	1	GSAB_PICPA	GSAB04 homo sapien
760	34	47.2	651	2	Q6MZW7	Q6csm4 yarrowia li	833	34	47.2	2043	1	Q8WQ87	Q8wq87 chiromomus
761	34	47.2	652	2	Q941X1	Q6mzw7 homo sapien	834	34	47.2	2052	1	UBR8_SCHPO	UBR873 schizosacch

835	34	47.2	2346	2	Q7RWC7	Q7rwc7 neurospora	908	33	45.8	166	2	Q9B158	Q9b158 ophiactis s
836	34	47.2	2482	2	Q7YIZ4	Q7yiz4 cryptospori	909	33	45.8	166	2	Q9B3M8	Q9b3m8 ophiactis s
837	34	47.2	2603	2	Q9X553	Q9x553 potorous tr	910	33	45.8	166	2	Q9B3N2	Q9b3n2 ophiactis s
838	34	47.2	2715	2	Q7PGW6	Q7pgw6 anopheles g	911	33	45.8	169	2	Q849R7	Q849r7 klebsiella
839	34	47.2	2746	2	Q8IMS2	Q8ims2 drosophila	912	33	45.8	170	2	Q8N2G2	Q8n2g2 homo sapien
840	34	47.2	2764	2	Q8O1399	Q8o1399 drosophila	913	33	45.8	170	2	Q849S9	Q849s9 klebsiella
841	34	47.2	2788	2	Q7QB39	Q7qb39 anopheles g	914	33	45.8	172	2	Q849S9	Q849s9 klebsiella
842	34	47.2	2802	2	Q8O1397	Q8o1397 drosophila	915	33	45.8	173	2	Q849S7	Q849s7 klebsiella
843	34	47.2	2802	2	Q8O1398	Q8o1398 drosophila	916	33	45.8	174	2	Q7RCK6	Q7rck6 plasmodium
844	34	47.2	2802	2	Q9VB32	Q9vb32 drosophila	917	33	45.8	175	2	Q8EXL2	Q8exl2 leptospira
845	34	47.2	3064	2	Q82XT8	Q82xt8 nitrosomona	918	33	45.8	177	2	Q6ZW67	Q6zw67 homo sapien
846	34	47.2	3111	2	Q74QP0	Q74qp0 versinia pe	919	33	45.8	178	2	Q849R8	Q849r8 klebsiella
847	34	47.2	3401	2	Q81B03	Q81b03 plasmodium	920	33	45.8	179	1	YPUI_BACSU	P35156 bacillus su
848	34	47.2	5704	2	Q7QVV9	Q7qv9 giardia lam	921	33	45.8	179	2	Q849T1	Q849t1 klebsiella
849	33.5	46.5	110	2	Q8OUC9	Q8ouc9 mus musculu	922	33	45.8	182	2	Q7OIH7	Q7oih7 arabidopsis
850	33.5	46.5	139	2	Q9L5W3	Q9l5w3 liberibacte	923	33	45.8	183	2	Q8EKA5	Q8eka5 shewanella
851	33.5	46.5	146	1	RPOB_LIBAF	P41187 liberibacte	924	33	45.8	188	2	Q966D9	Q966d9 caenorhabdi
852	33.5	46.5	178	1	RPOB_LIBAS	P36251 liberibacte	925	33	45.8	189	2	Q9NHV3	Q9nhv3 babesia equ
853	33.5	46.5	216	2	Q73LZ5	Q73lz5 traponema d	926	33	45.8	191	2	Q8FP82	Q8fp82 candida gra
854	33.5	46.5	218	2	Q6SHG7	Q6shg7 uncultured	927	33	45.8	192	2	Q55978	Q55978 human immun
855	33.5	46.5	251	2	Q81T43	Q81t43 bacillus an	928	33	45.8	193	2	Q9X8G0	Q9x8g0 streptomyce
856	33.5	46.5	292	2	Q895Z9	Q895z9 clostridium	929	33	45.8	194	1	YA46_RALSO	P58633 raietonia s
857	33.5	46.5	336	1	Y883_METJA	Q58293 methanococc	930	33	45.8	200	2	O07498	O07498 bacillus fi
858	33.5	46.5	343	1	GP57_HUMAN	Q9p1p4 homo sapien	931	33	45.8	204	2	Q8RH16	Q8rh16 fusobacteri
859	33.5	46.5	415	2	Q8UG69	Q8j969 brachydanio	932	33	45.8	205	2	Q839R3	Q839r3 bacillus ce
860	33.5	46.5	426	1	AROA_PASPI	Q8vp65 pasteurella	933	33	45.8	205	2	Q81NX5	Q81nx5 bacillus an
861	33.5	46.5	426	1	AROA_VTBPA	Q87qx9 vibrio para	934	33	45.8	205	2	Q6HH47	Q6hh47 bacillus th
862	33.5	46.5	427	1	AROA_BUCAI	P57396 buchnera ap	935	33	45.8	207	2	Q6FZZ4	Q6fzz4 bartonella
863	33.5	46.5	429	1	Q8UZF9	Q8uzf9 cercopithe	936	33	45.8	207	2	Q9AQJ6	Q9aqj6 acinetobact
864	33.5	46.5	476	2	Q9LNV8	Q9lnv8 arabidopsis	937	33	45.8	209	1	EFTS_CYAME	Q85fr4 cyanidiosch
865	33.5	46.5	496	2	Q8T0T6	Q8t0t6 drosophila	938	33	45.8	215	2	Q6ZL06	Q6zlu6 burkholderi
866	33.5	46.5	526	2	Q69F76	Q69f76 liberibacte	939	33	45.8	215	2	Q63S79	Q63s79 burkholderi
867	33.5	46.5	815	2	Q9ESX7	Q9esx7 cavia porce	940	33	45.8	216	2	Q8SON5	Q8son5 oryza sativ
868	33.5	46.5	845	2	Q76KL2	Q76kl2 cavia porce	941	33	45.8	222	2	Q6CLW7	Q6clw7 kluyveromyc
869	33.5	46.5	876	2	Q99N77	Q99n77 rattus norv	942	33	45.8	222	2	Q9N5R0	Q9n5r0 caenorhabdi
870	33.5	46.5	893	2	Q9ESX6	Q9esx6 cavia porce	943	33	45.8	222	2	Q83565	Q83565 traponema p
871	33.5	46.5	907	2	Q8AWX1	Q8awx1 xenopus tiro	944	33	45.8	223	2	Q849S0	Q849s0 klebsiella
872	33.5	46.5	930	1	TRPE_MOUSE	Q61l43 mus musculu	945	33	45.8	224	2	Q97ZN9	Q97zn9 sulfolobus
873	33.5	46.5	930	2	Q99N78	Q99n78 rattus norv	946	33	45.8	226	2	Q7PL26	Q7pl26 drosophila
874	33.5	46.5	1275	2	Q62658	Q62658 canis fami	947	33	45.8	230	2	Q97I15	Q97i15 clostridium
875	33	45.8	69	2	Q7MPD8	Q7mpd8 vibrio vuln	948	33	45.8	232	1	RL1_BACST	P04447 bacillus st
876	33	45.8	69	2	Q8DE83	Q8de83 vibrio vuln	949	33	45.8	232	2	Q76BE1	Q76be1 amia calva
877	33	45.8	76	2	Q7RI38	Q7ri38 plasmodium	950	33	45.8	232	2	Q9ZLC9	Q9zlc9 helicobacte
878	33	45.8	86	2	Q41123	Q41123 paramedium	951	33	45.8	236	2	Q980Y8	Q980y8 sulfolobus
879	33	45.8	88	2	Q6CYD5	Q6cyd5 kluyveromyc	952	33	45.8	238	2	Q9MP32	Q9mp32 dolichoderu
880	33	45.8	90	2	Q7FAD3	Q7fad3 oryza sativ	953	33	45.8	239	2	Q03190	Q03190 leptomyrmex
881	33	45.8	100	2	Q7MG54	Q7mc54 vibrio vuln	954	33	45.8	240	2	Q7PC07	Q7pc07 rickettsia
882	33	45.8	111	2	Q9YB17	Q9yb17 aeropyrum p	955	33	45.8	240	2	Q92HW2	Q92hw2 rickettsia
883	33	45.8	112	2	Q86450	Q86450 pseudanabae	956	33	45.8	240	2	Q68WM7	Q68wm7 rickettsia
884	33	45.8	122	2	Q8GS70	Q8gs70 oryza sativ	957	33	45.8	241	2	Q75FM8	Q75fm8 leptospira
885	33	45.8	128	2	Q6LTT5	Q6l1t5 photobacter	958	33	45.8	243	2	Q8RW00	Q8rw00 triticum ae
886	33	45.8	129	2	Q6C921	Q6c921 yarrowia li	959	33	45.8	243	2	Q8CWH3	Q8cwh3 versinia pe
887	33	45.8	135	2	Q6C921	Q6c921 homo sapien	960	33	45.8	245	1	PYHD_NPVVN	Q25469 malacoema
888	33	45.8	138	2	Q9Y349	Q9y349 homo sapien	961	33	45.8	246	1	SURE_PASMU	P57955 pasteurella
889	33	45.8	140	2	Q97TH1	Q97th1 clostridium	962	33	45.8	247	2	Q7W8D9	Q7w8d9 bordetella
890	33	45.8	140	2	Q72AJ1	Q72aj1 desulfovibr	963	33	45.8	247	2	Q7WLZ8	Q7wlz8 bordetella
891	33	45.8	140	2	Q9WZM9	Q9wzm9 thermotoga	964	33	45.8	249	2	Q62M44	Q62m44 burkholderi
892	33	45.8	144	2	Q9V1S1	Q9v1s1 pyrococcus	965	33	45.8	249	2	Q63S22	Q63s22 burkholderi
893	33	45.8	144	2	Q73DJ9	Q73dj9 bacillus ce	966	33	45.8	251	2	Q74M76	Q74m76 nanoarchaeu
894	33	45.8	146	2	Q8DY20	Q8dy20 streptococc	967	33	45.8	251	2	Q8LFE0	Q8lfe0 arabidopsis
895	33	45.8	146	2	Q854J9	Q8e4j9 streptococc	968	33	45.8	251	2	Q9LSW8	Q9lsw8 arabidopsis
896	33	45.8	153	2	Q57985	Q57985 pyrococcus	969	33	45.8	252	2	Q7PGI1	Q7pgil anopheles g
897	33	45.8	153	2	Q53934	Q53934 shewanella	970	33	45.8	254	2	Q9ZD39	Q9zd39 rickettsia
898	33	45.8	154	2	Q8SZN6	Q8szn6 drosophila	971	33	45.8	257	1	H161_VIBVY	Q9ksw8 vibrio vuln
899	33	45.8	154	2	Q6WFX1	Q6wfx1 cryptothlad	972	33	45.8	257	1	HIS6_VIBCH	Q87qk6 vibrio para
900	33	45.8	154	2	Q849R9	Q849r9 klebsiella	973	33	45.8	257	1	HIS6_VIBPA	Q88q5 vibrio vuln
901	33	45.8	155	2	Q6MR19	Q6mr19 bdellovibri	974	33	45.8	257	1	HIS6_VIBVU	Q7mah0 wolinnella s
902	33	45.8	157	2	Q9B3N4	Q9b3n4 ophiactis s	975	33	45.8	259	2	Q7MSH0	Q76ls8 staphylococ
903	33	45.8	158	2	Q6FL78	Q6fl78 candida gla	976	33	45.8	266	2	Q8E0L3	Q8e0l3 streptococc
904	33	45.8	161	2	Q849T0	Q849t0 klebsiella	977	33	45.8	266	2	Q8E687	Q8e687 streptococc
905	33	45.8	166	2	Q8SEF9	Q8sef9 ophiactis s	978	33	45.8	269	2	Q8ZYH3	Q8zyh3 pyrobaculum
906	33	45.8	166	2	Q8SGA5	Q8sga5 ophiactis s	979	33	45.8	270	2	Q8F5I0	Q8f5i0 leptospira

981 33 45.8 271 1 AROE PYRFU Q8u0a6 pyrococcus
 982 33 45.8 271 1 HIS6 ARCFU Q29439 archaeoglob
 983 33 45.8 273 2 QNHV4 Q9nhy4 babesia equ
 984 33 45.8 275 1 NADE ECOS7 Q8xd9 escherichia
 985 33 45.8 275 1 NADE ECOL6 Q8fn06 escherichia
 986 33 45.8 275 1 NADE ECOL1 P18843 escherichia
 987 33 45.8 275 1 NADE STALP Q8cnp1 staphylococ
 988 33 45.8 279 2 Q9UUA6 Q9uuu6 schizosacch
 989 33 45.8 280 2 Q64BW2 Q64bw2 bcdulvibri
 990 33 45.8 280 2 Q6WKK1 Q6mk1 bdellovibri
 991 33 45.8 281 1 RNZN ARATH Q8lgu7 arabidopsis
 992 33 45.8 281 2 Q88AC9 Q88ac9 pseudomonas
 993 33 45.8 281 2 Q88R39 Q88r39 pseudomonas
 994 33 45.8 286 2 Q80TD9 Q80td9 mus musculus
 995 33 45.8 289 2 Q62347 Q62347 caenorhabdi
 996 33 45.8 289 2 Q8RSU3 Q8rsu3 klebsiella
 997 33 45.8 289 2 Q8RSU4 Q8rsu4 klebsiella
 998 33 45.8 290 1 BLO2 KLEOX P23954 klebsiella
 999 33 45.8 290 2 Q8RLU6 Q8rlu6 klebsiella
 1000 33 45.8 290 2 Q8RSU5 Q8rsu5 klebsiella

ALIGNMENTS

RESULT 1

GA56 HUMAN
 ID GAS6_HUMAN STANDARD; PRT; 721 AA.
 AC Q14393; Q727N3;
 DC 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth-arrest-specific protein 6 precursor (GAS-6).
 GN Name=GAS6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=93330291; PubMed=8336730;
 RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
 RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
 RT member of the vitamin K-dependent proteins related to protein S, a
 RT negative coregulator in the blood coagulation cascade.";
 RL Mol. Cell. Biol. 13:4976-4985(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RA Munoz X., Sumoy L., de Frutos P., Sala N.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Uterus;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami T., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Sutterch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-85 FROM N.A.
 RA Maree A.O., Hillmann A., McRedmond J.P., Fitzgerald D.J.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP RECEPTOR INTERACTION.
 RX PubMed=7854420; DOI=10.1038/373623a0;
 RA Varnum B.C., Hunt C., Elliott G., Garcia A., Bartley T.D.,
 RA Fridell Y.W., Hunt R.W., Trail G., Clogston C., Toso R.J.,
 RA Yanagihara D., Bennett L., Sylber M., Merewether L.A., Tseng A.,
 RA Escobar E., Liu E.T., Yamane H.K.;
 RT "Axl receptor tyrosine kinase stimulated by the vitamin K-dependent
 RT protein encoded by growth-arrest-specific gene 6.";
 RL Nature 373:623-626(1995).
 RN [7]
 RP RECEPTOR INTERACTION.
 RX PubMed=7867073; DOI=10.1016/0092-8674(95)90520-0;
 RA Stitt T.N., Conn G., Gore M., Lai C., Bruno J., Radziejewski C.,
 RA Mattsson K., Fisher J., Gies D.R., Jones P.F., Maslakowski P.,
 RA Ryan T.E., Tobkes N.J., Chen D.H., Distefano P.S., Long G.L.,
 RA Basilico C., Goldfarb M.P., Lemke G., Glass D.J., Yancopoulos G.D.;
 RT "The anticoagulation factor protein S and its relative, Gas6, are
 RT ligands for the Tyro 3/Axl family of receptor tyrosine kinases.";
 RL Cell 80:661-670(1995).
 RN [8]
 RP ALTERNATIVE SPLICING (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX PubMed=9326368; DOI=10.1016/S0014-5793(97)01094-6;
 RA Marcandalli P., Gostissa M., Varnum B., Goruppi S., Schneider C.;
 RT "Identification and tissue expression of a splice variant for the
 RT growth arrest-specific gene gas6.";
 RL FEBS Lett. 415:56-58(1997).
 RN [9]
 RP RECEPTOR INTERACTION.
 RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;
 RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
 RA Mizuno K.;

RT Identification of the product of growth arrest-specific gene 6 as a
common ligand for Axl, Sky, and Mer receptor tyrosine kinases.;
J. Biol. Chem. 271:30022-30027(1996).
[10]
RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND PROCESSING.
RX PubMed=9326369; DOI=10.1016/S0014-5793(97)01093-4; Clogston C.,
RA Goruppi S., Yamane H., Marcandalli P., Garcia A., Clogston C.,
RA Gostissa M., Varnum B., Schneider C.;
RT "The product of a gas6 splice variant allows the release of the domain
responsible for Axl tyrosine kinase receptor activation.";
RL FEBS Lett. 415:59-63(1997).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 261-721 (ISOFORM 2), AND
MUTAGENESIS OF PHE-530; LEU-663 AND TYR-703.
RX PubMed=8621659; DOI=10.1074/jbc.271.16.9785;
RA Mark M.R., Chen J., Hammonds R.G., Sadick M., Godowski P.J.;
RT "Characterization of Gas6, a member of the superfamily of G domain-
containing proteins, as a ligand for Rse and Axl";
RL J. Biol. Chem. 271:9785-9789(1996).
RN [12]
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
and MER whose signaling is implicated in cell growth and survival,
cell adhesion and cell migration. Plays a role in thrombosis by
amplifying platelet aggregation and secretion in response to known
agonists (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonym=gas6SV;
CC IsoId=Q14393-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q14393-2; Sequence=VSP_010494;
CC Name=3;
CC IsoId=Q14393-3; Sequence=VSP_010492, VSP_010493, VSP_010494;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Plasma. Isoform 1 and isoform 2 are widely
expressed. Isoform 1 is the predominant form in spleen.
CC -!- PTM: Isoform 1 is proteolytically processed after secretion to
yield a N-terminal 36 kDa protein and a C-terminal 50 kDa protein
including the laminin G-like domains which activates AXL.
CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
dependent carboxylation. These residues are essential for the
binding of calcium (By similarity).
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL: LI3720; AAA58494.1; --
CC EMBL: AY256843; AAO84057.1; --
CC EMBL: AY256830; AAO84057.1; JOINED.
CC EMBL: AY256831; AAO84057.1; JOINED.
CC EMBL: AY256832; AAO84057.1; JOINED.
CC EMBL: AY256833; AAO84057.1; JOINED.
CC EMBL: AY256834; AAO84057.1; JOINED.
CC EMBL: AY256835; AAO84057.1; JOINED.
CC EMBL: AY256836; AAO84057.1; JOINED.
CC EMBL: AY256837; AAO84057.1; JOINED.
CC EMBL: AY256838; AAO84057.1; JOINED.
CC EMBL: AY256839; AAO84057.1; JOINED.
CC EMBL: AY256840; AAO84057.1; JOINED.
CC EMBL: AY256841; AAO84057.1; JOINED.
CC EMBL: AY256842; AAO84057.1; JOINED.
CC EMBL: AK126533; BAC86580.1; --
CC EMBL: BC038984; AAB38984.1; --

DR EMBL: AY170372; AAO41859.1; --
DR PIR: B48089; B48089.
DR PDB: 1H30; X-ray; A=257-678.
DR Genew: HGNC:4168; GAS6.
DR MIM: 600441; --
DR GO: GO:0005102; F:receptor binding; TAS.
DR GO: GO:0008283; P:cell proliferation; TAS.
DR GO: GO:0007165; P:signal transduction; TAS.
Query Match 100.0%; Score 72; DB 1; Length 721;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFVSAKSVKSLYL 15
DB 327 VPFVSAKSVKSLYL 341
|||||
RESULT 2
GAS6 MOUSE
ID GAS6 MOUSE STANDARD; PRT; 674 AA.
AC Q61592; Q99K57;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-arrest-specific protein 6 precursor (GAS-6).
GN Name=Gas6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330291; PubMed=8336730;
RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
member of the vitamin K-dependent proteins related to protein S, a
negative coregulator in the blood coagulation cascade.";
RL Mol. Cell. Biol. 13:4976-4985(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.U., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX PubMed=11175853; DOI=10.1038/84667;
RA Angelillo-Scherer A., de Frutos P., Aparicio C., Melis E., Savi P.,
RA Lupu F., Arnout J., Dewerchin M., Hoylaerts M., Herbert J., Collen D.,
RA Dahlback B., Carmeliet P.;
RT "Deficiency or inhibition of Gas6 causes platelet dysfunction and
protects mice against thrombosis";
RL Nat. Med. 7:215-221(2001).
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
and MER whose signaling is implicated in cell growth and survival,

cell adhesion and cell migration (By similarity). plays a role in thrombosis by amplifying platelet aggregation and secretion in response to known agonists.

-!- SUBUNIT: Monomer (By similarity).

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K dependent carboxylation. These residues are essential for the binding of calcium (By similarity). show protection against thrombosis, but no spontaneous bleeding.

-!- SIMILARITY: Contains 4 EGF-like domains.

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

-!- SIMILARITY: Contains 2 laminin G-like domains.

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EMBL; X59846; CAA42507.1; -.

DR EMBL; BC005444; AA05444.1; -.

DR PIR; A48089; A48089.

DR HSP; P00740; ICFH.

DR MGD; MGI:95660; Gas6.

DR InterPro; IPR00152; Asx hydroxyl S.

DR InterPro; IPR008985; ConA like lec_gl.

DR InterPro; IPR00742; EGF 2.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR002383; GLA blood.

DR InterPro; IPR001791; Laminin G.

DR InterPro; IPR003129; TSP N.

DR InterPro; IPR00294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00054; Laminin G; 2.

DR PRINTS; PR0001; GLABLOOD.

DR SMART; SM00179; EGF CA; 3.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01186; EGF 2; 3.

DR PROSITE; PS00026; EGF 3; 4.

DR PROSITE; PS01187; EGF CA; 3.

DR PROSITE; PS00011; GLA 1; 1.

DR PROSITE; PS00998; GLA 2; 1.

DR PROSITE; PS00025; LAM G DOMAIN; 2.

KW Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid; Growth regulation; Repeat; Signal; Vitamin K.

FT SIGNAL 1 27 Potential.

FT CHAIN 28 674 Growth-arrest-specific protein 6.

FT DOMAIN 50 91 Gla.

FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).

FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).

FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).

FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).

FT DOMAIN 295 467 Laminin G-like 1.

FT DOMAIN 474 666 Laminin G-like 2.

FT METAL 326 326 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 328 328 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 437 437 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 652 652 Calcium (By similarity).

FT DISULFID 117 130 By similarity.

FT DISULFID 122 139 By similarity.

FT DISULFID 141 150 By similarity.

FT DISULFID 157 168 By similarity.

FT DISULFID 164 177 By similarity.

FT DISULFID 179 192 By similarity.

FT DISULFID 198 209 By similarity.

FT DISULFID 204 218 By similarity.

FT DISULFID 220 233 By similarity.

FT DISULFID 239 248 By similarity.

FT DISULFID 244 257 By similarity.

FT DISULFID 259 274 By similarity.

FT DISULFID 280 280 By similarity.

FT DISULFID 441 467 By similarity.

FT DISULFID 639 666 By similarity.

FT CARBOHYD 417 417 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 488 488 N-linked (GlcNAc..) (Potential).

FT CONFLICT 530 530 Missing (in Ref. 1).

SQ SEQUENCE 674 AA; 74609 MW; 7C41P7693903F401 CRC64;

Query Match 95.8%; Score 69; DB 1; Length 674;

Best Local Similarity 93.3%; Pred. No. 0.0014;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15

DB 281 VPFSMAKSVKSLYL 295

RESULT 3

GA6_RAT STANDARD; PRT; 674 AA.

AC Q63772;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Growth-arrest-specific protein 6 precursor (Gas-6) (Growth-

DE Potentiating factor) (GPF).

GN Name=Gas6;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1] TaxID=10116;

RP SEQUENCE FROM N.A.

RP MEDLINE=95197586; PubMed=7890695; DOI=10.1074/jbc.270.11.5702;

RA Nakano T., Higashino K., Kikuchi N., Kishino J., Nomura K., Fujita H., Ohara O., Arita H.;

RT "Vascular smooth muscle cell-derived, Gla-containing growth-

RT potentiating factor for Ca(2+)-mobilizing growth factors.";

RL J. Biol. Chem. 270:5702-5705(1995).

RN [2]

RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RX PubMed=7559388; DOI=10.1074/jbc.270.39.22681;

RA Ohashi K., Nagata K., Toshima J., Nakano T., Arita H., Tenda H., Suzuki K., Mizuno K.;

RT "Stimulation of sky receptor tyrosine kinase by the product of growth arrest-specific gene 6.";

RL J. Biol. Chem. 270:22681-22684(1995).

RN [3]

RP RECEPTOR INTERACTION

RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;

RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H., Mizuno K.;

RT "Identification of the product of growth arrest-specific gene 6 as a common ligand for Axl, Sky, and Mer receptor tyrosine kinases.";

RL J. Biol. Chem. 271:30022-30027(1996).

RN [4]

RP GAMMA-CARBOXYGLUTAMIC ACIDS.

RX PubMed=9163328;

RA Nakano T., Kawamoto K., Kishino J., Nomura K., Higashino K., Arita H.;

RT "Requirement of gamma-carboxyglutamic acid residues for the biological activity of Gas6: contribution of endogenous Gas6 to the proliferation of vascular smooth muscle cells.";

RL Biochem. J. 323:387-392(1997).

CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3 and MER whose signaling is implicated in cell growth and survival,

cell adhesion and cell migration. Plays a role in thrombosis by amplifying platelet aggregation and secretion in response to known agonists (By similarity).

-!- SUBUNIT: Monomer (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Plasma.

-!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K dependent carboxylation. These residues are essential for the binding of calcium (Probable).

-!- SIMILARITY: Contains 4 EGF-like domains.

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

-!- SIMILARITY: Contains 2 laminin G-like domains.

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EMBL; D42148; BAA07719.1; --
 DR PIR; I55476; I55476.
 DR HSP; P00740; LCFH.
 DR RGD; 61913; Gas6.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR003129; TSP N.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00054; Laminin G; 2.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX HYDROXYL; 4.
 DR PROSITE; PS00022; EGF 1; 1.
 DR PROSITE; PS01186; EGF 2; 3.
 DR PROSITE; PS00026; EGF 3; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS00011; GLA 1; 1.
 DR PROSITE; PS00998; LAM G DOMAIN; 2.
 DR PROSITE; PS00025; LAM G DOMAIN; 2.
 DR Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid; Growth regulation; Repeat; Signal; Vitamin K.
 KW SIGNAL 1 27 Potential.
 FT CHAIN 28 674 Growth-arrest-specific protein 6.
 FT DOMAIN 50 91 Gla.
 FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).
 FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).
 FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 295 467 Laminin G-like 1.
 FT DOMAIN 474 666 Laminin G-like 2.
 FT METAL 326 326 Calcium (By similarity).
 FT METAL 328 328 Calcium (via carbonyl oxygen) (By similarity).
 FT METAL 437 437 Calcium (via carbonyl oxygen) (By similarity).
 FT METAL 652 652 Calcium (By similarity).
 FT DISULFID 117 130 By similarity.
 FT DISULFID 122 139 By similarity.
 FT DISULFID 141 150 By similarity.
 FT DISULFID 157 168 By similarity.
 FT DISULFID 164 177 By similarity.
 FT DISULFID 179 192 By similarity.

FT DISULFID 198 209 By similarity.
 FT DISULFID 204 218 By similarity.
 FT DISULFID 220 233 By similarity.
 FT DISULFID 239 248 By similarity.
 FT DISULFID 244 257 By similarity.
 FT DISULFID 259 274 By similarity.
 FT DISULFID 280 566 By similarity.
 FT DISULFID 441 467 By similarity.
 FT DISULFID 639 666 By similarity.
 FT CARBOHYD 189 189 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 674 AA; 74637 MW; FBF8F8B8664D6F2E CRC64;

Query Match 95.8%; Score 69; DB 1; Length 674;
 Best Local Similarity 93.3%; Pred. No. 0.0014;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSVAKSVKSLYL 295
 ||||:|||||||
 ||||:|||||||

RESULT 4
 Q6IRL1 PRELIMINARY; PRT; 674 AA.
 ID Q6IRL1
 AC Q6IRL1
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Gas6 protein.
 GN Name=Gas6;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwald J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 CC Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL; BC070881; AAH70881.1; -.
 DR HSP; P00736; IAPQ.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0007155; F:cell adhesion; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.


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DR InterPro; IPR008985; ConA_like_1ec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA; 2.
DR Pfam; PF00594; Glaf; 1.
DR Pfam; PF02210; Laminin_G_2; 2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 674 AA; 74671 MW; CC9A5EBD04480AE7 CRC64;

Query Match 95.8%; Score 69; DB 2; Length 674;
Best Local Similarity 93.3%; Pred. No. 0.0014;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLGL 15
| | | | |
Db 281 VPFSMAKSVKSLYLGL 295

RESULT 5
Q6PAE0 PRELIMINARY; PRT; 668 AA.
AC Q6PAE0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68463 protein.
GN Name=MGC68463;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettunen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC060355; AAH60355.1; -.
DR HSSP; P00743; LAPO.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_1ec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00594; Glaf; 1.
DR Pfam; PF02210; Laminin_G_2; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 668 AA; 74905 MW; 8BEE5232F4EF3916 CRC64;

Query Match 63.9%; Score 46; DB 2; Length 668;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLGL 15
| | | | |
Db 278 IFFASEKSKNSLYLG 292

RESULT 6
YLD1_CABEL STANDARD; PRT; 374 AA.
ID YLD1_CABEL
AC Q03566;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor C38C10.1.
GN ORFNames=C38C10.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398; DOI=10.1039/368032a0;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey I., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnenhammer E., Staden K.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RG "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- FUNCTION: Not known. Putative receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC -----
CC EMBL; Z19153; CAA79546.1; -;
CC FIRM; S28285; S28285.
CC HSSP; P02699; 1P88.
CC WormBase; WBGene00006576; tkr-1.
CC WormPep; C38C10.1; CR00104.
CC InterPro; IPR000276; GPCR Rhodpsn.
CC InterPro; IPR001681; Neurokin_receptor.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOOPSN.
CC PRINTS; PR00244; NEUROKININR.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Hypothetical protein;
KW Transmembrane.
KW DOMAIN 1 12 Extracellular (Potential).
FT TRANSMEM 13 37 1 (Potential).
FT DOMAIN 38 45 Cytoplasmic (Potential).
FT TRANSMEM 46 66 2 (Potential).
FT DOMAIN 67 83 Extracellular (Potential).
FT TRANSMEM 84 104 3 (Potential).
FT DOMAIN 105 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT DOMAIN 148 172 Extracellular (Potential).
FT TRANSMEM 173 193 5 (Potential).
FT DOMAIN 194 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 285 Extracellular (Potential).
FT TRANSMEM 286 374 7 (Potential).
FT DOMAIN 287 374 Cytoplasmic (Potential).
SQ SEQUENCE 374 AA; 42940 MW; 1311AE2743014C01 CRC64;
Query Match 61.1%; Score 44; DB 1; Length 374;
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFVSAKSVKSLY 13
DB 142 LPFAIAASVNSLY 154
RESULT 7
UVR_C MYCAA
ID UVR_C MYCAA STANDARD; PRT; 571 AA.
AC O84899;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UvrABC system protein C (UvrC protein) (Excinuclease ABC subunit C).
GN Name=uvrC;
OS Mycoplasma agalactiae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG2;
RX MEDLINE=9832980; PubMed=9664578; DOI=10.1006/mcpr.1998.0160;
RA Subramaniam S., Bergonier D., Poumarat F., Capaul S., Schlatter Y.,
RA Nicolet J., Frey J.;
RT "Species Identification of Mycoplasma bovis and Mycoplasma agalactiae
RT based on the uvrC genes by PCR.";
RL Mol. Cell. Probes 12:161-169(1998).
CC -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC processing of DNA lesions. UvrC both incises the 5' and 3' sides
CC of the lesion. The N-terminal half is responsible for the 3'
CC incision and the C-terminal half is responsible for the 5'
CC incision (By similarity).
CC -!- SUBUNIT: Interacts with uvrB in an incision complex (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the uvrC family.
CC -!- SIMILARITY: Contains 1 UVR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF003960; AAC32310.1; -;
CC HAMAP; MF_00203; -; 1.
CC InterPro; IPR010994; RUVA 2 like.
CC InterPro; IPR001943; UvrB/C.
CC InterPro; IPR009055; UvrB C.
CC InterPro; IPR004791; UvrC ABC.
CC InterPro; IPR001162; UvrC C.
CC InterPro; IPR00305; UvrC N.
CC Pfam; PF01541; GIY-YIG; 1.
CC Pfam; PF02151; UVR; 1.
CC ProDom; PD005870; UvrC C; 1.
CC SMART; SM00465; GIYC; 1.
CC TIGRPFAMs; TIGR00194; uvrC; 1.
CC PROSITE; PS50151; UVR; 1.
CC PROSITE; PS50164; UVR; 1.
CC PROSITE; PS50165; UVR; 2; 1.
CC DNA excision; DNA recombination; DNA repair; Excision nuclease;
KW SOS response.
FT DOMAIN 184 219 UVR.
SQ SEQUENCE 571 AA; 66214 MW; 74403690A5FE203C CRC64;
Query Match 61.1%; Score 44; DB 1; Length 571;
Best Local Similarity 72.7%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFVSAKSVKSLY 11
DB 142 LPFAIAASVNSLY 154

```

Db          557 VPFNVAKSIKN 567

RESULT 8
ID Q624E5 PRELIMINARY; PRT; 417 AA.
AC Q624E5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 25-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Limonene cyclase like protein.
GN Name=OSJNB0084L07.20-3; Synonyms=OSJNB0002L09.8-3;
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0084L07.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0002L09.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005179; BAC83915.1; -.
DR EMBL; AP005877; BAD31849.1; -.
DR InterPro; IPR004263; Exostosin.
DR Pfam; PF03016; Exostosin; 1.
SQ SEQUENCE 417 AA; 44610 MW; 67668E9A53B1DC6A CRC64;

Query Match 59.7%; Score 43; DB 2; Length 417;
Best Local Similarity 61.5%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFNVAKSVKSLY 13
:|||||:|:|
Db 323 LPFSVVMVKMIY 335

RESULT 9
ID Q624E7 PRELIMINARY; PRT; 606 AA.
AC Q624E7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative pectin-glucuronyltransferase.
GN Name=OSJNB0084L07.20-1; Synonyms=OSJNB0002L09.8-1;
OC Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0084L07.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0002L09.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005179; BAC83913.1; -.
DR EMBL; AP005877; BAD31848.1; -.
DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR004263; Exostosin.
DR Pfam; PF03016; Exostosin; 1.
KW Transferase.
SQ SEQUENCE 606 AA; 65830 MW; F90248E809A18266 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 606;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFNVAKSVKSLY 13
:|||||:|:|
Db 323 LPFSVVMVKMIY 335

RESULT 10
ID Q6DFA5 PRELIMINARY; PRT; 669 AA.
AC Q6DFA5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Gas6-prov protein.
GN Name=gas6-prov;
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocytes;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocytes;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocytes;
RC Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC076835; AAH76835.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.

```

DR GO: GO:0007155; P-cell adhesion; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl S.
 DR InterPro; IPR000985; ConA_like_lec_gl.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR003129; TSP_N.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_3.
 DR Pfam; PF07645; EGF_CA; 2.
 DR Pfam; PF00594; Glr; 1.
 DR Pfam; PF00054; Laminin_G.1; 1.
 DR Pfam; PF02210; Laminin_G.2; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
 KW EGF-like domain.
 SQ SEQUENCE 669 AA; 75232 MW; A8D1E362540F643 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 669;
 Best Local Similarity 60.0%; Pred. No. 72;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 279 LPFASEKSRNSLYLG 293

RESULT 11
 QY9984 PRELIMINARY; PRT; 252 AA.
 ID QY9984
 AC QY9984
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein APE2401.
 GN OrderedLocustNames=APE2401;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000064; BA081416.1; -.
 DR FIR; H72469; H72469.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 252 AA; 25912 MW; 527C1D8A70FFDC14 CRC64;

Query Match 58.3%; Score 42; DB 2; Length 252;
 Best Local Similarity 61.5%; Pred. No. 41;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 13
 DB 34 VAFSILRSLSLYL 46

RESULT 12
 BLAN ENTCL
 ID BLAN ENTCL STANDARD; PRT; 292 AA.
 AC P52663;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Imipenem-hydrolyzing beta-lactamase precursor (EC 3.5.2.6)
 DE (Carbapenemase) (NMC-A).
 GN Name=nmcA;
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-34.
 RC STRAIN=NOR-1;
 RX MEDLINE=94329582; PubMed=8052644;
 RA Naas T., Nordmann P.;
 RT "Analysis of a carbapenem-hydrolyzing class A beta-lactamase from
 RT Enterobacter cloacae and of its LysR-type regulatory protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:7693-7697(1994).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.89 ANGSTROMS).
 RC STRAIN=NOR-1;
 RX MEDLINE=99395084; PubMed=10464248; DOI=10.1074/jbc.274.36.25260;
 RA Mourey L., Kotra L.P., Belletini J., Bulichev A., O'Brien M.,
 RA Miller M.J., Mobashery S., Samama J.-P.;
 RT "Inhibition of the broad spectrum nonmetallo-carbapenemase of class A
 RT (NMC-A) beta-lactamase from Enterobacter cloacae by monocyclic beta-
 RT lactams.";
 RL J. Biol. Chem. 274:25260-25265(1999).
 CC -!- FUNCTION: Hydrolyzes carbapenems such as imipenem, which are
 CC extended-spectrum beta-lactam antibiotics.
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.
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 DR EMBL; Z21956; CAA79967.1; -.
 DR FIR; S35915; S35915.
 DR PDB; 1BUE; X-ray; A=28-292.
 DR PDB; 1BUL; X-ray; @=28-292.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; FALSE_NEG.
 KW 3D-structure; Antibiotic resistance; Direct protein sequencing;
 KW Hydrolase; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 292 Imipenem-hydrolyzing beta-lactamase.
 FT ACT_SITE 71 71 Acyl-ester intermediate.
 FT SITE 236 238 Substrate binding (By similarity).
 FT DISULFID 70 240
 FT TURN 30 31
 FT HELIX 32 42
 FT TURN 43 43
 FT STRAND 45 52

"A yeast protein similar to bacterial two-component regulators.";
 Science 262:566-569(1993).
 [2]
 RT SEQUENCE FROM N.A.
 RN STRAIN=9288C / AB972;
 RC MEDLINE=97313266; PubMed=9169870;
 RA Churche C.M., Bowman S., Badcock K., Bankier A., Brown D.,
 Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
 Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
 Moule S., Odell K., Pearson D., Raftandream M.A., Rice P., Rowley N.,
 Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
 "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IX.";
 Nature 387:84-87(1997).
 RL Nature 387:84-87(1997).
 RN [3].
 RP MUTAGENESIS OF HIS-576 AND ASP-1144.
 RX MEDLINE=94239498; PubMed=8183345; DOI=10.1038/369242a0;
 RA Maeda T., Wurgler-Murphy S.M., Saïto H.;
 "A two-component system that regulates an osmosensing MAP kinase
 cascade in yeast.";
 RT Nature 369:242-245(1994).
 RL Nature 369:242-245(1994).
 CC -!- FUNCTION: Forms part of a two-component regulatory system
 CC -!- SLN1/SSK1 activated by changes in the osmolarity of the
 CC extracellular environment. This system controls the SSK2/SSK22->
 CC PBS2->HOG1 pathway. Inactive SLN1 allows the unphosphorylated SSK1
 CC protein to activate SSK2 and SSK22, two MAPKKs that further
 CC stimulate the PBS2-HOG1 MAPK cascade. In low osmolarity media, the
 CC activated SLN1 histidine kinase represses the activation of the
 CC PBS2-HOG1 kinase cascade through phosphorylation of SSK1.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- PTM: Activation probably requires a transfer of a phosphate group
 CC between a His in the transmitter domain and an Asp of the receiver
 CC domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; Z38059; CAA86131.1; -;
 DR EMBL; U01835; AAC48912.1; -;
 DR PIR; S48387; S48387.
 DR PDB; 10XB; X-ray; B=1087-1220.
 DR PDB; 10XK; X-ray; B/D/F/H/J/L=1087-1220.
 DR Germline; 139682; -;
 DR SGD; S000001409; SLN1.
 DR GO; GO:0004673; F:protein-histidine kinase activity; IDA.
 DR GO; GO:0007234; P:osmosensory signaling pathway via two-compo. .; IDA.
 DR GO; GO:0042542; P:response to hydrogen peroxide; IMP.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR004358; Bact_sens_pr_C.
 DR InterPro; IPR011006; CheY like.
 DR InterPro; IPR009082; His_Kin_homodim.
 DR InterPro; IPR003661; His_Kin_N.
 DR InterPro; IPR005467; His_kinase.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00512; HisKA; 1.
 DR Pfam; PF00072; Response_reg; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HisKA; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS01109; HIS_KIN; 1.
 DR PROSITE; PS01109; RESPONSE REGULATORY; 1.
 DR 3D-structure; Kinase. Phosphorylation; Sensory transduction;
 KW Transferase; Transmembrane; Two-component regulatory system.
 KW DOMAIN 1 22 Cytoplasmic (Potential).
 FT TRANSMEM 23 46
 FT DOMAIN 47 333
 FT TRANSMEM 334 354
 FT DOMAIN 355 1220
 FT DOMAIN 573 928
 FT DOMAIN 1089 1210
 FT MOD_RES 576 576
 MOD_RES 1144 1144
 FT CARBOHYD 100 100
 FT CARBOHYD 138 138
 FT CARBOHYD 142 142
 FT CARBOHYD 181 181
 FT CARBOHYD 224 224
 FT CARBOHYD 272 272
 FT MUTAGEN 576 576
 FT MUTAGEN 891 891
 FT MUTAGEN 1144 1144
 SQ SEQUENCE 1220 AA; 134434 MW; 45PFE24A8165486B CRC64;

Potential.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 Histidine kinase.
 Response regulatory.
 Phosphohistidine (by autocatalysis)
 (Probable).
 4-aspartylphosphate (Probable).
 N-linked (GlcNAc. .) (Potential).
 N-linked (GlcNAc. .) (Potential).
 N-linked (GlcNAc. .) (Potential).
 N-linked (GlcNAc. .) (Potential).
 N-linked (GlcNAc. .) (Potential).
 H->Q: Inactive.
 H->D: In SLN1-1; slow growth.
 D->N: Inactive.
 MW; 45PFE24A8165486B CRC64;
 Query Match 58.3%; Score 42; DB 1; Length 1220;
 Best Local Similarity 81.8%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 VPFSVAKSVKS 11
 Db 955 VKFSVAKSIKS 965
 RESULT 16
 ID Q9VLA0 PRELIMINARY; PRT; 4345 AA.
 AC Q9VLA0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE CG15828-PA.
 ORFNames=CG15828;
 GN Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Paclebe J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betancourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL FlyBase;
RG FlyBase;
RN [6]
RP SEQUENCE FROM N.A.
RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003625; AAF52796.1; -;
DR FlyBase; FBgn0032136; CG15828.
DR GO; GO:0005319; F:lipid transporter activity; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR InterPro; IPR001454; DUF1081.
DR InterPro; IPR001747; Lipid transport N.
DR InterPro; IPR011030; LV superhelical.
DR InterPro; IPR001846; VWF D.
DR Pfam; PF06448; DUF1081; 1.
DR Pfam; PF01347; Vitellogenin_N; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00638; LPD_N; 1.
DR SMART; SM00216; VWD; 1.
SQ SEQUENCE 4345 AA; 495238 MW; 30AAC8439A52165F CRC64;

Query Match 58.3%; Score 42; DB 2; Length 4345;
Best Local Similarity 63.6%; Pred. No. 7.2e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSL 12

Db 2115 PFAVAKNIKSI 2125
||:||||:|
RESULT 17
Q7KTG2 PRELIMINARY; PRT; 4374 AA.
ID O7KTG2
AC Q7KTG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG15828-PB.
GN ORFNames=CG15828;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclebe J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Ye J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Paclebe J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS003625; AAS64667.1; -;
DR GO; GO:0005319; Flippid transporter activity; IEA.
DR GO; GO:0008669; Flippid transport; IEA.
DR InterPro; IPR009454; DUF1081.
DR InterPro; IPR001747; Lipid transprt N.
DR InterPro; IPR011030; LV superhelical.
DR Pfam; PF06448; DUF1081; 1.
DR Pfam; PF01347; Vitellinogenin_N; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00638; LPD_N; 1.
DR SMART; SM00216; VWD; 1.
SQ SEQUENCE 4374 AA; 498710 MW; C13F0DB2453D0F95 CRC64;
Query Match 58.3%; Score 42; DB 2; Length 4374;
Best Local Similarity 63.6%; Pred. No. 7.3e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 2 PFSVAKSVKSL 12
DB 2144 PFAVAKNIKS 2154
RESULT 18
Q9QKB0 PRELIMINARY; PRT; 218 AA.
AC Q9QKB0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZH 548;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134508; AAD56355.1; -;
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 1
FT SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;

FT NON_TER 1 1
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 23982 MW; F23A1BDB31F30308 CRC64;
Query Match 56.9%; Score 41; DB 2; Length 218;
Best Local Similarity 57.1%; Pred. No. 54;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFKNSKKVYL 91
RESULT 19
Q9QKB1 PRELIMINARY; PRT; 242 AA.
AC Q9QKB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP12;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134507; AAD56354.1; -;
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 1
FT NON_TER 242 242
FT SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;
Query Match 56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFKNSKKVYL 91
RESULT 20
Q9QKB2 PRELIMINARY; PRT; 242 AA.
AC Q9QKB2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H EGY93;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134506; AAD56353.1; -;
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 1
FT NON_TER 242 242
FT SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 21
Q9QKB3 PRELIMINARY; PRT; 242 AA.
AC Q9QKB3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B EGY93;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thionane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134505; AAD56352.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 22
Q9QKB4 PRELIMINARY; PRT; 242 AA.
AC Q9QKB4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=384-97.1;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thionane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134504; AAD56351.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 26410 MW; 74AA8D7353461FBA CRC64;

Query Match 56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 23
Q8JUF8 PRELIMINARY; PRT; 243 AA.
AC Q8JUF8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 protein (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA01-1322;
RA Miller B.R., Godsey M.S., Crabtree M.B., Al-Mazrao Y., Al-Jeffri M.H.,
RA Abdoon A.M., Al-Seghayer S.M., Ksiazek T.G.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF393745; AAM73695.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 26497 MW; 8E44AA8D7353461F CRC64;

Query Match 56.9%; Score 41; DB 2; Length 243;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 24
Q9QKC6 PRELIMINARY; PRT; 243 AA.
AC Q9QKC6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lunyo;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thionane Y., Bouloy M.;
RT "Genetic reassortment of Rift valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134492; AAD56339.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 26480 MW; 792801271AF69C60 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 243;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
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Db 78 VPFAVFNKSKVYL 91

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RESULT 25
Q9QKB5
ID Q9QKB5 PRELIMINARY; PRT; 244 AA.
AC Q9QKB5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=An D106417;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT Thiongane Y., Bouloy M.;
RL "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134503; AAD56350.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26569 MW; D709FEA092739DE5 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 244;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 26
Q9QKB8
ID Q9QKB8 PRELIMINARY; PRT; 244 AA.
AC Q9QKB8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=An D106417;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT Thiongane Y., Bouloy M.;
RL "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134500; AAD56347.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26570 MW; 80B294AA95C8F05E CRC64;

Query Match 56.9%; Score 41; DB 2; Length 244;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 27
Q9QKB4
ID Q9QKB4 PRELIMINARY; PRT; 245 AA.
AC Q9QKB4;

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Q9QKB9
ID Q9QKB9 PRELIMINARY; PRT; 244 AA.
AC Q9QKB9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar D104769;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT Thiongane Y., Bouloy M.;
RL "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134499; AAD56346.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26711 MW; CAA54862A9BD1449 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 244;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 28
Q9QKC1
ID Q9QKC1 PRELIMINARY; PRT; 245 AA.
AC Q9QKC1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar D38457;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT Thiongane Y., Bouloy M.;
RL "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134497; AAD56344.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 245
SQ SEQUENCE 245 AA; 26660 MW; 2BD996075AA93B3F CRC64;

Query Match 56.9%; Score 41; DB 2; Length 245;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:|
Db 78 VPFAVFNKSKVYL 91

RESULT 29
Q9QKC4
ID Q9QKC4 PRELIMINARY; PRT; 245 AA.
AC Q9QKC4;

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DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H 047502;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134494; AAD56341.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 245
SQ SEQUENCE 245 AA; 26651 MW; B224AD8BDCE89B4 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 245;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFNKSKVYL 91

RESULT 30
Q9QKB6 ID Q9QKB6 PRELIMINARY; PRT; 246 AA.
AC Q9QKB6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=An K6087;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134502; AAD56343.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26794 MW; 766A4F9E1B312F5B CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFNKSKVYL 91

RESULT 31
Q9QKB7 ID Q9QKB7 PRELIMINARY; PRT; 246 AA.
AC Q9QKB7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
```

```
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Smithburn;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134501; AAD56348.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26759 MW; 7DBC4674FC4D0BAC CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFNKSKVYL 91

RESULT 32
Q9QKC0 ID Q9QKC0 PRELIMINARY; PRT; 246 AA.
AC Q9QKC0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar D38611;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134498; AAD56345.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26773 MW; F7DD00B294AA95C8 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFNKSKVYL 91

RESULT 33
Q9QKC2 ID Q9QKC2 PRELIMINARY; PRT; 246 AA.
AC Q9QKC2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
```

```

OX NCBI_TaxID=11588;
RN SEQUENCE FROM N.A.
RP STRAIN=H D47408;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134496; AAD56343.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26761 MW; 79BCDDE390EB809A CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VFAVFKNSKVVYL 91
|||||:|:|:|

RESULT 34
Q9QKC3 PRELIMINARY; PRT; 246 AA.
AC Q9QKC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; sRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H D47311;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134495; AAD56342.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26759 MW; EF66A3B294B81758 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VFAVFKNSKVVYL 91
|||||:|:|:|

RESULT 35
Q9QKC5 PRELIMINARY; PRT; 246 AA.
AC Q9QKC5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; sRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
```

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RC STRAIN=Ar B1976;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134493; AAD56340.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26804 MW; 446D2C1C6D282E58 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VFAVFKNSKVVYL 91
|||||:|:|:|

RESULT 36
Y419_METJA STANDARD; PRT; 354 AA.
ID Y419_METJA
AC Q57862;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein MJ0419.
GN OrderedoccNames=MJ0419;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC NCBI_TaxID=21190;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC
CC EMBL; U67494; AAB98417.1; -.
CC PIR; C64352; C64352.
CC TIGR; MJ0419; -.
CC InterPro; IPR002760; DUF70.
CC Pfam; PF01901; DUF70; 1.
CC Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 29
FT TRANSMEM 31
FT TRANSMEM 51
FT TRANSMEM 76
FT TRANSMEM 96
FT TRANSMEM 109
FT TRANSMEM 129
FT TRANSMEM 144
FT TRANSMEM 164
FT TRANSMEM 185
FT TRANSMEM 205
FT TRANSMEM 278
FT TRANSMEM 298
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FT TRANSMEM 306 326 Potential.
FT TRANSMEM 327 347 Potential.
SQ SEQUENCE 354 AA; 40036 MW; D6C7180C6418A641 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 354;
Best Local Similarity 53.8%; Pred. No. 87;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FSVAKSVKSLYL 15
: ||| || |||
Db 298 YKLAKDVRGIVYL 310

RESULT 37
Q7N4C9 PRELIMINARY; PRT; 355 AA.
AC Q7N4C9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarities with unknown protein.
GN OrderedLocusNames=plu2412;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Sude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanos A., Powell K., Siguer P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BK571867; CAE14776.1; -.
DR PhotoList; plu2412; -.
KW Complete proteome.
SQ SEQUENCE 355 AA; 41645 MW; 2A2D08E121C8578A CRC64;

Query Match 56.9%; Score 41; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFVSAKSVKSLYL 14
|||: |||: |||
Db 70 VPFVSAIKYIYL 83

RESULT 38
Q8JU22 PRELIMINARY; PRT; 377 AA.
AC Q8JU22;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor-like protein.
GN Name=L0011.
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22710395; PubMed=12827464;
RA Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Abolnik C., Lu Z.,
RA Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
RT "Comparative sequence analysis of the South African vaccine strain and
RT two virulent field isolates of Lumpy skin disease virus.";
RL Arch. Virol. 148:1335-1356(2003).

DR EMBL; AF409137; AAN02577.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000355; Chmkine receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00857; CCHMKOKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 377 AA; 42992 MW; 57C476D32A897E36 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 377;
Best Local Similarity 64.3%; Pred. No. 93;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VPFVSAKSVKSLYL 14
: ||| ||| |||
Db 303 LPFSVTVFVSLYL 316

RESULT 39
VQ3L CAPVK STANDARD; PRT; 381 AA.
AC Q86917;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE G-protein coupled receptor homolog Q2/3L.
GN Name=Q2/3L;
OS Capripoxvirus (strain KS-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=10269;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266308; PubMed=7747471;
RA Cao J.X., Gershon P.D., Black D.N.;
RT "Sequence analysis of HindIII Q2 fragment of capripoxvirus reveals a
RT putative gene encoding a G-protein-coupled chemokine receptor
RT homologue.";
RL Virology 209:207-212(1995).
CC -!- FUNCTION: Putative chemokine receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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DR EMBL; S78201; AAC32894.1; -.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 91 Extracellular (Potential).
FT TRANSMEM 92 112 1 (Potential).
FT DOMAIN 113 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 2 (Potential).
FT DOMAIN 148 165 Extracellular (Potential).
FT TRANSMEM 166 186 3 (Potential).
FT DOMAIN 187 206 Cytoplasmic (Potential).
FT TRANSMEM 207 227 4 (Potential).
```

FT DOMAIN 228 251 Extracellular (Potential).
FT TRANSMEM 252 272 5 (Potential).
FT DOMAIN 273 294 Cytoplasmic (Potential).
FT TRANSMEM 295 315 6 (Potential).
FT DOMAIN 316 336 Extracellular (Potential).
FT TRANSMEM 337 357 7 (Potential).
FT DOMAIN 358 381 Cytoplasmic (Potential).
FT CARBOHYD 2 2 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 15 15 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 19 19 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 41 41 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 50 50 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 56 56 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 62 62 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 381 AA; 43421 MW; 287E8736E56C90C8 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
:|||||
Db 307 LPFSVTVFVSSLYL 320

RESULT 40

Q8JTYO PRELIMINARY; PRT; 381 AA.
AC Q8JTYO;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE CC chemokine receptor-like protein.
GN Name=LW011;
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22710395; PubMed=12827464;
RA Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Abolnik C., Lu Z.,
RA Vreede F.T., Rajdaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
RT "Comparative sequence analysis of the South African vaccine strain and
RT two virulent field isolates of Lumpy skin disease virus.";
RL Arch. Virol. 148:1335-1356(2003).
DR EMBL: AF409138; AAN02735.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000355; Chkine receptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 381 AA; 43398 MW; AD97874F3B7COA13 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
:|||||
Db 307 LPFSVTVFVSSLYL 320

RESULT 41

Q91MZ3 PRELIMINARY; PRT; 381 AA.
ID Q91MZ3

AC Q91MZ3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE LSDV011 CC chemokine receptor-like protein S78201.
GN Name=LSDV011;
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21329495; PubMed=11435593;
RA Tullman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "Genome of lumpy skin disease virus.";
RL J. Virol. 75:7122-7130(2001).
DR EMBL: AF325528; AAK94972.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 381 AA; 43407 MW; 287E81ED56C90C8 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
:|||||
Db 307 LPFSVTVFVSSLYL 320

RESULT 42

Q91TZ3 PRELIMINARY; PRT; 381 AA.
ID Q91TZ3
AC Q91TZ3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE G-protein-coupled chemokine receptor-like protein.
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Neethling;
RA Stipinovich C., Vreede F.T., Kara P.D., Wallace D.B., Nel L.H.,
RA Viljoen G.J.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF336128; AAK43551.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 381 AA; 43349 MW; AD979B9EF67COA13 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;


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OY 1 VPFSVAKSVKSLYL 14
DB 307 LPFSTVTVFVSSLYL 320
:|||||
:|||||

RESULT 43
ATC2 YEAST
ID ATC2 YEAST STANDARD; PRT; 1173 AA.
AC P3829;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calcium-transporting ATPase 2 (EC 3.6.3.8) (Vacuolar Ca(2+)-ATPase).
GN Name=PMC1; OrderedLocNames=YGL006W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94124630; PubMed=7507493; DOI=10.1083/jcb.124.3.351;
RA Cunningham K.W., Fink G.R.;
RT "Calcineurin-dependent growth control in Saccharomyces cerevisiae
RT mutants lacking PMC1, a homolog of plasma membrane Ca2+ ATPases.";
RL J. Cell Biol. 124:351-363(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313265; PubMed=9169869;
RA Tettelin H., Agostoni Carbone M.L., Albermann K., Albers K.,
RA Arroyo K., Backes U., Barreiros T., Bertani I., Bjournson A.J.,
RA Brueckner M., Bruschi C.V., Carignani G., Castagnoli L., Cerdan E.,
RA Clemence M.L., Coblenz A., Coglievina M., Coissac E., Defoor E.,
RA Del Bino S., Delius H., Delner D., de Wergifosse P., Dufon B.,
RA Durand P., Entian K.-D., Exaso P., Escribano V., Fabiani L.,
RA Farmann B., Feroli F., Feuermann M., Frontali L., Garcia-Gonzalez M.,
RA Garcia-Saez M.I., Goffeau A., Guerreiro P., Hani J., Hansen M.,
RA Hebling U., Hernandez K., Heumann K., Hilger F., Hofmann B.,
RA Indge K.J., James C.M., Klima R., Kottler P., Kramer B., Kramer W.,
RA Lauquin G., Leuther H., Louis E.J., Maillier E., Marconi A.,
RA Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,
RA Melchiorretto P., Mewes H.-W., Minenkova O., Mueller-Auer S.,
RA Nawrocki A., Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L.,
RA Paolucci S., Plevani P., Portetelle D., Portillo F., Potier S.,
RA Purnelle B., Rieger M., Riles L., Rinaldi T., Robben J.,
RA Rodrigues-Pousada C., Rodriguez-Beimonte E., Rodriguez-Torres A.M.,
RA Rose M., Ruzzi M., Saliola M., Sanchez-Perez M., Schaefer B.,
RA Schaefer M., Scharfe M., Schmidheini T., Schreier A., Skala J.,
RA Souciet J.-L., Steensma H.Y., Talla E., Thierry A., Vandenbol M.,
RA van der Aart Q.J.M., van Dyck L., Vanoni M., Verhasselt P., Voet M.,
RA Volckaert G., Wambutt R., Watson M.D., Weber N., Wedler E., Wedler H.,
RA Wipfli P., Wolf K., Wright L.F., Zaccaria P., Zimmermann M.,
RA Zollner A., Kleine K.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome VII.";
RL Nature 387:81-84(1997).
CC -!- FUNCTION: This magnesium-dependent enzyme catalyzes the hydrolysis
CC of ATP coupled with the transport of calcium. Transports the
CC calcium to the vacuole and participates in the control of the
CC cytosolic free calcium.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+) (Cis) = ADP + phosphate +
CC Ca(2+) (Trans).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
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DR EMBL; U03060; AAC48919.1; -.
DR EMBL; Z72528; CAA96706.1; -.
DR PIR; S48877; S48877.
DR GerMOnline; J41054; -.
DR SGD; S000002974; PMCL.
DR GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
DR GO; GO:0005388; P:calcium-transporting ATPase activity; IMP.
DR GO; GO:0006874; P:calcium ion homeostasis; IMP.
DR GO; GO:0006816; P:calcium ion transport; IMP.
DR InterPro; IPR006408; ATPase-IIB_Ca.
DR InterPro; IPR001757; ATPase_EI-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; EI-E2_ATPase_reg.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; EI-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01517; ATPase-IIB_Ca; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 7.
DR PROSITE; PS00154; ATPase_EI-E2; 1.
KW ATP-binding; Calcium transport; Hydrolase; Magnesium; Phosphorylation;
KW Transmembrane.
FT DOMAIN 1 114 Cytoplasmic (Potential).
FT TRANSMEM 115 139 Potential.
FT DOMAIN 140 152 Extracellular (Potential).
FT TRANSMEM 153 173 Potential.
FT DOMAIN 174 349 Cytoplasmic (Potential).
FT TRANSMEM 350 368 Potential.
FT DOMAIN 369 388 Extracellular (Potential).
FT TRANSMEM 389 409 Potential.
FT DOMAIN 410 899 Cytoplasmic (Potential).
FT TRANSMEM 900 922 Potential.
FT DOMAIN 923 929 Extracellular (Potential).
FT TRANSMEM 930 950 Potential.
FT DOMAIN 951 976 Cytoplasmic (Potential).
FT TRANSMEM 977 998 Potential.
FT DOMAIN 999 1010 Extracellular (Potential).
FT TRANSMEM 1011 1029 Potential.
FT DOMAIN 1030 1065 Cytoplasmic (Potential).
FT TRANSMEM 1066 1086 Potential.
FT DOMAIN 1087 1099 Extracellular (Potential).
FT TRANSMEM 1100 1120 Potential.
FT DOMAIN 1121 1173 Cytoplasmic (Potential).
FT ACT_SITE 445 445 4-aspartylphosphate intermediate (By similarity).
SQ SEQUENCE 1173 AA; 130860 MW; 5BD9ECFF8508F396 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 1173;
Best Local Similarity 46.2%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 PFSVAKSVKSLYL 14
DB 1089 PFSIARQTKSMWI 1101
|||||
|||||

RESULT 44
VGLM RVFVZ
ID VGLM RVFVZ STANDARD; PRT; 1197 AA.
AC P21401.
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE M polyprotein precursor [Contains: Nonstructural protein NS-M;
DE Glycoprotein G1; Glycoprotein G2].
GN Name=M;
OS Rift valley fever virus (strain ZH-548 M12) (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11589;
RN [1]
```

RP SEQUENCE FROM N.A.
RX MEDLINE=89204917; PubMed=2705307;
RA Takenara K., Min M.K., Battles J.K., Sugiyama K., Emery V.C.,
RA Dalrymple J.M., Bishop D.H.L.;
RT "Identification of mutations in the M RNA of a candidate vaccine
strain of Rift Valley fever virus.";
RL Virology 169:452-457(1989)
CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins
CC including nonstructural protein NS-M, glycoprotein G1, and
CC glycoprotein G2.
CC
CC -1- SIMILARITY: Belongs to the phleboviruses M polyprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M25276; AAA47449.1; -;
CC PIR; A30183; VGVURF.
CC InterPro; IPR010826; Phlebovirus G1.
CC InterPro; IPR009878; Phlebovirus G2.
CC InterPro; IPR009879; Phlebovirus NSM.
CC Pfam; PF07243; Phlebovirus G1; 1.
CC Pfam; PF07245; Phlebovirus G2; 1.
CC Pfam; PF07246; Phlebovirus NSM; 1.
CC Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
CC Glycoprotein G1.
CC CHAIN 1 153 Nonstructural protein NS-M.
FT CHAIN 154 690 Glycoprotein G1.
FT CHAIN 691 1197 Glycoprotein G2.
FT CARBOHYD 88 88 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 438 438 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 794 794 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1035 1035 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1077 1077 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 1197 AA; 130804 MW; 860B822CD968767F CRC64;
Query Match 56.9%; Score 41; DB 1; Length 1197;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSYL 14
DB 343 VPFAVFKSKKYL 356
RESULT 45
VGLM RVFV STANDARD; PRT; 1206 AA.
AC P03518; Q86494; Q86495;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE M polyprotein precursor [Contains: Nonstructural protein NS-M;
DE Glycoprotein G1; Glycoprotein G2].
GN Name=M;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OC NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86045943; PubMed=2998042;
RA Collett M.S., Purchio A.P., Keegan K., Frazier S., Hays W.,
RA Anderson D.K., Parker M.D., Schmaljohn C.S., Schmidt J.,
RA Dalrymple J.M.;
RT "Complete nucleotide sequence of the M RNA segment of Rift Valley
RT fever virus.";
RL Virology 144:228-245(1985).
CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins
CC including nonstructural protein NS-M, glycoprotein G1, and
CC glycoprotein G2.

CC -1- SIMILARITY: Belongs to the phleboviruses M polyprotein family.
CC -----
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CC -----
CC EMBL; M11157; AAA47450.1; -;
CC PIR; A04110; VGVURV.
CC InterPro; IPR010826; Phlebovirus G1.
CC InterPro; IPR009878; Phlebovirus G2.
CC InterPro; IPR009879; Phlebovirus NSM.
CC Pfam; PF07243; Phlebovirus G1; 1.
CC Pfam; PF07245; Phlebovirus G2; 1.
CC Pfam; PF07246; Phlebovirus NSM; 1.
CC Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
CC Glycoprotein G1.
CC CHAIN 1 153 Nonstructural protein NS-M.
FT CHAIN 154 690 Glycoprotein G1.
FT CHAIN 691 1206 Glycoprotein G2.
FT CARBOHYD 88 88 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 438 438 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 794 794 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1035 1035 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1077 1077 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 1206 AA; 132053 MW; D2E801719285924 CRC64;
Query Match 56.9%; Score 41; DB 1; Length 1206;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSYL 14
DB 343 VPFAVFKSKKYL 356
RESULT 46
QSEEL1 PRELIMINARY; PRT; 3457 AA.
AC Q6EEL1
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Polyprotein.
OS Maize chlorotic dwarf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Sequiviridae;
OC Waukavirus.
OC NCBI_TaxID=51354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Severe;
RX PubMed=15246276; DOI=10.1016/j.virol.2004.04.039;
RA Chaouch-Hamada R., Redinbaugh M.G., Gingery R.E., Willie K.,
RA Hogenhout S.A.;
RT "Accumulation of Maize chlorotic dwarf virus proteins in its plant
RT host and leafhopper vector.";
RL Virology 325:379-388(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Severe;
RA Chaouch-Hamada R., Redinbaugh M.G., Gingery R.E., Willie K.,
RA Hogenhout S.A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY362551; AAR14150.1; -;
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001091; Met_trans_CN4.
DR InterPro; IPR009003; Pept_ser_Cys

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DR InterPro; IPR000605; RNA helicase.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
DR InterPro; IPR001205; RNA_pol_PSD.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.
DR PROSITE; PS00093; N4_MTASE; UNKNOWN_1.
KW Polyprotein.
SQ SEQUENCE 3457 AA; 388956 MW; 3B388792325D9C5E CRC64;

Query Match          56.9%; Score 41; DB 2; Length 3457;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSL 12
Db 1386 VPFSAKTAQVL 1397

RESULT 47
ID O66712 PRELIMINARY; PRT; 250 AA.
AC O66712;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein aq391.
GN OrderedLocusNames=AQ_391;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RT Nature 392:353-358(1998).
DR EMBL; AE000688; AAC06677.1; -.
DR PIR; D70335; D70335.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR009051; Helical_ferredoxn.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 250 AA; 29458 MW; 46FBD1A3576A434B CRC64;

Query Match          55.6%; Score 40; DB 2; Length 250;
Best Local Similarity 53.8%; Pred. No. 93;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSLY 13
Db 181 IPFDVGKSVKTAW 193

RESULT 48
ID Q93CR3 PRELIMINARY; PRT; 405 AA.
AC Q93CR3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE O-antigen polymerase.
GN Name=wzy;
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

DR InterPro; IPR000605; RNA helicase.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
DR InterPro; IPR001205; RNA_pol_PSD.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.
DR PROSITE; PS00093; N4_MTASE; UNKNOWN_1.
KW Polyprotein.
SQ SEQUENCE 3457 AA; 388956 MW; 3B388792325D9C5E CRC64;

Query Match          56.9%; Score 41; DB 2; Length 3457;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSL 12
Db 1386 VPFSAKTAQVL 1397

RESULT 47
ID O66712 PRELIMINARY; PRT; 250 AA.
AC O66712;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein aq391.
GN OrderedLocusNames=AQ_391;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RT Nature 392:353-358(1998).
DR EMBL; AE000688; AAC06677.1; -.
DR PIR; D70335; D70335.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR009051; Helical_ferredoxn.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 250 AA; 29458 MW; 46FBD1A3576A434B CRC64;

Query Match          55.6%; Score 40; DB 2; Length 250;
Best Local Similarity 53.8%; Pred. No. 93;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSLY 13
Db 181 IPFDVGKSVKTAW 193

RESULT 48
ID Q93CR3 PRELIMINARY; PRT; 405 AA.
AC Q93CR3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE O-antigen polymerase.
GN Name=wzy;
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481970; PubMed=11598067;
RX DOI=10.1128/IAI.69.11.6923-6930.2001;
RA Wang L., Qu W., Reeves P.R.;
RT "Sequence analysis of four Shigella boydii O-antigen loci: implication
RT for Escherichia coli and Shigella relationships."
RL Infect. Immun. 69:6923-6930(2001).
DR EMBL; AF402315; AAL27351.1; -.
SQ SEQUENCE 405 AA; 46810 MW; 0F1002BF45B083FA CRC64;

Query Match          55.6%; Score 40; DB 2; Length 405;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 VPFSV---AKSVKSLYL 14
Db 335 IPFTIGLCGKSIKSYL 352

RESULT 49
ID Q9U7C8 PRELIMINARY; PRT; 413 AA.
AC Q9U7C8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative calmodulin-binding protein Cam-BP46.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Day D.H., Henley C., Myre M.A.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140043; AAD56609.1; -.
DR DictyBase; DB0201645; cmdb.
DR InterPro; IPR008615; FNIP.
DR Pfam; PF05725; FNIP; 6.
SQ SEQUENCE 413 AA; 46581 MW; FB1054612318FEDF CRC64;

Query Match          55.6%; Score 40; DB 2; Length 413;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 15
Db 176 PLVIPKSLRSLFLG 189

RESULT 50
ID HEM1 CHLVI STANDARD; PRT; 424 AA.
AC P28452; O87494;
DT 01-DEC-1992 (Rel. 24, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Glutamyl-tRNA reductase (EC 1.2.1.-) (GluTR).
GN Name=hema;
OS Chlorobium vibrioforme.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Prosthecochloris.
OX NCBI_TaxID=1098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=f. thiosulfatophilum / NCIB 8327;
RX MEDLINE=92171712; PubMed=1793335;
RA Majumdar D., Avissar Y.J., Wyche J.H., Beale S.I.;
RT "Structure and expression of the Chlorobium vibrioforme hema gene."
RL Arch. Microbiol. 156:281-289(1991).
RN [2]
```

RP REVISIONS TO C-TERMINUS.
RA Willows R.D., Beale S.I.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Glutamyl-tRNA(Glu) + NADPH = glutamate-1-
CC semialdehyde + NADP(+) + tRNA(Glu).
CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.
CC Involved in chlorophyll biosynthesis.
CC -!- SIMILARITY: belongs to the glutamyl-CRNA reductase family.
CC -----
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CC -----
DR EMBL: M96364; AAC23112.1; -;
DR EMBL: AF080069; AAC61856.1; -;
DR PIR: A48359; A48359.
DR HSP: Q42843; 1B29.
DR HAMAP: MF 00087; -; 1.
DR InterPro: IPR00343; GlutR.
DR Pfam: PF00745; GlutR dimer; 1.
DR Pfam: PF05201; GlutR_N; 1.
DR Pfam: PF05200; GlutR_NAD_bind; 1.
DR TIGRFAMs: TIGR01035; hemaA; 1.
DR PROSITE: PS00747; GLUTR; 1.
KW Chlorophyll biosynthesis; NADP; Oxidoreductase;
KW Porphyrin biosynthesis.
FT ACT_SITE 50 50 Nucleophile (By similarity).
FT ACT_SITE 99 99 Proton acceptor (By similarity).
SQ SEQUENCE 424 AA; 47968 MW; E65D0DBB8C1F9625 CRC64;

Query Match 55.6%; Score 40; DB 1; Length 424;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAKSVKS 11
Db 145 PFSVAKVKVT 154
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Search completed: July 7, 2005, 09:35:41
Job time : 60.0687 secs

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